

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 18:41:36 ; Search time 1978 Seconds
(without alignments)
517.281 Million cell updates/sec

Title: US-10-608-296-38
Perfect score: 18
Sequence: 1 ccacacctattcatactc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	357	10	G67590	G67590 csnppla2g1b
2	18	100.0	418	6	CQ922146	CQ922146 Sequence
3	18	100.0	447	6	AX377240	AX377240 Sequence
4	18	100.0	496	6	CS071001	CS071001 Sequence
5	18	100.0	559	6	CQ723247	CQ723247 Sequence
6	18	100.0	562	6	AR380655	AR380655 Sequence
7	18	100.0	562	6	AX332734	AX332734 Sequence
8	18	100.0	562	6	AX333340	AX333340 Sequence
9	18	100.0	562	6	AX333743	AX333743 Sequence
10	18	100.0	562	8	HUMPLA2RA	M21054 Human lung
11	18	100.0	569	6	E02268	E02268 cDNA encodi
12	18	100.0	600	6	AX377262	AX377262 Sequence
13	18	100.0	644	6	BD209899	BD209899 Human nuc
14	18	100.0	644	6	AX014213	AX014213 Sequence
15	18	100.0	654	6	CS071209	CS071209 Sequence
16	18	100.0	3375	8	HUMPLA2A1	M22970 Human pancr
17	18	100.0	8368	8	AY438977	AY438977 Homo sapi
18	18	100.0	13612	6	AX377239	AX377239 Sequence

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 Burczynski,M.E., Twine,N.C., Slonim,D.K., Trepicchio,W.L., Strahs,A., Immerman,F. and Dörner,A.J.

TITLE Methods for prognosis and treatment of solid tumors

JOURNAL Patent: WO 2004097052-A 3346 11-NOV-2004; Wyeth (US); Burczynski, Michael E. (US)

FEATURES source Location/Qualifiers 1. .418 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

ORIGIN Query Match 100.0%; Score 18; DB 6; Length 418; Best Local Similarity 100.0%; Pred. No. 60; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 275 CCACACCTATTTCATCTC 292

RESULT 3

AX377240

LOCUS AX377240 447 bp DNA linear PAT 18-MAR-2002

DEFINITION Sequence 2 from Patent WO0212562.

ACCESSION AX377240

VERSION AX377240.1 GI:19573529

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Kazemi,A., Kliem,S.E. and Koshy,B.

TITLE Haplotypes of the pla2glb gene

JOURNAL Patent: WO 0212562-A 2 14-FEB-2002; Genaisance Pharmaceuticals, Inc. (US)

FEATURES source Location/Qualifiers 1. .447 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

ORIGIN Query Match 100.0%; Score 18; DB 6; Length 447; Best Local Similarity 100.0%; Pred. No. 59; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 276 CCACACCTATTTCATCTC 293

RESULT 4

CS071001/c

LOCUS CS071001 496 bp DNA linear PAT 05-MAY-2005

DEFINITION Sequence 164 from Patent WO2001032927.

ACCESSION CS071001

VERSION CS071001.1 GI:63088405

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Sornasse,T., Seilhamer,J.J. and Watson,G.A.

TITLE Tissue specific genes of diagnostic import

JOURNAL Patent: WO 2001032927-A 164 10-MAY-2001; Incyte Genomics, Inc. (US)

FEATURES source Location/Qualifiers 1. .496 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

ORIGIN Query Match 100.0%; Score 18; DB 6; Length 496; Best Local Similarity 100.0%; Pred. No. 59; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 209 CCACACCTATTTCATCTC 192

RESULT 5

CQ723247

LOCUS CQ723247 559 bp DNA linear PAT 03-FEB-2004

DEFINITION Sequence 9181 from Patent WO02068579.

ACCESSION CQ723247

VERSION CQ723247.1 GI:42284104

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.

TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof

JOURNAL Patent: WO 02068579-A 9181 06-SEP-2002; PE Corporation (NY) (US)

FEATURES source Location/Qualifiers 1. .559 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

ORIGIN Query Match 100.0%; Score 18; DB 6; Length 559; Best Local Similarity 100.0%; Pred. No. 59; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 311 CCACACCTATTTCATCTC 328

RESULT 6

AR380655

LOCUS AR380655 562 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 1200 from patent US 6607879.

ACCESSION AR380655

VERSION AR380655.1 GI:40088289

KEYWORDS .

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 562)

AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.

TITLE Compositions for the detection of blood cell and immunological response gene expression

JOURNAL Patent: US 6607879-A 1200 19-AUG-2003; Incyte Corporation; Palo Alto, CA

FEATURES source Location/Qualifiers 1. .562 /organism="unknown" /mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 562;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTCTACTC 18
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Db 313 CCACACCTATTCTACTC 330

RESULT 7
AX332734
LOCUS AX332734 562 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 3243 from Patent WO0194629.
ACCESSION AX332734
VERSION AX332734.1 GI:18123368
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 3243 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
source 1. .562
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 562;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTCTACTC 18
|||||
Db 313 CCACACCTATTCTACTC 330

RESULT 8
AX333340
LOCUS AX333340 562 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 3849 from Patent WO0194629.
ACCESSION AX333340
VERSION AX333340.1 GI:18123974
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 3849 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
source 1. .562
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 562;

Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTCTACTC 18
|||||
Db 313 CCACACCTATTCTACTC 330

RESULT 9
AX333743
LOCUS AX333743 562 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 4252 from Patent WO0194629.
ACCESSION AX333743
VERSION AX333743.1 GI:18124462
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 4252 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
source 1. .562
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 562;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTCTACTC 18
|||||
Db 313 CCACACCTATTCTACTC 330

RESULT 10
HUMPLA2RA
LOCUS HUMPLA2RA 562 bp mRNA linear PRI 03-JUN-1994
DEFINITION Human lung phospholipase A-2 (PLA-2) mRNA, complete cds, clone
lung-1(hcDNA).
ACCESSION M21054 M14965
VERSION M21054.1 GI:190012
KEYWORDS phospholipase A2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 562)
AUTHORS Seilhamer, J.J., Randall, T.L., Yamanaka, M. and Johnson, L.K.
TITLE Pancreatic phospholipase A2: isolation of the human gene and cDNAs
from porcine pancreas and human lung
JOURNAL DNA 5 (6), 519-527 (1986)
PUBMED 3028739
COMMENT Original source text: Homo sapiens lung cDNA to mRNA.
FEATURES Location/Qualifiers
source 1. .562
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="lung"
38. .484
/EC_number="3.1.1.4"
/codon_start=1
/product="phospholipase"

/protein_id="AAA36450.1"
/db_xref="GI:190013"
/translation="MKLLVLAVLLTVAAADSGISPRAVWQFRKMICKVIPGSDPPFLEY
NNYGCYGLGSGTPVDLDCQTHDNCYDQAKKLDSCKELLDPYHTYYSYSCSGS
AITCSSKNKECEAFICNCDRNAAICFSKAPYNKAHKNLDTKKYCQS"

ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 562;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCATCTC 18
|||||
Db 313 CCACACCTATTCATCTC 330

RESULT 11

E02268
LOCUS E02268 569 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding human phospholipase A2.
ACCESSION E02268
VERSION E02268.1 GI:2170505
KEYWORDS JP 1990065781-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 569)
Tamaki,M., Takimoto,N., Nakamura,E., Teraoka,H., Ogawa,M. and
Matsubara,K.

TITLE PRODUCTION OF PHOSPHOLIPASE AZ OF HUMAN PANCREAS
JOURNAL Patent: JP 1990065781-A 1 06-MAR-1990;

COMMENT

SHIONOGI & CO LTD
OS Homo sapiens
PN JP 1990065781-A/1
PD 06-MAR-1990
PF 29-AUG-1988 JP 1988214666
PI TAMAKI MIKIO, TAKIMOTO NORIKO, NAKAMURA ETSUO, TERAOKA
HIROSHI, PI OGAWA MICHIO, MATSUBARA KENICHI
PC C12N9/18//C12N15/55,(C12N9/18,C12R1:865);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue type=pancreas;
CC *source: clone=HpL11;
Key Location/Qualifiers
FH
FT CDS 25..471
FT /product='human phospholipase A2 precursor' FT
FT sig_peptide 25..90
FT mat_peptide 91..468
FT /product='human phospholipase A2 mature FT
FT peptide'
FT 5'UTR 1..24
FT polyA_signal 503..508.
Location/Qualifiers
1..569
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

FEATURES

source

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 569;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCATCTC 18
|||||
Db 300 CCACACCTATTCATCTC 317

RESULT 12

AX377262
LOCUS AX377262 600 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 24 from Patent WO0212562.
ACCESSION AX377262
VERSION AX377262.1 GI:19573550
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Kazemi,A., Kliem,S.E. and Koshy,B.
Haplotypes of the pla2glb gene
Patent: WO 0212562-A 24 14-FEB-2002;
Genaissance Pharmaceuticals, Inc. (US)

REFERENCE

AUTHORS
TITLE
JOURNAL
Genaissance Pharmaceuticals, Inc. (US)
Location/Qualifiers
1..600
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES

source

variation

misc_feature 61..120
/note="pS1: polymorphic base G or A"

variation

misc_feature 181..240
/note="Ns represent sequence between polymorphic sites"

variation

misc_feature 301..360
/note="Ns represent sequence between polymorphic site"

variation

misc_feature 421..480
/note="pS4: polymorphic base G or A"

variation

misc_feature 541..600
/note="Ns represent sequence between polymorphic site"

variation

misc_feature 541..600
/note="Ns represent sequence following PS5"

variation

misc_feature 541..600
/note="Ns represent sequence between polymorphic site"

variation

misc_feature 541..600
/note="Ns represent sequence between polymorphic site"

variation

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/note="Ns represent sequence between polymorphic site"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 600;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCATCTC 18
|||||

Db 372 CCACACCTATTCATCTC 389

RESULT 13

BD209899
LOCUS BD209899 644 bp DNA linear PAT 17-JUL-2003
DEFINITION Human nucleic acid sequence originating in normal pancreas.
ACCESSION BD209899
VERSION BD209899.1 GI:33019669
KEYWORDS JP 2002512022-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 644)
Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and
Rosenthal,A.

REFERENCE

AUTHORS

Human nucleic acid sequence originating in normal pancreas
Patent: JP 2002512022-A 3 23-APR-2002;
METAGEN GESELLSCHAFT FUER GENOM FORSCHUNG MBH
OS Homo sapiens (human)
PN JP 2002512022-A/3

TITLE

JOURNAL

COMMENT

PD 23-APR-2002
PF 08-APR-1999 JP 2000544778
PR 19-APR-1998 DE 198 18 598.7
PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
PI EDGAR DAHL,
PI ANDRE ROSENTHAL
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12P21/08, C12N15/00, C12N5/00
PC Human nucleic acid sequence originating in normal pancreas. FH
CC Human nucleic acid sequence originating in normal pancreas. FH
Key Location/Qualifiers
FT source 1. .644
FT /organism='Homo sapiens (human)'.
FEATURES
source
1. .644
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 644;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTCTACTC 18
|||||
Db 337 CCACACCTATTCTACTC 354
RESULT 14
AX014213
LOCUS 644 bp DNA linear PAT 07-SEP-2000
DEFINITION
Sequence 6 from Patent WO9954446.
ACCESSION AX014213
VERSION AX014213.1 GI:10040614
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pilarczyk,C.
Human nucleic acid sequences from normal pancreas tissue
Patent: WO 9954446-A 6 28-OCT-1999;
TITLE
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
FEATURES
source
1. .644
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 644;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTCTACTC 18
|||||
Db 337 CCACACCTATTCTACTC 354
RESULT 15
CS071209
LOCUS 654 bp DNA linear PAT 05-MAY-2005
DEFINITION
Sequence 372 from Patent WO2001032927.
ACCESSION CS071209
VERSION CS071209.1 GI:63088613
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Sornasse,T., Seilhamer,J.J. and Watson,G.A.
Tissue specific genes of diagnostic import
Patent: WO 2001032927-A 372 10-MAY-2001;
JOURNAL Incyte Genomics, Inc. (US)
FEATURES
source
1. .654
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 654;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTCTACTC 18
|||||
Db 428 CCACACCTATTCTACTC 445
RESULT 16
HUMPLA2A1
LOCUS 3375 bp DNA linear PRI 07-JAN-1995
DEFINITION
Human pancreatic phospholipase A-2 (PLA-2) gene, exons 1 to 3.
ACCESSION M22970 M14965
VERSION M22970.1 GI:190008
KEYWORDS phospholipase A2.
SEGMENT 1 of 2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 3375)
Seilhamer,J.J., Randall,T.L., Yamanaka,M. and Johnson,L.K.
Pancreatic phospholipase A2: isolation of the human gene and cDNAs
from porcine pancreas and human lung
DNA 5 (6), 519-527 (1986)
JOURNAL
PUBMED
COMMENT Original source text: Homo sapiens pulverized liver DNA.
FEATURES
source
1. .3375
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="12q23-qter"
/tissue type="pulverized liver"
<537. .570
/gene="PLA2A"
/note="G00-120-715"
/number=1
571. .2262
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/note="G00-120-715"
/number=1
2263. .2422
/gene="PLA2A"
/note="G00-120-715"
/number=2
2423. .3222
/gene="PLA2A"
/note="G00-120-715"
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3223. .3350
/gene="PLA2A"
/note="G00-120-715"
/number=3
exon
intron
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intron
exon


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intron      3351. .>3375
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/note="G00-120-715"
/number=3
ORIGIN      5 bp upstream of PstI site.
Query Match      100.0%; Score 18; DB 8; Length 3375;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
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Db      3304 CCACACCTATTTCATCTC 3321

RESULT 17
AY438977
LOCUS      AY438977      8368 bp      DNA      linear      PRI 29-OCT-2003
DEFINITION Homo sapiens phospholipase A2, group IB (pancreas) (PLA2G1B) gene,
complete cds.
ACCESSION  AY438977
VERSION     AY438977.1 GI:37953284
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE   1 (bases 1 to 8368)
AUTHORS    Rieder,M.J., Livingston,R.J., Daniels,M.R., Chung,M.-W.,
Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D.,
Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and Nickerson,D.A.
TITLE      Direct Submission
JOURNAL    Submitted (16-OCT-2003) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
COMMENT    To cite this work please use: NIEHS-SNPs, Environmental Genome
Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
(URL: http://egp.gs.washington.edu).
FEATURES
source
1..8368
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
repeat_region 101..257
/rpt_family="MIR"
/rpt_type=dispersed
variation      205
/frequency="0.01"
/replace="a"
variation      306
/frequency="0.01"
/replace="a"
repeat_region 326..538
/rpt_family="Alu"
/rpt_type=dispersed
misc_feature   354..496
/note="Region not scanned for variation"
gene           875..6548
/gene="PLA2G1B"
join(875..944,2644..2803,3603..3730,6347..6548)
/gene="PLA2G1B"
/product="phospholipase A2, group IB (pancreas)"
join(911..944,2644..2803,3603..3730,6347..6471)
/gene="PLA2G1B"
/codon_start=1
/product="phospholipase A2, group IB (pancreas)"
/protein_id="AAR05441.1"
/db_xref="GI:37953285"
/translation="MKLLVLAVLLTVAAADSGISPRVWQFRKMVKVIPGSDPPFLEY
NNYGCYGLGGSGTPVDLKDCCQTHDNCYDQAKKLDCKFLLDNPYTHYSYSCSGS
AITCSSKNKECEAFICNCDRNAAICFSKAPYNKAHKNLDTKKYCQS"
repeat_region 1174..1307
/rpt_family="Alu"
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variation      1286
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/gene="PLA2G1B"
/frequency="0.01"
/replace="g"
repeat_region 1319..1588
/rpt_family="Alu"
/rpt_type=dispersed
variation      1343
/gene="PLA2G1B"
/frequency="0.03"
/replace="a"
variation      1593
/gene="PLA2G1B"
/frequency="0.02"
/replace="t"
repeat_region 1605..1669
/rpt_family="L2"
/rpt_type=dispersed
misc_feature   1638..2188
/gene="PLA2G1B"
/note="Region not scanned for variation"
repeat_region 1670..1975
/rpt_family="Alu"
/rpt_type=dispersed
repeat_region 1976..2038
/rpt_family="L2"
/rpt_type=dispersed
repeat_region 2086..2165
/rpt_family="L2"
/rpt_type=dispersed
repeat_region 2194..2319
/rpt_family="Alu"
/rpt_type=dispersed
misc_feature   2319..2453
/gene="PLA2G1B"
/note="Region not scanned for variation"
variation      3027
/gene="PLA2G1B"
/frequency="0.25"
/replace="t"
repeat_region 3165..3431
/rpt_family="Alu"
/rpt_type=dispersed
variation      3262
/gene="PLA2G1B"
/frequency="0.01"
/replace="t"
variation      3321
/gene="PLA2G1B"
/frequency="0.01"
/replace="a"
variation      3396
/gene="PLA2G1B"
/frequency="0.03"
/replace="g"
variation      3630
/gene="PLA2G1B"
/frequency="0.10"
/replace="c"
variation      3702
/gene="PLA2G1B"
/frequency="0.15"
/replace="a"
variation      3768
/gene="PLA2G1B"
/frequency="0.01"
/replace="t"
variation      3818
/gene="PLA2G1B"
/frequency="0.01"
/replace="a"
repeat_region 3846..3964
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repeat_region /rpt_family="MIR"
/rpt_type=dispersed
3977. .4280
repeat_region /rpt_family="Alu"
/rpt_type=dispersed
4281. .4346
/rpt_family="L2"
repeat_region /rpt_type=dispersed
4347. .4634
/rpt_family="Alu"
variation /rpt_type=dispersed
4386
/gene="PLA2G1B"
/frequency="0.08"
/replace="t"
repeat_region 4635. .4723
/rpt_family="L2"
variation /rpt_type=dispersed
5013
/gene="PLA2G1B"
/frequency="0.10"
/replace="a"
repeat_region 5103. .5404
/rpt_family="Alu"
variation /rpt_type=dispersed
5133
/gene="PLA2G1B"
/frequency="0.01"
/replace="c"
5543
/gene="PLA2G1B"
/frequency="0.01"
/replace="c"
5555
/gene="PLA2G1B"
/frequency="0.01"
/replace="t"
5556
/gene="PLA2G1B"
/frequency="0.15"
/replace="g"
5577. .5629
repeat_region /rpt_family="L1"
/rpt_type=dispersed
5580
/gene="PLA2G1B"
/frequency="0.09"
/replace="g"
5675
/gene="PLA2G1B"
/frequency="0.09"
/replace="g"
5779. .6083
repeat_region /rpt_family="Alu"
/rpt_type=dispersed
5929
/gene="PLA2G1B"
/frequency="0.01"
/replace="a"
5949
/gene="PLA2G1B"
/frequency="0.01"
/replace="g"
6039
/gene="PLA2G1B"
/frequency="0.01"
/replace="a"
6082
/gene="PLA2G1B"
/frequency="0.14"
/replace="t"

Query Match 100.0%; Score 18; DB 8; Length 8368;

Best Local Similarity 100.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 3684 CCACACCTATTTCATCTC 3701

RESULT 18
AX377239
LOCUS AX377239 13612 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 1 from Patent WO0212562.
ACCESSION AX377239
VERSION AX377239.1 GI:19573528
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Kazemi,A., Kliem,S.E. and Koshy,B.
TITLE Haplotypes of the pla2glb gene
JOURNAL Patent: WO 0212562-A 1 14-FEB-2002;
Genaissance Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
1. .13612
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
3845
variation /note="PS1: polymorphic base G or A"
3968
variation /note="PS2: polymorphic base A or G"
6060
variation /note="PS2: polymorphic base A or G"
6844
variation /note="PS4: polymorphic base G or A"
9531
variation /note="PS5: polymorphic base G or A"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 13612;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 6826 CCACACCTATTTCATCTC 6843

RESULT 19
AC003982/c
LOCUS AC003982 122302 bp DNA linear PRI 18-MAR-1999
DEFINITION Homo sapiens PAC clone 166H1 from 12q, complete sequence.
ACCESSION AC003982
VERSION AC003982.1 GI:2769695
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 122302)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
PUBMED 9847074
REFERENCE 2 (bases 1 to 122302)
AUTHORS Bradshaw,H., Wu,X. and Ozersky,P.
TITLE The sequence of Homo sapiens PAC clone 166H1
JOURNAL Unpublished (1999)
REFERENCE 3 (bases 1 to 122302)

AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 4 (bases 1 to 122302)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT SUBMITTED BY: WUGSC
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

This clone was originally isolated in the laboratory of Professor Graeme Bell, Howard Hughes Medical Institute and Departments of Biochemistry and Molecular Biology, and Medicine, The University of Chicago, Chicago, IL, USA. The clone was provided by the laboratory of Dr. Roger Cox at The Wellcome Trust Centre For Human Genetics, Oxford, UK. Some contig information was also obtained from Yamagata et al., Nature 384:455-8 (1996).

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-1, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.
The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is 278C19; the clone sequenced to the right is 15E1. Actual start of this clone is at base position 1 of 166H1; actual end is at 122302 of 166H1.

FEATURES

source	1. .122302 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="12" /map="12q" /clone="166H1" /clone_lib="RPCI-1"
repeat_region	1. .238 /rpt_family="Alu"
repeat_region	239. .265 /rpt_family="AT_rich"
repeat_region	268. .565 /rpt_family="Alu"
repeat_region	1001. .1309 /rpt_family="Alu"
repeat_region	1440. .1745 /rpt_family="Alu"
repeat_region	1909. .1940 /rpt_family="Alu"
repeat_region	1955. .1983 /rpt_family="MER1_type"
repeat_region	2063. .2362 /rpt_family="Alu"
repeat_region	2516. .2650 /rpt_family="Alu"
repeat_region	2674. .2730 /rpt_family="L1"
repeat_region	2735. .2788 /rpt_family="(GAAAA)n"
repeat_region	2790. .3077 /rpt_family="Alu"
repeat_region	3081. .3139 /rpt_family="L1"
repeat_region	3716. .4020 /rpt_family="Alu"
repeat_region	4196. .4492 /rpt_family="Alu"
gene	4560. .14034 /gene="WUGSC:H 166H1.1"
CDS	join(4560. .5056,13418. .13748,13882. .14034) /gene="WUGSC:H 166H1.1" /note="unknown_function; 60% similar to Z50177 (PID:g927403) (PID:g927402); H_166H1.1" /codon_start=1 /evidence=not experimental /protein_id="AAB95634.1" /db_xref="GI:2769696" /translation="MKMSFALTFRSAKRWIANPSQPCSKASIGLFPVSPPLDPEKV KELQRFITLSKRLLVMTGAGISTESGIPDYRSEKVGLYARTDRRPIQHGDFVRSAPIR ORYWARNFVGMWPQFSSHQPNPAHWALSTWEKLGKLYLWLVTONVDALHTKAGSRRLTEL HGCMGRAYCSVSFLGSRVLCDCGEQTPRGVQLQERFQVLNPTWSAEAHGLAPDGDVF LSEEQVRSFQVPTCVQCQGGHLKPDVVPFGDTVNPDKVDFVHKRVKEADSLLVVGSSLQ VYSGYRFLTAWEEKLPIAILNIGPTRSDDLACLKLNRCGELLPLIDPC"
repeat_region	5366. .5655 /rpt_family="Alu"
repeat_region	5672. .5798 /rpt_family="Alu"
repeat_region	5802. .5834 /rpt_family="(TA)n"
repeat_region	5834. .5857 /rpt_family="POLY_A"
repeat_region	5870. .6184 /rpt_family="Alu"
repeat_region	6224. .6268 /rpt_family="(CA)n"
repeat_region	6269. .6558 /rpt_family="Alu"
repeat_region	6729. .7029 /rpt_family="Alu"
repeat_region	7051. .7172 /rpt_family="Alu"
repeat_region	7192. .7500 /rpt_family="Alu"
repeat_region	7518. .7820 /rpt_family="Alu"
repeat_region	8207. .8500 /rpt_family="Alu"
repeat_region	8576. .8878 /rpt_family="Alu"
repeat_region	9023. .9154 /rpt_family="Alu"
repeat_region	9165. .9470 /rpt_family="Alu"
repeat_region	9887. .10188 /rpt_family="Alu"
repeat_region	10221. .10342 /rpt_family="L1"
repeat_region	10408. .10707 /rpt_family="Alu"
repeat_region	10713. .11014 /rpt_family="Alu"

* 7113 7212: gap of unknown length
* 7213 13283: contig of 6071 bp in length
* 13284 13383: gap of unknown length
* 13384 20660: contig of 7277 bp in length
* 20661 20760: gap of unknown length
* 20761 34473: contig of 13713 bp in length
* 34474 34573: gap of unknown length
* 34574 44394: contig of 9821 bp in length
* 44395 44494: gap of unknown length
* 44495 57126: contig of 12632 bp in length
* 57127 57226: gap of unknown length
* 57227 80266: contig of 23040 bp in length
* 80267 80366: gap of unknown length
* 80367 109398: contig of 29032 bp in length
* 109399 109498: gap of unknown length
* 109499 149812: contig of 40314 bp in length
* 149813 149912: gap of unknown length
* 149913 220384: contig of 70472 bp in length.

FEATURES

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1. .220384
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-836M11"
2157. .2256
/estimated_length=unknown
7113. .7212
/estimated_length=unknown
13284. .13383
/estimated_length=unknown
20661. .20760
/estimated_length=unknown
34474. .34573
/estimated_length=unknown
44395. .44494
/estimated_length=unknown
57127. .57226
/estimated_length=unknown
80267. .80366
/estimated_length=unknown
109399. .109498
/estimated_length=unknown
149813. .149912
/estimated_length=unknown

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 220384;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 71201 CCACACCTATTTCATCTC 71184

RESULT 21
MMPAX83
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
MMPAX83
M.musculus Pax-8 gene, exon 3. 463 bp DNA linear ROD 04-JUL-1997
X99593
X99593.1 GI:1850884
Pax-8 gene.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
1
Okladnova,O., Poleev,A., Fantes,J., Lee,M., Plachov,D. and Horst,J.
The genomic organization of the murine Pax 8 gene and
characterization of its basal promoter
Genomics 42 (3), 452-461 (1997)

9205117
2 (bases 1 to 463)
Okladnova,O.
Direct Submission
Submitted (18-JUL-1996) O. Okladnova, Institut fuer Humangenetik,
Uni Muenster, Vesaliusweg 12-14, D- 48149 Muenster, Germany, FRG
FEATURES
Location/Qualifiers
1. .463
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="2B"
112. .277
/gene="Pax-8"
112. .277
/gene="Pax-8"
/usedin=X99592:pax8_cds
/usedin=X99592:pax8_mrna
/label=ex3
ORIGIN
Query Match 94.4%; Score 17; DB 9; Length 463;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 24 CACACCTATTTCATCTC 40
RESULT 22
AY157583
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AY157583
Mus musculus transcription factor Pax8 gene, exons 3 through 7 and
partial cds.
AY157583
AY157583.1 GI:25247296
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
2 (bases 1 to 7821)
Maxime,B., Abdallah,S., Markus,M., Annette,N. and Meinrad,B.
Direct Submission
Submitted (01-OCT-2002) Research Institute of Molecular Pathology,
Dr. Bohr-Gasse 7, Vienna A-1030, Austria
FEATURES
Location/Qualifiers
1. .7821
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129/Sv"
/db_xref="taxon:10090"
join(<3063. .3228,4657. .4854,6114. .6202,6591. .6716,
6979. .>7154)
/product="transcription factor Pax8"
join(<3063. .3228,4657. .4854,6114. .6202,6591. .6716,
6979. .>7154)
/codon_start=3
/product="transcription factor Pax8"
/protein_id="AAN72308.1"
/db_xref="GI:25247297"
/translation="HGGLNQLGGAFVNGRPPLPEVVQRIVDLAHQGVPCDISRQLRV
SHGCVSKILGRYETGSIRPGVIGGSKPKVATPKVEKIGDYKRONPTMFAWEIRDRL
LAEGVCDNDTVPSVSSINRIIRTKVQQFNLPMDSCVATKSLSPGHTLIPSSAVTPPE
SPQSDLSGTSYINGLLGIAQPGNDNKRKMDSDQDSCRLSIDSSSSSPRKHLRTD
TFSQHLEALECFFERQHYPEAYASPSHTKGEQ"

misc_feature

clone_end:Sp6
4927..5761
/note="clone_boundary
clone_end:Sp6
site:
end_sequence:RXBNK60TVB"
4927..5712
/note="clone_boundary
clone_end:Sp6
site:
end_sequence:RXBNK60TV"
complement(146702..147615)
/note="clone_boundary
clone_end:T7
site:
end_sequence:RXBNK60TJB"

misc_feature

misc_feature

ORIGIN

Query Match

Best Local Similarity

Matches

17;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

2

CACACCTATTTCATCTC 18

|||||

Db

54484

CACACCTATTTCATCTC 54468

RESULT 24

BX323576

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX323576

Zebrafish DNA sequence from clone DKEYP-77A12 in linkage group 7, complete sequence.

BX323576

BX323576.9 GI:51591805

HTG.

Danio rerio (zebrafish)

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 163069)

Johnson,C.

Direct Submission

Submitted (27-AUG-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 27, 2004 this sequence version replaced gi:50724700.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the

length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEYP-77A12 is from a Zebrafish BAC library

VECTOR: pIndigoBAC-5.

FEATURES

Location/Qualifiers

1..163069

/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clone="DKEYP-77A12"

/clone_lib="DanioKeypilot"

ORIGIN

Query Match

Best Local Similarity

Matches

17;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

Qy

2

CACACCTATTTCATCTC 18

|||||

Db

100672

CACACCTATTTCATCTC 100688

RESULT 25

AL732528/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL732528

Mouse DNA sequence from clone RP23-218B17 on chromosome 2, complete sequence.

AL732528

AL732528.12 GI:22798098

HTG.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 166465)

Oliver,K.

Direct Submission

Submitted (06-SEP-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Sep 12, 2002 this sequence version replaced gi:22213682.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-218B17 is from the RPCI-23 Mouse PAC Library

constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6.

FEATURES

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Location/Qualifiers
1. .166465
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="2"
/clone="RP23-218B17"
/clone_lib="RPCI-23"

ORIGIN

Query Match 94.4%; Score 17; DB 9; Length 166465;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
|||||
Db 125209 CACACCTATTTCATCTC 125193

RESULT 26

BX571839/c

LOCUS BX571839 168648 bp DNA linear VRT 21-JUL-2004
DEFINITION Zebrafish DNA sequence from clone DKEY-259P7 in linkage group 16, complete sequence.

ACCESSION

VERSION BX571839.8 GI:50470903

KEYWORDS

SOURCE HTG.

ORGANISM

Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 168648)
Humphries,M.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (20-JUL-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zf1sh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 21, 2004 this sequence version replaced gi:50399659.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zf1sh-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep
Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.
Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those

beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-259P7 is from a Zebrafish BAC library
VECTOR: pIndigoBAC-5.

FEATURES

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Location/Qualifiers
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/organism="Danio rerio"
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/clone="DKEY-259P7"
/clone_lib="DanioKey"

ORIGIN

Query Match 94.4%; Score 17; DB 5; Length 168648;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
|||||
Db 100066 CACACCTATTTCATCTC 100050

RESULT 27

AC099634

LOCUS

DEFINITION

AC099634 177551 bp DNA linear HTG 14-JUN-2003
Mus musculus clone RP24-126P14, WORKING DRAFT SEQUENCE, 19 unordered pieces.

ACCESSION

VERSION AC099634.2 GI:31745422

KEYWORDS

SOURCE HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 177551)

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 177551)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP24-126P14
Unpublished
2 (bases 1 to 177551)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

JOURNAL

Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 177551)

REFERENCE

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,

Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Illiev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (14-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 14, 2003 this sequence version replaced gi:16947881.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html.

TITLE
JOURNAL
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: Ll17389
Center clone name: 126_P_14
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 171576 bases at least Q40
Consensus quality: 173582 bases at least Q30
Consensus quality: 174212 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 175751; sum-of-contigs
Quality coverage: 6.9 in Q20 bases; agarose-fp
Quality coverage: 6.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 9555: contig of 9555 bp in length
* 9556 9655: gap of 100 bp
* 9656 10295: contig of 640 bp in length
* 10296 10395: gap of 100 bp
* 10396 11093: contig of 698 bp in length
* 11094 11193: gap of 100 bp
* 11194 12358: contig of 1165 bp in length
* 12359 12458: gap of 100 bp
* 12459 13510: contig of 1052 bp in length
* 13511 13610: gap of 100 bp
* 13611 16664: contig of 3054 bp in length
* 16665 16764: gap of 100 bp
* 16765 19485: contig of 2721 bp in length
* 19486 23382: contig of 100 bp
* 23383 23482: gap of 100 bp
* 23483 25198: contig of 1716 bp in length
* 25199 31520: contig of 6222 bp in length
* 31521 31620: gap of 100 bp
* 31621 39389: contig of 7769 bp in length
* 39390 39489: gap of 100 bp
* 39490 47996: contig of 8507 bp in length
* 47997 48096: gap of 100 bp

* 48097 59411: contig of 11315 bp in length
* 59412 59511: gap of 100 bp
* 59512 70527: contig of 11016 bp in length
* 70528 70627: gap of 100 bp
* 70628 80578: contig of 9951 bp in length
* 80579 80678: gap of 100 bp
* 80679 94343: contig of 13665 bp in length
* 94344 94443: gap of 100 bp
* 94444 106090: contig of 11647 bp in length
* 106091 106190: gap of 100 bp
* 106191 129001: contig of 22811 bp in length
* 129002 129101: gap of 100 bp
* 129102 177551: contig of 48450 bp in length.

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="RP24-126P14"
 /clone_lib="RPCI-24 Male Mouse BAC"
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gap

misc_feature

Query Match

Best Local Similarity

Matches

17;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

2

CACACCTATTCACTC 18

|||||

48878

CACACCTATTCACTC 48894

Db

RESULT 28

BX247878/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted. Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-26605 is from a CHORI-211 BAC library VECTOR: pTARBAC2.1. Location/Qualifiers

misc_feature

/estimated_length=100

59512. .70527

/note="assembly_fragment"

70528. .70627

/estimated_length=100

70628. .80578

gap

misc_feature

Query Match

Best Local Similarity

Matches

17;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

QY

2

CACACCTATTCACTC 18

|||||

48878

CACACCTATTCACTC 48894

Db

RESULT 28

BX247878/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted. Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-26605 is from a CHORI-211 BAC library VECTOR: pTARBAC2.1. Location/Qualifiers

source

1. .190715

/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clone="CH211-26605"

/clone_lib="CHORI-211"

Query Match

Best Local Similarity

Matches

17;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

ORIGIN

QY

2

CACACCTATTCACTC 18

|||||

88799

CACACCTATTCACTC 88783

Db

RESULT 29

AC105464/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC105464

Rattus norvegicus clone CH230-25001, WORKING DRAFT SEQUENCE.

AC105464

AC105464.4 GI:24942074

HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 203746)

Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwackeleme,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,

Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 203746)
Worley,K.C.

Direct Submission
Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 203746)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 13, 2002 this sequence version replaced gi:23101651. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GNAB
Center clone name: CH230-25001

----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 195938 bases at least Q40
Consensus quality: 197488 bases at least Q30
Consensus quality: 198349 bases at least Q20
Estimated insert size: 202264; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 203746: contig of 203746 bp in length.

FEATURES
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clone_end:Sp6"

misc_feature
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misc_feature
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/note="wgs_end_extension
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misc_feature
1. .203746
/note="wgs_end_extension
clone_end:Sp6"

ORIGIN
Query Match 94.4%; Score 17; DB 14; Length 203746;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
|||||
Db 7055 CACACCTATTTCATCTC 7039

RESULT 30
AC136410
LOCUS
DEFINITION Rattus norvegicus clone CH230-489H14, WORKING DRAFT SEQUENCE, 5 ordered pieces.
AC136410
AC136410.3 GI:51948542
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 213533)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., Mcleod,M., Mcneill,T., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokemeleh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,

Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 213533)

Rat Genome Sequencing Consortium
Direct Submission
Submitted (01-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 213533)
Worley,K.C.
Direct Submission
Submitted (15-SEP-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 9, 2004 this sequence version replaced gi:25188275.

COMMENT

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help.tmc.edu
----- Project Information
Center project name: KAIJ
Center clone name: CH230-489H14
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 322827 bases at least Q40
Consensus quality: 326270 bases at least Q30
Consensus quality: 328526 bases at least Q20
Estimated insert size: 372074; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone
* The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. The indicated order and orientation of each sequence has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing.
* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 28444: contig of 28444 bp in length
28445 30144: gap of 1700 bp
30145 79409: contig of 49265 bp in length
79410 80509: gap of 1100 bp
80510 92997: contig of 12488 bp in length
92998 94297: gap of 1300 bp
94298 185713: contig of 91416 bp in length
185714 187713: gap of 2000 bp
187714 213533: contig of 25820 bp in length.

FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-489H14"
1. 28444
/note="assembly_name:Contigl48"
28445. 30144
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28445. 30144
/estimated_length=1700
30145. 79409
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79410. 80509
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79410. 80509
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185714. 187713
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ORIGIN

Query Match 94.4%; Score 17; DB 14; Length 213533;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACT 17
|||||
Db 87350 CCACACCTATTCTACT 87366

RESULT 31
AC119364/c

LOCUS
DEFINITION
AC119364
Rattus norvegicus clone CH230-179F6, WORKING DRAFT SEQUENCE, 2
unordered pieces.
AC119364
AC119364.5 GI:25009122
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 234063)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,


```
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
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Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
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Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
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Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
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Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
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Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
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Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,J., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
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Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 250548)
Worley,K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 250548)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2002 this sequence version replaced gi:21909266.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
----- Project name: GYRL
Center clone name: CH230-29N17
----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 235756 bases at least Q40
Consensus quality: 237808 bases at least Q30
Consensus quality: 239171 bases at least Q20
Estimated insert size: 257025; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 249385: contig of 249385 bp in length
* 249386 249485: gap of unknown length
* 249486 250548: contig of 1063 bp in length.
FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%;   Pred. NO. 1.4e+02;
Matches 17;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      2  CACACCTATTTCATCTC 18
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Db      234445 CACACCTATTTCATCTC 234429

RESULT 33
AC095794
LOCUS
DEFINITION
AC095794 259335 bp DNA linear HTG 13-NOV-2002
Rattus norvegicus clone CH230-9F15, *** SEQUENCING IN PROGRESS ***,
5 unordered pieces.
AC095794
AC095794.5 GI:24940895
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE
1 (bases 1 to 259335)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gregoregis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokemeleh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,J., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 250548)
Worley,K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 250548)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2002 this sequence version replaced gi:21909266.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
----- Project name: GYRL
Center clone name: CH230-29N17
----- Summary Statistics
```

REFERENCE AUTHORS TITLE JOURNAL	Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelimeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Rose,R., Ruiz,S.J., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.		TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL
	Direct Submission Unpublished 2 (bases 1 to 259335) Worley,K.C. Direct Submission Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 259335) Rat Genome Sequencing Consortium. Direct Submission Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 13, 2002 this sequence version replaced gi:22773035. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.		
REFERENCE AUTHORS TITLE JOURNAL	Consensus quality: 240241 bases at least Q20 Estimated insert size: 241666; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation ----- * NOTE: Estimated insert size may differ from sequence length * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). * NOTE: This is a 'working draft' sequence. It currently * consists of 5 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * 1 245368: contig of 245368 bp in length * 245369 245468: gap of unknown length * 245469 254303: contig of 8835 bp in length * 254304 254403: gap of unknown length * 254404 256377: contig of 1974 bp in length * 256378 256477: gap of unknown length * 256478 257611: contig of 1134 bp in length * 257612 257711: gap of unknown length * 257712 259335: contig of 1624 bp in length.		COMMENT
	FEATURES Location/Qualifiers source 1..259335 /organism="Rattus norvegicus" /mol_type="genomic DNA" /db_xref="taxon:10116" /clone="CH230-9F15" 1..1341 /note="wgs end_extension clone_end:Sp6" 6828..7544 /note="clone_boundary clone_end:Sp6 site: end_sequence:BH340872" 135172..136506 /note="wgs contig" 245369..245468 /estimated_length=unknown 245469..247036 /note="wgs contig" 254304..254403 /estimated_length=unknown 256378..256477 /estimated_length=unknown 257612..257711 /estimated_length=unknown misc_feature 1..1341 /note="wgs end_extension clone_end:Sp6" 6828..7544 /note="clone_boundary clone_end:Sp6 site: end_sequence:BH340872" 135172..136506 /note="wgs contig" 245369..245468 /estimated_length=unknown 245469..247036 /note="wgs contig" 254304..254403 /estimated_length=unknown 256378..256477 /estimated_length=unknown 257612..257711 /estimated_length=unknown gap 245369..245468 /estimated_length=unknown 245469..247036 /note="wgs contig" 254304..254403 /estimated_length=unknown 256378..256477 /estimated_length=unknown 257612..257711 /estimated_length=unknown gap 245469..247036 /note="wgs contig" 254304..254403 /estimated_length=unknown 256378..256477 /estimated_length=unknown 257612..257711 /estimated_length=unknown ORIGIN Query Match 94.4%; Score 17; DB 14; Length 259335; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 2 CACACCTATTTCATCTC 18 Db 93238 CACACCTATTTCATCTC 93254 RESULT 34 DQ097951 LOCUS DEFINITION Homo sapiens nonfunctional T cell receptor alpha variable 8-5 (TRAV8-5) gene, complete sequence. ACCESSION DQ097951 VERSION DQ097951.1 GI:70913413 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ----- Project Information Center project name: GDDK Center clone name: CH230-9F15 ----- Summary Statistics Assembly program: Phrap; version 0.990329 Consensus quality: 234689 bases at least Q40 Consensus quality: 238072 bases at least Q30			

REFERENCE 1 (bases 1 to 2005)
AUTHORS Mackelprang,R., Livingston,R.J., da Ponte,S.H., Rieder,M.J., Yi,Q., Subrahmanyam,L., Montoya,M. and Nickerson,D.A.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2005) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT This work was supported by the National Institutes of Health (AI45279) and a Program for Genomic Applications (HL66682 and HL66642) (URL: http://chum.gs.washington.edu).
FEATURES
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1. .2005
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variation
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variation
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328
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339. .1559
gene
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339. .1559
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1006
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Best Local Similarity 94.4%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1432 CCACACCTATTCTACAC 1449
RESULT 35
AY135687
LOCUS AY135687 64211 bp DNA linear ROD 11-DEC-2002
DEFINITION Mus musculus argonaute 1 protein (Agol) gene, partial cds.
ACCESSION AY135687
VERSION AY135687.1 GI:26449032
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 64211)
AUTHORS Carmell,M.A., Xuan,Z., Zhang,M.Q. and Hannon,G.J.
TITLE The Argonaute family: tentacles that reach into RNAi, development control, stem cell maintenance, and tumorigenesis
JOURNAL Genes Dev. 16 (21), 2733-2742 (2002)
PUBMED 12414724
REFERENCE 2 (bases 1 to 64211)
AUTHORS Adams,M. and Mural,R.
TITLE Direct Submission
JOURNAL Submitted (24-JUL-2002) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
FEATURES
source
1. .64211
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gap /estimated_length=54
15643. .15790
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/protein_id="AAN75579.1"
/db_xref="GI:26449033"
/translation="MSDHGRRLLPDSVLTGVFTAGAYLPPLQQVFOAPRRPPIGTV GKPIKLLANYFEVDIPKIDVYHYEVDIKPKCPRRVNREVVEYMQFKPQIFGDRKP VYDGKNIYVTALPIGNERNVDFTIPGEGKDRIFKVISIKWLAIVSWRMLHEALVSG QIPVPLESVQALDVAMRHLSMRYPVGRSFPSPPEGYHPLGGREVFVGFHQSVRP AMWKMLNIDVSATAFYKAQPVIEFMCEVLDIRNIDEQPKPLTDSQVRVFTKEIKGLK

VEVTHCGQMKRYRVCVTRRPASHQTFPLQLESGQTVECTVAQYFKQKYNLQLKYPH
LPCLQVGQEQKHTYLPLEVCNIVAGQRCIKKLTDNQTSMTIKATARSAPDRQBEISRL
MKNASYNLDPYIQEFGIKVKDDMTEVTGRVLPAPILQYGGNRRAIATPNQGYWDMRGK
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DSVEPMFRHLKNTYSGLQIIVILPGKTPVYAEVKRVGDTLLGMATQCVQVKNVVKTS
PQTLNCLCKINKVLGGINNILVPHQRYERLLALSRGPPGESSAVFQQPVIPLGADV
HPPAGDGKKPSITAVVGSMDAHPSTRYCATVRVORPRQEIIEDLSYMWRELLIQFYKST
RFKPTRIIFYRDGVPEGQLPQILHYELLAIRAIDACIKLEKDYQPGITYIVVQKRHHTRL
FCADKNERIGKSNIPAGCTVTDNTITHPFEDFVLCSSHAGIQGTSRPSHYVVLWDDNR
FТАDELQILTYQLCHTYVRCTRSVSIPAPAYYARLVAFRARYHLVDKEHD"
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43039. .43264
/estimated_length=226

ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 64211;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
|||||

Db 63505 CCACACCTATTTCATAATC 63522

RESULT 36
AC151470

LOCUS AC151470 68792 bp DNA linear HTG 02-SEP-2004
DEFINITION Xenopus tropicalis, WORKING DRAFT SEQUENCE, 5 ordered pieces.
ACCESSION AC151470
VERSION AC151470.1 GI:51854487
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE Xenopus tropicalis (SiTurana tropicalis)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 68792)
Tindall,A.J., Pownall,M.E., Morris,I.D. and Isaacs,H.V.
The Xenopus tropicalis peroxidasin gene is expressed within the
developing neural tube and pronephric kidney

Dev. Dyn. (2004) In press
REFERENCE 2 (bases 1 to 68792)
DOE Joint Genome Institute.
Direct Submission
Submitted (02-SEP-2004) Production Genomics Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA
94598-1698, USA

COMMENT
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 5364: contig of 5364 bp in length
* 5365 5464: gap of unknown length
* 5465 6272: contig of 808 bp in length
* 6273 6372: gap of unknown length
* 6373 66225: contig of 59853 bp in length
* 66226 66325: gap of unknown length
* 66326 67110: contig of 785 bp in length
* 67111 67210: gap of unknown length
* 67211 68792: contig of 1582 bp in length.

FEATURES
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1. .68792
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
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6273. .6372
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ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 68792;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
|||||

Db 9134 CCACTCCTATTTCATCTC 9151

RESULT 37
AC006262/c

LOCUS AC006262 107573 bp DNA linear PRI 21-SEP-2001
DEFINITION Homo sapiens chromosome 19, BAC BC264576 (CTC-297N14), complete
sequence.
ACCESSION AC006262
VERSION AC006262.2 GI:15718550
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 106320)
AUTHORS Lamerdin,J.E., McCready,P.M., Skowronski,E., Viswanathan,V.,
Burkhart-Schultz,K., Gordon,L., Dias,J., Ramirez,M., Stilwagen,S.,
Phan,H., Velasco,N., Do,L., Regala,W., Terry,A., Garnes,J.,
Danganan,L., Erler,A., Christensen,M., Georgescu,A., Avila,J.,
Liu,S., Attix,C., Andreise,T., Trankheim,M., Amico-Keller,G.,
Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G.,
Kronmiller,B., Arellano,A., Sanders,C., Ow,D., Nolan,M., Trong,S.,
Kobayashi,A., Olsen,A.S. and Carfano,A.V.

TITLE Sequence analysis of a 1.9 Mb region in 19ql3.2 between APOE and
D19S412

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 107573)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA

REFERENCE 3 (bases 1 to 106320)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA

REFERENCE 4 (bases 1 to 107573)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-2001) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA

COMMENT
On Sep 21, 2001 this sequence version replaced gi:4079612.
Map and sequence oriented from centromere to q telomere. BC264576
overlaps BC282485 (CTC-344H19, AC007785) to the left from bases 1
to 20,296 of this accession, and overlaps BC82621 (CTB-139A18,
AC007193) to the right from bases 106,317 to 107,573 of this
accession. This sequence does not represent the entire insert of
BC264576. Additional chromosome 19 map and sequence information may
be obtained at: <http://www-bio.1lnl.gov/bbrp/genome/genome.html>.

FEATURES
source
1. .107573
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
/map="19ql3.2 between APOE and D19S412"
/clone="CTC-297N14"

Query Match		91.1%;	Score 16.4;	DB 8;	Length 107573;
Best Local Similarity		94.4%;	Pred. No. 3.2e+02;		
Matches	17;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	1 CCACACCTATTCTACTC 18				
Db	17921 CCACACCTATTCTATACAC 17904				
RESULT 38					
AE017349_08/c					
WPCOMMENT					
Sequence split into 12 fragments LOCUS AE017349 Accession AE017349					
Fragment Name		Begin	End		
AE017349_00		1	110000		
AE017349_01		100001	210000		
AE017349_02		200001	310000		
AE017349_03		300001	410000		
AE017349_04		400001	510000		
AE017349_05		500001	610000		
AE017349_06		600001	710000		
AE017349_07		700001	810000		
AE017349_08		800001	910000		
AE017349_09		900001	1010000		
AE017349_10		1000001	1110000		
AE017349_11		1100001	1178688		
Continuation (9 of 12) of AE017349 from base 800001 (AE017349 Cryptococcus neoformans va					
Query Match		91.1%;	Score 16.4;	DB 15;	Length 110000;
Best Local Similarity		94.4%;	Pred. No. 3.1e+02;		
Matches	17;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	1 CCACACCTATTCTACTC 18				
Db	70977 CCACACCTCTTCTACTC 70960				
RESULT 39					
AY386265					
LOCUS	AY386265 134431 bp DNA linear VRL 20-JAN-2004				
DEFINITION	Bovine papular stomatitis virus strain BV-AR02, complete genome.				
ACCESSION	AY386265				
VERSION	AY386265.1 GI:40019124				
KEYWORDS					
SOURCE	Bovine papular stomatitis virus				
ORGANISM	Bovine papular stomatitis virus				
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Parapoxvirus.					
REFERENCE	1 (bases 1 to 134431)				
AUTHORS	Delhon,G., Tulman,E.R., Afonso,C.L., Lu,Z., de la				
Concha-Bermejillo,A., Lehmkuhl,H.D., Piccone,M.E., Kutish,G.F. and					
Rock,D.L.					
TITLE	Genomes of the Parapoxviruses Orf Virus and Bovine Papular				
Stomatitis Virus					
JOURNAL	J. Virol. 78 (1), 168-177 (2004)				
PUBMED	14671098				
REFERENCE	2 (bases 1 to 134431)				
AUTHORS	Kutish,G.F.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-SEP-2003) African Swine Fever Research, Plum Island				
Animal Disease Center, U.S. Department of Agriculture, Agricultural					
Research Service, P.O. Box 848, Greenport, NY 11944-0848, USA					
Location/Qualifiers					
1. .134431					
FEATURES	/organism="Bovine papular stomatitis virus"				
source					
/mol_type="genomic DNA"					
/strain="BV-AR02"					
/isolate="ORFB"					
/isolation_source="three week old calf with oral lesions,					
then passaged in primary lamb kidney cells"					
/db_xref="taxon:129727"					
/country="USA: Arkansas"					

CDS	complement(513.. .956)
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/evidence=not experimental	
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/protein_id="AAR98359.1"	
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/translation="MSALRRLAATAAAALVALGILLGALFRPAAPALPAAFVEPGPARAD	
GSAELVCLVVGGAQHMAAEEAAGAAALSPAYPAAAGVRSFASARKGPLLQLQEVTVAVQ	
DVAALDADAEEFACVAFAGFRAAAAYARPVAEWRRLRREEL"	
CDS	complement(1097.. .2587)
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/codon_start=1	
/product="ORF003 ankyrin repeat protein"	
/protein_id="AAR98360.1"	
/db_xref="GI:41018755"	
/translation="MESALYDYFFTRGPDVRASEVRQLLSLGADVNTGGFGNTALHT	
YLHYDGPDPPEVVRCLLEAGAHVDAVDRCCGALAPELYLLNSKSFDAELFAKLLFGPRT	
DTAFREFLSKVLYGAVVHRPFDOITTERVVDTLVALGADVNRGVVDRTPLHACLTGLA	
ARADTVRLLRHGADLNSMDVYSMTPMVLLRSSDATLELVRLLDAGSDMRITDFRC	
NTLLHQHAESYRPRPAIFEEELISRGCDPLATNVFGNTPLHSMATISSCKNTLLIQPFVR	
AGLDIDALNVRYGASPLHFATGHRNDAAAALVAAGARIIDLRNRGITPLDNIVAHNL	
GRAMRAVIKRSPPEHVAADALARAEEVTPETTRQCVAVVVAHLGAAALADPDKHAHA	
DFIRICLADTAVLRVTFTGDPPLCSALDLLRRMDNLPADPPRAILRLIARLVVYGPD	
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LRVLKTLMRGCQTIDILLSRFMSSLLREYVLRNDRDFSACSWEMFELVRAGANVNDG	
IGFTRTLHACMGVRTNVFMVNSILKLGADVRAADVYGATPLGALLKSPSACVELVEL	
LVAAGSDVCTVDARHNNLLHQHAQRRPSAAVIRRLIELGCDPTALNSSGNTPLHLMA	
AHTSCKRSLIQPLFDAGVADVNRARYDTTPLHVAHAHRNDKACARLLALGADVTLRS	
FTGKTPLAHMI VNDHITCIDRALDARPAVAVAESLAEVGRVRSRCVAVVVAHI	
GAHALPEPVRSQAFAEAECEAETALMRAVRVGTPTATPLLDVVCSTPTPPATLVRRRSA	
KSLKILSIYRDVLQORLVHMRHSALVDSLVMRIGPCPLPADVVVALVLRVPTPLQURT	
CDS	complement(4331.. .4627)
/codon_start=1	
/evidence=not experimental	
/product="ORF005 hypothetical protein"	
/protein_id="AAR98362.1"	
/db_xref="GI:41018757"	
/translation="MSGTPRYGMYDQGGNYKGTANDPGGACKRPHSLSSGGSSSDGSG	
WGSWMGGPPPAKKHCGGGGIGFAGMYGGSGGGICGGVKGVSGGINGGISKI"	
CDS	complement(4904.. .5362)
/codon_start=1	
/product="ORF006 vascular endothelial growth factor"	
/protein_id="AAR98363.1"	
/db_xref="GI:41018758"	
/translation="MKCLIVCMQWSLALLCLQCVKWMQAAPTSSNGNHEVEKWSDVY	
DNSRCQPMKTPVKVSDIYDNTNDRHSPPCVTLMRCGGCCNDESLECVPTETSNVTMQ	
IMTTSAYNDGTSGGISSGMREMSFLQHNKCECRPKSTPPPETTESHRR"	
CDS	complement(5458.. .5949)
/note="similar to Vaccinia virus strain Copenhagen F2L"	
/codon_start=1	
/product="ORF007 dUTPase"	
/protein_id="AAR98364.1"	
/db_xref="GI:41018759"	
/translation="MEFVENHFACDALRVVRLSPNATLPTRGSPRAAGYDILCSACDCI	
VPAGGRRVVFTDLQIQLPDGCYGRVAPRSGLAVKHKFDVGAGVIDADYRGNVGVVLFN	
FGHNDFEVKTGDRIAQLICERAAFPDVEEVACLDDTERGAGGFGSTGVTERTCTTW	
YVN"	
CDS	complement(6025.. .7581)
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/codon_start=1	
/product="ORF008 ankyrin repeat protein"	
/protein_id="AAR98365.1"	
/db_xref="GI:41018760"	
/translation="MLRESVFSSHEDLLFRYLETGSVPDLVVVRALVATDADVNFRG	

EYGRTPHLCVLVARNANCADIVETLLEAGADVNRADVCGYTPLHCYVQHDYVQLRVV
 ETMLAAGAEVRTEGFEVFDNVLSFLASCGSTGSEADIVRLIRAGADVRESDAYDM
 TALHVVARNPAARPVLGLMLEAGADVDRAMDXGVTPLAVLLSSTGVNDELVAMMLRA
 GADPRARDMDGRTLHLHATVPRAKESIMRTLVDSGCDPAGIDTGNFTALHYMAMYGT
 CRRPVVSFLLEKGLDMDRQNDAGQTALYRAAVFNPAACRRLLIQMGADLAPVAATGFCA
 VAEVFRNRNDFKSAALLERKPPIDLLVALVTATNWGFFFPDSEAAILLCVHSLVARGA
 GERVAEPVLGKYADAVRECEAEIRAMREVRNADTTLLDVLRADESAKAHVHPNALL
 DRVHAFKVYGNALFGKVMRMLRMSLAEHVAGLPCALPPEIVTISILSYMSYEELMG
 LRTALLAPAR"

complement(7713. .9110)
 /note="similar to Vaccinia virus strain Copenhagen F11L
 and Molluscum contagiosum virus MC018L"
 /codon_start=1
 /evidence=not_experimental
 /product="ORF009 hypothetical protein"
 /protein_id="AAR98366.1"
 /db_xref="GI:41018761"

/translation="MTWCGLARMSSTLSFRRLSYGRSSCVPRTCGMPMRPRIRNSD
 EDSEYDDNVPGYDPDSVDAAPVARPLVLTVPGASRPVLDSVFERIIPDVSALVTH
 LGEWTEIRLFESPFRAPVRVCRSVLARIYDAEMAFEVKOCQALKRHGEWYMRQKV
 SPDMAFVALICIRNEGVAALAVNTKYLNTNITVGSIVFPVAVRGMFLPLPHIGGEAE
 YIILTMPTQDLLDQGDVFPSPVDQDAQIIRTAASAEATKRACVLVSDLITLRIELE
 CYHRICKLMIVISEFGDLYSNVGAKMITESVDIAKMGSDVDVGGENCEDVGVASAVA
 LCRRASSRRRRPVSVMNRSHLLNIGLNLFAMFAQCAGTGPHPDLSLMARMEKDLO
 DMYARFTELWDTVLEKAAADLDSTLPRTEVLEKFIHLQVCNSPAGIERNQLVQRLTMLA
 GSGYRLTGSGEVGPV"

complement(9147. .11078)
 /note="similar to Vaccinia virus strain Copenhagen F12L
 and Molluscum contagiosum virus MC019L"
 /codon_start=1
 /product="ORF010 EEV maturation protein"
 /protein_id="AAR98367.1"
 /db_xref="GI:41018762"

/translation="MLGFWKVCNSLTSKQAWDEQLVATDLVPGEYALAKARDGKTII
 FDAQSVRDAAIIVPLSLKSTRITCTFVDPHRDALDPPAASTORFAIVSRDDPACYIPES
 SSPFLDILRRSEDEPELLAAFEENPPAGARSDIDELNQWLSDAGLYHLRMVSTDAPV
 RLGTVPVRKQTLDDIMNVCVGVYAIWVKDPASVYTRPDTEVLAHDAARTAAQASSWAQPH
 LHSPSTSCVAAWFCYRCGGDGRVQLHSIVMNTGMVFRGSPARMVVRRELLMWLATCKEH
 MTVYGFYSFFDSRQVFALAGKWTLSLNTLLSKLGNRVTFVDLARFAPGTLFSEYC
 EFWGGACVEVPEDIVPDENPAVAEDAASVAAQALMDAARSHQAALARIFPSCDMAAF
 NGLREMVLGNAARGCGACPMHSSALDMVNAALFIEEAGANPAPADARCFRLSSPLREA
 ASKRYPAGKPHFVTELTGLLSIALCEVERSEVLRIPVLPDPDDEQDLRFSVVLTSVD
 IETANRLKGYISIRVIAALEWRSEEVLRGTGIEAQMAATRELNIPQTSNLMRSIASMPL
 PLDPDSSPSGRSSAVVRAFAASYCRSTIHLIERVDSHFSGNFVVRHGYDRFWRVDRV
 AKHLTGVSGIQEVLPAVAR"

complement(11155. .12291)
 /note="similar to Vaccinia virus strain Copenhagen F13L
 and Molluscum contagiosum virus MC021L"
 /codon_start=1
 /product="ORF011 EEV phospholipase"
 /protein_id="AAR98368.1"
 /db_xref="GI:41018763"

/translation="MWPFSSIPVGAECRVVETLPAEVSSLQVGNMSTFECFSAIVESA
 TKFLYIASFCNLTGSTRGVVDKDKLCTLAKSGVNVTVLVDVQSKDRDAEELREAGVN
 YVKVKVSGRDDVGNLGSFWSINAGQWYVGSASLTGSGISNIKNLGVYSTNRHLATDL
 MNRYNTFYSMIVEPKVPFSRLCCAMITPTATDFHLDHAGGGVFFSDAPEKFLGFYRTL
 DEDLVLHRIDSAKNSIDLSSLVVPVIRHADRVVEYPRIMDALLRAAIDRSVVRVIV
 TEWKNAADPLSVSAARTLNDFGVGSIDISTRLSIPGRDDAANNTKLLIVDDTFAHVTV
 ANMDGTHYKYHAFVSVNAEKGDIVNQLSAVFERDWRFSQYCKPIN"
 complement(12312. .12569)

/codon_start=1
 /evidence=not_experimental
 /product="ORF012 hypothetical protein"
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 /db_xref="GI:41018764"

/translation="MRVHGARRNLDEVIDQLLDDMOIDGDIFFEVPDCTPDWVDALD
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 12910. .13131
 /codon_start=1
 /evidence=not_experimental
 /product="ORF013 hypothetical protein"
 /protein_id="AAR98370.1"
 /db_xref="GI:41018765"

/translation="MCLCGIFFPCAEWLVRRVNRLLIIVRRRVGGEPAYVSVVQACDD
 YTFEFDAAQQSVSLLRAGAEAAATPIARV"
 complement(13212. .13493)
 /note="similar to Molluscum contagiosum virus MC026L"
 /codon_start=1
 /product="ORF014 modified RING finger protein"
 /protein_id="AAR98371.1"
 /db_xref="GI:41018766"

/translation="MPIKVKSWKVAVKSLACPPVCYICKSKASEGCLNNAACPGACPF
 VMVCGHYHRHCLGPANTDVCVCRSVLQKADIPDETASDAVIREFML"
 complement(13500. .15110)
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 /evidence=not_experimental
 /product="ORF015 hypothetical protein"
 /protein_id="AAR98372.1"
 /db_xref="GI:41018767"

/translation="MDEELILLGFMDSEMPLSHMNKLRRLTKLRMNSFAVIMCLR
 EAILRKWLPSGSILGTDISDDVRLLEFVVSEVDSARENIPEYLVTVQWTHNADIFDE
 CMREAMEALFGDSVQRLAMGVVESRYPHLVAERCNSCLAALMPEDASVRFVNAILRYS
 GNMAGIVDRSREAGSHEELADMVRQQHASKIRMPRVVGAVVARVVEMDIEGLKTYC

Query Match 91.1%; Score 16.4; DB 13; Length 134431;
 Best Local Similarity 94.4%; Pred. No. 3.le+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCACACCTATTCACTAC 18
 |||||
 Db 96522 CCACACCTATTAACTAC 96539

RESULT 40
 AC160234/c
 LOCUS
 DEFINITION
 AC160234
 AC160234.2 GI:63055136
 HTG; HTGS_PHASE2; HTGS_DRAFT.
 Rhinolophus ferrumequinum (greater horseshoe bat)
 ORGANISM
 Rhinolophus ferrumequinum
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Chiroptera; Microchiroptera;
 Rhinolophidae; Rhinolophinae; Rhinolophus.
 1 (bases 1 to 138685)
 Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A.,
 Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,
 Engle,J., Fuksenko,T., Gestole,M., Greene,A., Guan,X., Gupta,J.,
 Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hunter,G.,
 Hurtle,B., Idol,J.R., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q.,
 Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H.,
 Masiello,C., Maskeri,B., McDowell,J., Mojidi,H.A., Mullikin,J.C.,
 Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A., Puri,O.,
 Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,
 Stantripop,S., Stephen,E., Taye,A., Thomas,J.W., Thomas,P.J.,
 Tsipouri,V., Ung,L., Vogt,J.L., Wetherby,K.D., Young,A. and
 Green,E.D.
 NISC Comparative Sequencing Initiative
 Unpublished
 2 (bases 1 to 138685)
 Green,E.D.
 Direct Submission
 Submitted (20-APR-2005) NIH Intramural Sequencing Center, 5625
 Fishers Lane, Rockville, MD 20852, USA
 3 (bases 1 to 138685)
 Green,E.D.
 Direct Submission
 Submitted (06-MAY-2005) NIH Intramural Sequencing Center, 5625
 Fishers Lane, Rockville, MD 20852, USA
 On May 6, 2005 this sequence version replaced gi:62751232.
 ----- Genome Center
 Center: NIH Intramural Sequencing Center
 Center code: NISC

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Web site: <http://www.nisc.nih.gov>
Contact: nisc_zoo@nhgri.nih.gov
----- Project Information
Center project name: ipi
Center clone name: 248B22

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is generally based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 137930 bases at least Q40
Consensus quality: 138141 bases at least Q30
Consensus quality: 138305 bases at least Q20
Insert size: 167000; agarose-fp
Insert size: 138385; sum-of-contigs
Quality coverage: 8.50x in Q20 bases; agarose-fp
Quality coverage: 10.26x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 27052: contig of 27052 bp in length
* 27053 27152: gap of unknown length
* 27153 105879: contig of 78727 bp in length
* 105880 105979: gap of unknown length
* 105980 130171: contig of 24192 bp in length
* 130172 130271: gap of unknown length
* 130272 138685: contig of 8414 bp in length.

FEATURES
source

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/db_xref="taxon:59479"
/clone="VMRC7-248B22"
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/note="BAC resource: <http://bacpac.chori.org/>"

misc_feature

1. .27052
/note="assembly_fragment
clone_end:other
vector_side:left"

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/estimated_length=unknown

misc_feature

27153. .105879
/note="assembly_fragment"

misc_feature

83540. .138685
/note="clone overlaps with GenBank Accession Number
AC160240 clone VMRC7-88J4 (center project name ipj)"

gap

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/estimated_length=unknown

misc_feature

105980. .130171
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gap

130172. .130271
/estimated_length=unknown

misc_feature

130272. .138685
/note="assembly_fragment"

ORIGIN

clone_end:SP6
vector_side:right"

Query Match 91.1%; Score 16.4; DB 14; Length 138685;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATACTC 18
|||||
Db 8910 CCACACCTATTTCCTACTC 8893
|||||

RESULT 41

AC159925

LOCUS

DEFINITION

AC159925 149184 bp DNA linear HTG 06-MAY-2005

Atelerix albiventris clone LB4-257D11, WORKING DRAFT SEQUENCE, 7

ordered pieces.

AC159925

AC159925.2 GI:63055118

HTG; HTGS PHASE2; HTGS DRAFT.

Atelerix albiventris (middle-African hedgehog)

Atelerix albiventris

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;

Erinaceinae; Atelerix.

1 (bases 1 to 149184)

Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A.,

Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,

Engle,J., Fuksenko,T., Gestole,M., Greene,A., Guan,X., Gupta,J.,

Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hunter,G.,

Hurle,B., Idol,J.R., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q.,

Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H.,

Masiello,C., Maskeri,B., McDowell,J., Mojidi,H.A., Mullikin,J.C.,

Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A., Puri,O.,

Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,

Stantripop,S., Stephen,E., Taye,A., Thomas,J.W., Thomas,P.J.,

Tsipouri,V., Ung,L., Vogt,J.L., Wetherby,K.D., Young,A. and

Green,E.D.

NISC Comparative Sequencing Initiative

Unpublished

2 (bases 1 to 149184)

Green,E.D.

Direct Submission

Submitted (14-APR-2005) NIH Intramural Sequencing Center, 5625

Fishers Lane, Rockville, MD 20852, USA

3 (bases 1 to 149184)

Green,E.D.

Direct Submission

Submitted (06-MAY-2005) NIH Intramural Sequencing Center, 5625

Fishers Lane, Rockville, MD 20852, USA

On May 6, 2005 this sequence version replaced gi:62543316.

----- Genome Center

Center: NIH Intramural Sequencing Center

Center code: NISC

Web site: <http://www.nisc.nih.gov>

Contact: nisc_zoo@nhgri.nih.gov

----- Project Information

Center project name: kdw

Center clone name: 257D11

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is generally based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

```
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 147467 bases at least Q40
Consensus quality: 147906 bases at least Q30
Consensus quality: 148268 bases at least Q20
Insert size: 145000; agarose-fp
Insert size: 148584; sum-of-contigs
Quality coverage: 7.95x in Q20 bases; agarose-fp
Quality coverage: 7.76x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 54387: contig of 54387 bp in length
* 54388 54487: gap of unknown length
* 54488 82572: contig of 28085 bp in length
* 82573 82672: gap of unknown length
* 82673 95830: contig of 13158 bp in length
* 95831 95930: gap of unknown length
* 95931 101313: contig of 5383 bp in length
* 101314 101413: gap of unknown length
* 101414 128146: contig of 26733 bp in length
* 128147 128246: gap of unknown length
* 128247 132000: contig of 3754 bp in length
* 132001 132100: gap of unknown length
* 132101 149184: contig of 17084 bp in length.
Location/Qualifiers
1. .149184
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/mol_type="genomic DNA"
/db_xref="taxon:9368"
/clone="LB4-257D11"
/clone_lib="LB4"
/clone="BAC resource: http://bacpac.chori.org/"
1. .54387
/note="assembly_fragment
clone_end:T7
vector_side:left"
26261. .149184
/note="clone overlaps with GenBank Accession Number
AC160584 clone LB4-23009 (center project name kdx)"
54388. .54487
/estimated_length=unknown
54488. .82572
/note="assembly_fragment"
82573. .82672
/estimated_length=unknown
82673. .95830
/note="assembly_fragment"
95831. .95930
/estimated_length=unknown
95931. .101313
/note="assembly_fragment"
101314. .101413
/estimated_length=unknown
101414. .128146
/note="assembly_fragment"
128147. .128246
/estimated_length=unknown
128247. .132000
/note="assembly_fragment"
132001. .132100
/estimated_length=unknown
132101. .149184
/note="assembly_fragment
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clone_end:SP6
vector_side:right"

ORIGIN
Query Match          91.1%;   Score 16.4;   DB 14;   Length 149184;
Best Local Similarity 94.4%;   Pred. No. 3.1e+02;
Matches 17;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      1 CCACACCTATTCTACTC 18
      | ||||| ||||| |||||
Db      100334 CAACACCTATTCTACTC 100351

RESULT 42
AC160584
LOCUS
DEFINITION
Atelerix albiventris clone LB4-23009, WORKING DRAFT SEQUENCE, 2
ordered pieces.
AC160584
ACCESSION
AC160584.2 GI:53028190
VERSION
HTG: HTGS_PHASE2; HTGS DRAFT.
KEYWORDS
Atelerix albiventris (middle-African hedgehog)
ORGANISM
Atelerix albiventris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;
Erinaceinae; Atelerix.
1 (bases 1 to 150567)
AUTHORS
Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A.,
Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,
Engle,J., Fuxsenko,T., Gestole,M., Greene,A., Guan,X., Gupta,J.,
Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hunter,G.,
Hurle,B., Idol,J.R., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q.,
Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H.,
Masiello,C., Maskeri,B., McDowell,J., Mojidi,H.A., Mullikin,J.C.,
Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A., Puri,O.,
Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,
Stantripop,S., Stephen,E., Taye,A., Thomas,J.W., Thomas,P.J.,
Tsipouri,V., Ung,L., Vogt,J.L., Wetherby,K.D., Young,A. and
Green,E.D.
TITLE
NISC Comparative Sequencing Initiative
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 150567)
AUTHORS
Green,E.D.
TITLE
Direct Submission
JOURNAL
Submitted (28-APR-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
3 (bases 1 to 150567)
Green,E.D.
TITLE
Direct Submission
JOURNAL
Submitted (05-MAY-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On May 5, 2005 this sequence version replaced gi:62945479.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
----- Project Information
Center project name: kdx
Center clone name: 230009

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig, has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is generally based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
```

```
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 149914 bases at least Q40
Consensus quality: 150134 bases at least Q30
Consensus quality: 150306 bases at least Q20
Insert size: 148000; agarose-fp
Insert size: 150467; sum-of-contigs
Quality coverage: 8.80x in Q20 bases; agarose-fp
Quality coverage: 8.66x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 27873 27972: contig of 27872 bp in length
* 27973 150567: contig of 122595 bp in length.
Location/Qualifiers
1. 150567
/organism="Atelerix albiventris"
/mol_type="genomic DNA"
/db_xref="taxon:9368"
/clone="LB4-23009"
/clone_lib="LB4"
/note="BAC resource: http://bacpac.chori.org/"
1. 122925
/note="clone overlaps with GenBank Accession Number
AC159925 clone LB4-257D11 (center project name kdw)"
1. 27872
/note="assembly_fragment
clone_end:T7
vector_side:left"
27873_ .27972
/estimated_length=unknown
27973_ .150567
/note="assembly_fragment
clone_end:SP6
vector_side:right"

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 150567;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| |||||
Db 73641 CAACACCTATTTCATCTC 73658

RESULT 43
AC105201/c
LOCUS AC105201 151032 bp DNA linear PRI 02-MAR-2002
DEFINITION Homo sapiens chromosome 18, clone RP11-244M2, complete sequence.
ACCESSION AC105201
VERSION AC105201.3 GI:18653689
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 151032)
REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 18, clone RP11-244M2
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 151032)
```

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (26-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 151032)

REFERENCE

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

Submitted (02-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 13, 2002 this sequence version replaced gi:18483543.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L22966
Center clone name: 244_M_2

FEATURES

source

Location/Qualifiers

1. .151032
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
/map="18"
/clone="RP11-244M2"
/clone_lib="RPCI-11 Human Male BAC"

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repeat_region 2582. .2606
/rpt_family="(TG)n"
repeat_region 3819. .4110
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repeat_region 4936. .4970
/rpt_family="(TG)n"
repeat_region 4997. .5019
/rpt_family="AT_rich"
repeat_region 5330. .5628
/rpt_family="AluSq"
repeat_region 5696. .5724
/rpt_family="AT_rich"
repeat_region complement(5866. .6277)
/rpt_family="MER66A"
repeat_region complement(6315. .6665)
/rpt_family="MER66A-int"
repeat_region complement(6883. .7113)
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repeat_region complement(7114. .7199)
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repeat_region complement(7200. .7739)
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repeat_region 14235. .14575
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repeat_region 14608. .14754
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repeat_region 14757. .14825
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repeat_region 14832. .14879
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repeat_region 15041. .15400
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26415. .26475
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26691. .26942
/rpt_family="L2"
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27183. .27344
/rpt_family="L2"
repeat_region 27472. .27492
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/rpt_family="L2"
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Best Local Similarity 94.4%; Pred. No. 3.le+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 71375 CCACACCTATTTCATACAC 71358

RESULT 44
AC016373
LOCUS AC016373 152106 bp DNA linear HTG 30-MAR-2000
DEFINITION Homo sapiens clone RP11-13M18, WORKING DRAFT SEQUENCE, 13 unordered
pieces.
ACCESSION AC016373
VERSION AC016373.3 GI:7341913
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 152106)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome, clone RP11-13M18
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 152106)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (25-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 30, 2000 this sequence version replaced gi:6624031.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE
JOURNAL

COMMENT

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3360
Center clone name: L3 M 18

----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 143567 bases at least Q40
Consensus quality: 147860 bases at least Q30
Consensus quality: 149348 bases at least Q20
Insert size: 180000; agarose-fp
Insert size: 150906; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1182: contig of 1182 bp in length
* 1183 1282: gap of 100 bp
* 1283 5050: contig of 3768 bp in length
* 5051 5150: gap of 100 bp
* 5151 7923: contig of 2773 bp in length
* 7924 8023: gap of 100 bp
* 8024 14304: contig of 6281 bp in length
* 14305 14404: gap of 100 bp
* 14405 20437: contig of 6033 bp in length
* 20438 20537: gap of 100 bp
* 20538 26636: contig of 6099 bp in length
* 26637 26736: gap of 100 bp
* 26737 31895: contig of 5159 bp in length
* 31896 31995: gap of 100 bp
* 31996 40274: contig of 8279 bp in length
* 40275 40374: gap of 100 bp
* 40375 47530: contig of 7156 bp in length
* 47531 47630: gap of 100 bp
* 47631 61004: contig of 13374 bp in length
* 61005 61104: gap of 100 bp
* 61105 74867: contig of 13763 bp in length
* 74868 74967: gap of 100 bp
* 74968 91818: contig of 16851 bp in length
* 91819 91918: gap of 100 bp
* 91919 152106: contig of 60188 bp in length.

FEATURES
source

1. .152106
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

misc_feature /clone="RP11-13M18"
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/note="assembly_fragment"
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/estimated_length=100
1283. .5050
/note="assembly_fragment"
5051. .5150
/estimated_length=100
5151. .7923
/note="assembly_fragment
clone_end:SP6
vector_side:right"
7924. .8023
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8024. .14304
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14305. .14404
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14405. .20437
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20438. .20537
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20538. .26636
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26637. .26736
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26737. .31895
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31896. .31995
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31996. .40274
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40275. .40374
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40375. .47530
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47531. .47630
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47631. .61004
/note="assembly_fragment"
61005. .61104
/estimated_length=100
61105. .74867
/note="assembly_fragment"
74868. .74967
/estimated_length=100
74968. .91818
/note="assembly_fragment"
91819. .91918
/estimated_length=100
91919. .152106
/note="assembly_fragment
clone_end:T7
vector_side:right"

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 152106;
Best Local Similarity 94.4%; Pred. No. 3.le+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATAC 18

|||||

Db 120884 CCACACCTATTTCATACAC 120901

RESULT 45

CR318635

LOCUS

DEFINITION

complete sequence.

ACCESSION

CR318635 154312 bp DNA linear VRT 12-MAY-2005
Zebrafish DNA sequence from clone CH211-253D2 in linkage group 23,
CR318635

CR318635.8	GI:63094294
HTG	
Danio rerio (zebrafish)	
Danio rerio	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.	
1 (bases 1 to 154312)	
Heath,P.	
Direct Submission	
Submitted (12-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk	
On May 7, 2005 this sequence version replaced gi:62954551.	
----- Genome Center	
Center: Wellcome Trust Sanger Institute	
Center code: SC	
Web site: http://www.sanger.ac.uk	
Contact: zfish-help@sanger.ac.uk	

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.	
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.	
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep	
Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.	
Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml	
CH211-253D2 is from a CHORI-211 BAC library	
VECTOR: pTARBAC2.1.	
Location/Qualifiers	
1. .154312	
/organism="Danio rerio"	
/mol_type="genomic DNA"	
/db_xref="taxon:7955"	
/clone="CH211-253D2"	
/clone_lib="CHORI-211"	
ORIGIN	
Query Match	91.1%; Score 16.4; DB 5; Length 154312;
Best Local Similarity	94.4%; Pred. No. 3.1e+02;
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	1 CCACACCTATTTCATACTC 18
Db	115546 CCACACCTATTTCACACTC 115563
RESULT 46	
AL354997	
LOCUS	156077 bp DNA linear PRI 18-MAY-2005
DEFINITION	Human DNA sequence from clone RP11-309H8 on chromosome 13 Contains two novel genes and a novel RING finger protein pseudogene,

complete sequence.	
AL354997	
AL354997.17	GI:12666245
HTG; RING.	
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 156077)	
Pelan,S.	
Direct Submission	
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk	
Clone requests: clonerequest@sanger.ac.uk	
On Feb 5, 2001 this sequence version replaced gi:12584390.	
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep	
This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13	
RP11-309H8 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm	
VECTOR: pBACe3.6	
----- Genome Center	
Center: Wellcome Trust Sanger Institute	
Center code: SC	
Web site: http://www.sanger.ac.uk	
Contact: vega@sanger.ac.uk	

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.	
Location/Qualifiers	
1. .156077	
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
/chromosome="13"	
/clone="RP11-309H8"	
/clone_lib="RPCI-11.2"	
/note="Clone left_end: RP11-309H8"	
complement(10967)	
join(complement(11000..11005)	
join(complement(32931..33002),	
complement(AL353635.17:28148..28173),	
complement(AL353635.17:27186..27323),	
complement(AL353635.17:25849..25909),	
complement(AL353635.17:22461..22941))	
/locus_tag="RP11-143O10.1-001"	
join(complement(32931..33002),	
complement(AL353635.17:28148..28173),	
complement(AL353635.17:27186..27323),	
complement(AL353635.17:25849..25909),	
complement(AL353635.17:22461..22941))	
/locus_tag="RP11-143O10.1-001"	
/note="match: ESTs: BG183515 BG183515.1 BG189865 BG189865.1 BG191871 BG191871.1"	
complement(44930..46212)	
/locus_tag="RP11-309H8.2-001"	
/pseudo	
complement(44930..46212)	
/locus_tag="RP11-309H8.2-001"	
FEATURES	
source	
misc_feature	
polyA_site	
polyA_signal	
gene	
mRNA	
gene	
CDS	

/note="match: proteins: Q8VI40"
/pseudo
/codon_start=1
58554..58797
/note="Sequence from AC016373, sequenced by Whitehead.
Assembly confirmed by restriction digest data."
join(69315..69474,75779..76352)
/locus_tag="RP11-309H8.3-001"
join(69315..69474,75779..76352)
/locus_tag="RP11-309H8.3-001"
/note="match: ESTs: BG182545 BG191981 BG209582"
74442..74460
/locus_tag="RP11-309H8.3-001"
/note="Weak data."
97179..97234
/note="Sequence from AC027145, sequenced by Whitehead.
Assembly confirmed by restriction digest data."
134856..134919
/note="Sequence from AC027145, sequenced by Whitehead.
Assembly confirmed by restriction digest data."
155978
/note="Clone_left_end: RP11-114G1"

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 156077;
Best Local Similarity 94.4%; Pred. No. 3.le+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 39509 CCACACCTATTCTATACAC 39526

RESULT 47
CNS05TEG/c
LOCUS
DEFINITION
Human chromosome 14 DNA sequence BAC R-55G7 of library RPCI-11 from
chromosome 14 of Homo sapiens (Human), complete sequence.
AL359218 4 GI:14329664
HTG; HTGS ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 160718)
Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
Gyapay,G., Saurin,W. and Weissenbach,J.
Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 160718)
Genoscope.
Direct Submission
Submitted (31-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jun 8, 2001 this sequence version replaced gi:12580647.

Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-98N22 (AC=AL163152)
Downstream BAC (overlapping the SP6 end) : C-2335L22

Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 7.46x in Q20 bases; sum-of-contigs

Overall quality chart :
Range : bases
0
1 - 9 : 1
10 - 19 : 12
20 - 29 : 69
30 - 39 : 98
40 - 49 : 976
50 - 59 : 3761
60 - 69 : 6619
70 - 79 : 18798
80 - 89 : 45434
90 - 99 : 84950

Percentage of bases with a quality value >= 40 : 99 %.
FEATURES
source
Location/Qualifiers
1..160718
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="R-55G7"
/clone_lib="RPCI-11"

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 160718;
Best Local Similarity 94.4%; Pred. No. 3.le+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 132546 CCACACCTATTCTACACTC 132529

RESULT 48
AC103218
LOCUS
DEFINITION
Rattus norvegicus clone CH230-47A7, *** SEQUENCING IN PROGRESS ***,
12 unordered pieces.
AC103218
AC103218.4 GI:23120606
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 163443)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 166500)

AUTHORS Lamerdin,J.E., McCready,P.M., Richardson,P., Sakaldasis,G., Burkhart-Schultz,K., Gordon,L., Scott,D., Johnson,G., Stiiwagen,S., Phan,H., Velasco,N., Do,L., Regala,W., Terry,A., Danganan,L., Erler,A., Christensen,M., Georgescu,A., Avila,J., Attix,C., Andreise,T., Amico-Keller,G., Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G., Kronmiller,B., Arellano,A., Sanders,C., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. and Carrano,A.V.

TITLE Sequence analysis of a 2.5 Mb region in 19ql3.2-13.3 between APOE and C5R1

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 166500)

AUTHORS Lamerdin,J.E.

TITLE Direct Submission

JOURNAL Submitted (11-JUN-1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA

COMMENT Map and sequence oriented from q centromere to telomere. BAC 282485 overlaps cosmid R30477 to the left from bases 1 to 4,419 of this accession, and overlaps BAC 264576 (CIT-B-297N14; AC006262) from bases 146,203 to 166,500. Additional chromosome 19 map and sequence information may be obtained at: <http://www-bio.llnl.gov/bbrp/genome/genome.html>.

FEATURES

source

1. .166500

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="19"

/map="19ql3.3 between DM and c5R1"

/clone="CIT-B-344H19"

/clone_lib="Cal Tech CIT-B BAC library"

/note="LLNL clone name: BC282485"

70. .145

/rpt_family="(TGAA)n"

complement(177. .453)

/rpt_family="AluJb"

complement(472. .712)

/rpt_family="MIR"

join(<746. .904,1157. .1239,4294. .4451,5875. .6036, 12784. .12994,13080. .13162,13903. .13958,14053. .14128, 14429. .14568,14726. .14804,14982. .15039,15813. .15885, 16025. .16122)

/note="Hypothetical arginine-rich gene product; Hypothetical CDS constructed from overlapping ESTs and Xgrail predictions. EST coverage is lacking for some portions of the CDS. Gene may be alternatively spliced, as multiple transcripts map into this region; alternatively, these individual clones may represent artifactual events during RT and cDNA creation"

/codon_start=3

/evidence=not experimental

/product="BC282485_1"

/protein_id="AAD38244.1"

/db_xref="GI:5042405"

/translation="TlAMDQPAGLQVDYVFRGVEHAVRVMVSGQVLELEVEDRMTADQ WRGEFDAGFIEDLTKGNFKQFNIFCHMLFSALTQSSSVTLDDLTVTDLES LRNRK MGRPGSLAPRSALNSKRYLILYISVEFDRIHYPLPLPYQGPDPVVLQGIIRSLKE ELGRLOGLDQNTDRDRENIWHLREQVSRlASEKLEAEOLGRSREALAGRAARQE AEALRGLVRGLELRQERGLGHRVAGRRGQDCRRRLAKELEEAKERSLARLKTLT SELALYKRGSGRGRPARPSPSPGTGGRALRFDPDTAFVKAKERKQREIQMKQQQRN RLGGSGGDGSPSVWSRQTQPPAALTGRGDAPNRSNRSSVDSFRSRCSASSCSDL EDFESLSRGGHRRRGKPPSPTPWSGSNMKSPPVershHQKSLANSGGWVPIKEYSSE HQAADMAEIDARLKAQYMNRLDMRS"

746. .904

/note="DDS similarity to overlapping ESTs: N39722 yx92e04.r1 Homo sapiens cDNA clone 269214 5'; (12. .170); 99% identity.~AA283147 zt14d07.r1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:713101 5'; (6. .163); 99% identity.~AA143160 z149d07.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505261 5'; (1. .43); 100%

misc_feature

identity.~AA142881 z149d07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505261 3'; (570. .527); 64% identity."

1157. .1239

/note="predicted exon, program: grail2exons human_1.3, frame: 0, quality: good, score: 62.000~DDS similarity to overlapping ESTs:

N39722 yx92e04.r1 Homo sapiens cDNA clone 269214 5'; (171. .255); 95% identity.~AA283147 zt14d07.r1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:713101 5'; (164. .247); 92% identity.~AA143160 z149d07.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505261 5'; (44. .126); 100% identity.~N28707 yx66d11.r1 Homo sapiens cDNA clone 266709 5'; (1. .66); 98% identity.~AA142881 z149d07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505261 3'; (526. .438); 82% identity."

1536. .1634

/rpt_family="(CA)n"

complement(1673. .1973)

/rpt_family="AluSx"

complement(2040. .2185)

/rpt_family="LINE2"

complement(2200. .2498)

/rpt_family="AluSx"

complement(2576. .2746)

/rpt_family="AluSg/x"

complement(2747. .3044)

/rpt_family="AluSx"

3048. .3750

/rpt_family="MER64"

3841. .4060

/rpt_family="MER64"

4294. .4451

/note="DDS similarity to overlapping ESTs: N39722 yx92e04.r1 Homo sapiens cDNA clone 269214 5'; (256. .438); 81% identity.~AA283147 zt14d07.r1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:713101 5'; (248. .400); 99% identity.~AA143160 z149d07.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505261 5'; (127. .281); 97% identity.~N28707 yx66d11.r1 Homo sapiens cDNA clone 266709 5'; (67. .222); 98% identity.~AA142881 z149d07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505261 3'; (437. .275); 97% identity."

complement(4789. .5083)

/rpt_family="AluSx"

5875. .5972

/note="DDS similarity to overlapping ESTs: N39722 yx92e04.r1 Homo sapiens cDNA clone 269214 5'; (439. .506); 71% identity.~AA143160 z149d07.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505261 5'; (282. .379); 100% identity.~AA142881 z149d07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505261 3'; (274. .175); 95% identity."

5875. .5898

/note="DDS similarity to N28707 yx66d11.r1 Homo sapiens cDNA clone 266709 5'; (223. .246); 100% identity."

5906. .6036

/note="predicted exon, program: grail2exons human_1.3, frame: 1, quality: excellent, score: 100.000"

complement(6148. .6443)

/rpt_family="AluSx"

complement(6608. .6648)

/rpt_family="LINE2"

complement(7118. .7340)

/rpt_family="MIR"

complement(7538. .7639)

/rpt_family="(CA)n"

complement(7792. .8054)

/rpt_family="MIR"

complement(8789. .9083)

/rpt_family="AluJo"

/note="match: ESTs: AA099036.1 AA371047.1 AA430277.1
AA677654.1 AI499778 AL079991 AU133297.1 AW347402
AW347402.1 AW409774.1 BE751213.1 BF315314 BF315314.1
BF338569 BF338569.1 BI197478.1 CA357296.1 H09468 H11271
H11271.1 T08839.1 TI2623.1 TI9257
match: cDNAs: AB006627 AB014534 AB014534.1 AF116573
AF116573.1 AF116574 AF116574.1 U48797"
join(complement(126444..126885),complement(3274..3461),
complement(AL355608.11:56896..57280),
complement(AL354981.41:54070..54177),
complement(AL392085.12:155681..155827),
complement(AL392085.12:123954..124121),
complement(AL392085.12:92563..92647),
complement(AL392085.12:91976..92050),
complement(AL392085.12:91070..91207),
complement(AL157829.24:141920..142070),
complement(AL157829.24:98954..99120),
complement(AL157829.24:83969..84157),
complement(AL157829.24:11736..11860),
complement(AL157829.24:7329..7433),
complement(AL157829.24:4108..4287),
complement(AL133284.13:85231..85496),
complement(AL133284.13:54013..54146),
complement(AL133284.13:52027..52175),
complement(AL133282.15:51488..51629),
complement(AL133282.15:6582..6682),
complement(AL133282.15:4738..4921),
complement(AL137024.27:148623..148860))
/gene="ASTN2"
/locus_tag="RP11-45A16.2-001"
/standard_name="OTTHUMP00000022742"
/note="match: proteins: O14525 O60799 O75129 O75998 Q61137
Q9QY74 Q9UHW6"
/codon_start=1
/product="astroractin 2"
/protein_id="CAH71966.1"
/db_xref="GI:55664665"
/db_xref="GOA:Q5VXG8"
/db_xref="InterPro:IPR001862"
/db_xref="InterPro:IPR003961"
/db_xref="UniProt/TREMBL:Q5VXG8"
/translation="MAAAGARLSPGPGSLRGPRLCFHPGPPPLPLLLFLLLLP
PPLLAGATAASREDPSPCLKTVTSTLPALRSDIDGWSGARAGAGTGAAGAAAA
ASPGSGSAGTAESRLLLFVRNELPGRIAVQDDLDNGETLFFFTLEMSGTAADISLVH
WRQWLNGTLFHVSMSSGLOAQATPTLOBPSEIVEEQMHILHISVMGGLIALLL
LLLFTVALYAQRWQKRRRIPOKSASTEATHIHYIPSVLLGPQARESFRSRLQTH
NSVIGVPIRETPIILDYDCEEDEPPRRANHVRSREDFGQVTHTLDSLGHPEEKVD
FEKGGISFGRAKGTSGSEADDETQLTFYTEQYRSRRRSKGLKSPVNNKTALTLIAS
SCILAMVCGSQMSCPLTVKTVLHVPEHFIADGSSFVSEGSYLDISDLNPAKLSLY
QINATSPVWRDLCGORTDACEQLCDPTGECSCHEGAPDPVHRHLCVRSDWGQSEG
PWPYTTLERGYDLVTGEQAPEKILRSTFSLGQLWLPVSKSFVVPVELSINPLASCK
TDVLVTEDPADVREBAMLSTYFETINDLLSFGPVRDCSRNNGGCTRNFKCVSDRQVD
SGCVCPEELKPMKDGSGCYDHSKIGIDCSGNGGCEQLCLQTLPLPYDATSSTIFM
FCGCVEEYKLAPDGKCLMLSDVCEGPKCLKPDSKFNDTLFGEMLHGVNRTQHVNQG
QVFQMTFRENNFTKDFPQLADGLLVIPLPVEEQRGVLSSEPLDQLLTGDIRYDEAM
GYPMVQWRVRSNLYRVKLSITITLAAGFTNVLKILTKESSRELLSFIQHYGSHYIAE
ALYGSELTCTIIHFPSSKKVQQLWLQYQKETTGLSKKELKSMPTFITYLSGLLTAQMLS
DDQLISGVEIRCEEKRCPSTCHLCRRPGKEQLSPTPVLLEINRVVPLYTLIQDNGTK
EAFKSALMSSYWCSGKGDVIDDWCRCDLSAFDANGLPNCSPLLQPVLRLSPTVEPSST
VVSLEWVDVQPAIGTKVSDYILQHKKVDEYTDITLYTGEFLSFADLLSGLGTSVAA
GRSHGEVPEVSIYSVIPKCLEPDLGYKFTLYAVDTRGRHSELSTVTLRTACPLVDDNK
ABEIADKIYNLYNGYTSKGEQQMAYNTLMESASMLFRVQHHYNSHYEKFPGDFVWRSE
DELGPRKAHLILRLERVSSHCSLLRSAYIQSVETVTPYLFRCRSEEVREPAGMWYSI
LKDTKITCEEKVMVSNARNTYGESGR"

misc_feature
misc_feature
misc_feature

/note="Clone right_end: RP11-567J2"
123824..123876
/note="Single clone region. Assembly confirmed by
restriction digest data."
126530..127179
/note="Single clone region. Sequence from reads from a
short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."

misc_feature 164932
/note="Clone_left_end: RP11-388N2"
ORIGIN
Query Match 91.1%; Score 16.4; DB 8; Length 166931;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
Db 94228 CCACACCTAGTCATCTC 94211
RESULT 51
AL606976/c 169465 bp DNA linear ROD 20-JUN-2002
LOCUS
DEFINITION
Mouse DNA sequence from clone RP23-113P22 on chromosome 4, complete
sequence.
ACCESSION
AL606976
VERSION
AL606976.25 GI:21537445
KEYWORDS
HTG.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 169465)
Pandian,R.
Direct Submission
Submitted (31-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 21, 2002 this sequence version replaced gi:21213218.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:.,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-113P22 is
from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6.
Location/Qualifiers
1..169465
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-113P22"
/clone_lib="RPCI-23"
FEATURES
source
1..169465
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-113P22"
/clone_lib="RPCI-23"
ORIGIN
Query Match 91.1%; Score 16.4; DB 9; Length 169465;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
Db 137483 CCACACCTATTTCATAATC 137466

RESULT 52	CR385076	172382 bp	DNA	linear	VRT 03-MAY-2005
LOCUS	Zebrafish DNA sequence from clone DKEY-230H18 in linkage group 2, complete sequence.				
DEFINITION	CR385076				
ACCESSION	CR385076.8	GI:62954692			
VERSION	HTG.				
KEYWORDS	Danio rerio (zebrafish)				
SOURCE	Danio rerio				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.				
REFERENCE	1 (bases 1 to 172382)				
AUTHORS	Hunter,G.				
TITLE	Direct Submission				
JOURNAL	Submitted (03-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk				
COMMENT	On Apr 28, 2005 this sequence version replaced gi:62909866. ----- Genome Center Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: zfish-help@sanger.ac.uk ----- During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted. Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-230H18 is from a Zebrafish BAC library VECTOR: pindigoBAC-5. Location/Qualifiers 1. 172382 /organism="Danio rerio" /mol_type="genomic DNA" /db_xref="taxon:7955" /clone="DKEY-230H18" /clone_lib="Daniokey"				
FEATURES	source				
ORIGIN	Query Match 91.1%; Score 16.4; DB 5; Length 172382; Best Local Similarity 94.4%; Pred. No. 3e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0; QY 1 CCACACCTATTTCATCTC 18 Db 144941 CCACACCATTCATCTC 144958				

RESULT 53	AC024399	185323 bp	DNA	linear	HTG 04-JUN-2000
LOCUS	Homo sapiens clone RP11-516D7, WORKING DRAFT SEQUENCE, 12 unordered pieces.				
DEFINITION	AC024399				
ACCESSION	AC024399.3	GI:8247873			
VERSION	HTG; HTGS_PHASE1; HTGS_DRAFT.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 185323)				
AUTHORS	Birren,B., Linton,L., Nusbaum,C. and Lander,E.				
TITLE	Homo sapiens, clone RP11-516D7				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 185323)				
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Landers,T., Largocque,K., Lehoczky,J., Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA				
COMMENT	On Jun 4, 2000 this sequence version replaced gi:7342078. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html ----- Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information Center project name: L6755 Center clone name: 516_D_7 ----- Summary Statistics Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 174909 bases at least Q40 Consensus quality: 180249 bases at least Q30 Consensus quality: 182452 bases at least Q20 Insert size: 188000; agarose-fp Insert size: 184223; sum-of-contigs Quality coverage: 4.7 in Q20 bases; agarose-fp Quality coverage: 4.8 in Q20 bases; sum-of-contigs ----- * NOTE: This is a 'working draft' sequence. It currently * consists of 12 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.				

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1520: contig of 1520 bp in length
* 1521 1620: gap of 100 bp
* 1621 4220: contig of 2600 bp in length
* 4221 4320: gap of 100 bp
* 4321 6884: contig of 2564 bp in length
* 6885 6984: gap of 100 bp
* 6985 10741: contig of 3757 bp in length
* 10742 10841: gap of 100 bp
* 10842 14568: contig of 3727 bp in length
* 14569 14668: gap of 100 bp
* 14669 22794: contig of 8126 bp in length
* 22795 22894: gap of 100 bp
* 22895 31230: contig of 8336 bp in length
* 31231 31330: gap of 100 bp
* 31331 45469: contig of 14139 bp in length
* 45470 45569: gap of 100 bp
* 45570 65126: contig of 19557 bp in length
* 65127 65226: gap of 100 bp
* 65227 92039: contig of 26813 bp in length
* 92040 92139: gap of 100 bp
* 92140 128331: contig of 36192 bp in length
* 128332 128431: gap of 100 bp
* 128432 185323: contig of 56892 bp in length.

FEATURES

source 1. .185323
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="RP11-516D7"
/clone_lib="RP11-516D7"
1. .1520
/note="assembly_fragment"
1521. .1620
/estimated_length=100
1621. .4220
/note="assembly_fragment"
4221. .4320
/estimated_length=100
4321. .6884
/note="assembly_fragment"
6885. .6984
/estimated_length=100
6985. .10741
/note="assembly_fragment"
10742. .10841
/estimated_length=100
10842. .14568
/note="assembly_fragment"
14569. .14668
/estimated_length=100
14669. .22794
/note="assembly_fragment"
22795. .22894
/estimated_length=100
22895. .31230
/note="assembly_fragment"
31231. .31330
/estimated_length=100
31331. .45469
/note="assembly_fragment"
45470. .45569
/estimated_length=100
45570. .65126
/note="assembly_fragment"
65127. .65226
/estimated_length=100
65227. .92039
/note="assembly_fragment"
clone_end:77
vector_side:right"

gap 92040. .92139
/estimated_length=100
misc_feature 92140. .128331
/note="assembly_fragment"
gap 128332. .128431
/estimated_length=100
misc_feature 128432. .185323
/note="assembly_fragment"
clone_end:SP6
vector_side:left"

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 185323;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 87585 CCACACCTATTCTACTC 87602

RESULT 54
AL6711173/c 201741 bp DNA linear ROD 25-JUL-2002
LOCUS AL6711173
DEFINITION Mouse DNA sequence from clone RP23-426N4 on chromosome 4, complete
sequence.
ACCESSION AL6711173 GI:21955531
VERSION AL6711173.12
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 201741)
AUTHORS Leongamornlert,D.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 25, 2002 this sequence version replaced gi:21738473.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-426N4 is from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6.

FEATURES

source Location/Qualifiers
1. .201741
/organism="Mus musculus"
/mol_type="genomic DNA"

<div><div>/db_xref="taxon:10090"</div><div>/chromosome="4"</div><div>/clone="RP23-426N4"</div><div>/clone_lib="RPCI-23"</div></div>									
ORIGIN									
<div><div>Query Match</div><div>Best Local Similarity</div><div>Matches</div><div>17; Conservative</div><div>91.1%; Score 16.4; DB 9; Length 201741; Pred. No. 3e+02; 0; Mismatches 1; Indels 0; Gaps 0;</div></div>									
QY	1	CCACACCTATTTCATCACTC	18						
Db	157556	CCACACATATTTCATCACTC	157539						
RESULT 55									
AC123163									
LOCUS	AC123163	209355 bp	DNA	linear	HTG 13-MAY-2003				
DEFINITION	Rattus norvegicus clone CH230-165P8, *** SEQUENCING IN PROGRESS								
***, 3 unordered pieces.									
AC123163									
AC123163.5	GI:30579265								
VERSION	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.								
KEYWORDS	Rattus norvegicus (Norway rat)								
SOURCE	Rattus norvegicus								
ORGANISM	Rattus norvegicus								
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.									
1 (bases 1 to 209355)									
REFERENCE									
AUTHORS	Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alibrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokemeleh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmami,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.								
Direct Submission									
Unpublished									
2 (bases 1 to 209355)									
Worley,K.C.									
Direct Submission									
Submitted (29-MAY-2002)	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA								
3 (bases 1 to 209355)									
Rat Genome Sequencing Consortium.									
Direct Submission									
Submitted (13-MAY-2003)	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA								
On May 13, 2003	this sequence version replaced gi:25188596.								
The sequence in this assembly	is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.								
-----	Genome Center								
Center:	Baylor College of Medicine								
Center code:	BCM								
Web site:	http://www.hgsc.bcm.tmc.edu/								
Contact:	hgsc-help@bcm.tmc.edu								
-----	Project Information								
Center project name:	GMNO								
Center clone name:	CH230-165P8								
-----	Summary Statistics								
Assembly program:	Atlas 3.0;								
Consensus quality:	190762 bases at least Q40								
Consensus quality:	194365 bases at least Q30								
Consensus quality:	197548 bases at least Q20								
Estimated insert size:	204166; sum-of-contigs estimation								
Quality coverage:	5x in Q20 bases; sum-of-contigs estimation								

* NOTE:	Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).								
* NOTE:	This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces								
* is not known	and their order in this sequence record is arbitrary. Gaps between the contigs are represented as								
* runs of N,	but the exact sizes of the gaps are unknown.								
* This record	will be updated with the finished sequence as soon as it is available and the accession number will								
* be preserved.									
* 1	182365: contig of 182365 bp in length								
* 182366	182465: gap of unknown length								
* 182466	208006: contig of 25541 bp in length								
* 208007	208106: gap of unknown length								
* 208107	209355: contig of 1249 bp in length.								
Location/Qualifiers									
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/organism="Rattus norvegicus"									
/mol_type="genomic DNA"									
/db_xref="taxon:10116"									
/clone="CH230-165P8"									
1. .1679									
/note="wgs_end_extension"									
clone_end:Sp6"									
3627. .4180									
FEATURES									
source									

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gap					
gap					
ORIGIN					
Query Match		91.1%;	Score 16.4;	DB 14;	Length 209355;
Best Local Similarity		94.4%;	Pred. No. 3e+02;		
Matches 17; Conservative		0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	CCACACCTATTTCATCTC	18		
Db		203249	CCACACCCATTCATCTC	203266	
RESULT 56					
AC118365/c					
LOCUS					
DEFINITION		AC118365	212446 bp	DNA	linear
		Rattus norvegicus clone CH230-273H4, *** SEQUENCING IN PROGRESS			
		***.			
ACCESSION		AC118365			
VERSION		AC118365.3	GI:22856535		
KEYWORDS		HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.			
SOURCE		Rattus norvegicus (Norway rat)			
ORGANISM		Rattus norvegicus			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.			
AUTHORS		1 (bases 1 to 212446)			
		Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokeleme,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.			
		Direct Submission			
		Unpublished			
		2 (bases 1 to 212446)			
		Worley,K.C.			
		Direct Submission			
		Submitted (17-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
		3 (bases 1 to 212446)			
		Rat Genome Sequencing Consortium.			
		Direct Submission			
		Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
		On Sep 14, 2002 this sequence version replaced gi:21745733.			
		The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.			
		----- Genome Center			
		Center: Baylor College of Medicine			
		Center code: BCM			
		Web site: http://www.hgsc.bcm.tmc.edu/			
		Contact: hgsc-help@bcm.tmc.edu			
		----- Project Information			
		Center project name: GTTT			
		Center clone name: CH230-273H4			
		----- Summary Statistics			
		Assembly program: Phrap; version 0.990329			
		Consensus quality: 183516 bases at least Q40			
		Consensus quality: 186007 bases at least Q30			
		Consensus quality: 187853 bases at least Q20			
		Estimated insert size: 196344; sum-of-contigs estimation			
		Quality coverage: 4x in Q20 bases; sum-of-contigs estimation			

		* NOTE: Estimated insert size may differ from sequence length			
		* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).			
		* NOTE: This is a 'working draft' sequence. It currently			
		* consists of 1 contigs. Gaps between the contigs			
		* are represented as runs of N. The order of the pieces			
		* is believed to be correct as given, however the sizes			
		* of the gaps between them are based on estimates that have			
		* provided by the submittor.			
		* This sequence will be replaced			
		* by the finished sequence as soon as it is available and			
		* the accession number will be preserved.			
		* 1 212446: contig of 212446 bp in length.			
		* Location/Qualifiers			
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		/db_xref="taxon:10116"			
		/clone="CH230-273H4"			
		1. .1081			
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		source			
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gap /estimated_length=100
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ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 221392;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACACTATTTCATCTC 18
|||||
Db 134193 CCACACTATTTCATACCC 134176

RESULT 59

AC098768/c

LOCUS

DEFINITION AC098768 221397 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-184P12, WORKING DRAFT SEQUENCE, 2

unordered pieces.

AC098768

AC098768.5 GI:30581306

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 221397)

REFERENCE

AUTHORS

Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
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Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
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Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
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Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
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Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montenayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Fränkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,

Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
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Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Umani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Woodden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

Direct Submission

Unpublished

2 (bases 1 to 221397)

Worley,K.C.

Direct Submission

Submitted (01-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 221397)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23268156.

The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GIRW

Center clone name: CH230-184P12

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 198467 bases at least Q40

Consensus quality: 201844 bases at least Q30

Consensus quality: 203826 bases at least Q20

Estimated insert size: 209357; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 11412: contig of 11412 bp in length

* 11413 11512: gap of unknown length

* 11513 221397: contig of 209885 bp in length.

Location/Qualifiers

1. 221397

/organism="Rattus norvegicus"

FEATURES
source

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11413. .11512
/estimated_length=unknown
11513. .13645
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complement(205657. .206268)
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clone_end:T7
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end sequence:BH261429"
218210. .221397
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clone_end:T7"

ORIGIN
Query Match      91.1%; Score 16.4; DB 14; Length 221397;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATCTC 18
      |||||
Db      146811 CCACACCTATCCATCTC 146794

RESULT 60
AC162180
LOCUS      AC162180      226160 bp      DNA      linear      ROD 30-JUL-2005
DEFINITION Mus musculus BAC clone RP23-126K16 from chromosome 9, complete
sequence.
AC162180 AC113972
VERSION   AC162180.2 GI:71533498
KEYWORDS  HTG.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 226160)
AUTHORS   Kanchi,K., Kozlowicz,A., Levy,A., Bielicki,L. and Haglund,K.
TITLE     The sequence of Mus musculus BAC clone RP23-126K16
JOURNAL   Unpublished (2001)
REFERENCE 2 (bases 1 to 226160)
AUTHORS   Wilson,R.K.
TITLE     Direct Submission
JOURNAL   Submitted (25-MAY-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 226160)
AUTHORS   Wilson,R.K.
TITLE     Direct Submission
JOURNAL   Submitted (30-JUL-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT   On Jul 30, 2005 this sequence version replaced gi:66571672.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
Center project name: M_BA0126K16
Drafting center: WIBR
```

NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.

This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is minimal.

If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

This sequence is the entire insert of the clone.

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FEATURES
source      Location/Qualifiers
1. .226160
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           /mol_type="genomic DNA"
           /db_xref="taxon:10090"
           /chromosome="9"
           /clone="RP23-126K16"
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           63376. .63467
misc_feature /note="Sequence derived from PCR product of project DNA"
           161629. .161909
unsure      /note="Unresolved simple sequence repeat."
           220317. .220375
misc_feature /note="Sequence derived from PCR product of project DNA"
           220785. .221239
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ORIGIN
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Query Match      91.1%; Score 16.4; DB 9; Length 226160;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATCTC 18
      |||||
Db      121803 CCACACATATTCATCTC 121820
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Search completed: May 10, 2006, 19:26:09
Job time : 1996 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM nucleic - nucleic search, using sw model
Run on: May 10, 2006, 02:29:57 ; Search time 672 Seconds
(without alignments)
178.519 Million cell updates/sec

Title: US-10-608-296-38
Perfect score: 18
Sequence: 1 ccacacctattcatactc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : N_Geneseq_21:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	ADI35111	Adi35111 Human PLA
2	18	100.0	18	ADJ10012	Adj10012 Extension
3	18	100.0	224	ABV98192	Abv98192 Human pan
4	18	100.0	224	ABV98533	Abv98533 Human pan
5	18	100.0	224	ABV97702	Abv97702 Human pan
6	18	100.0	224	ABV98622	Abv98622 Human pan
7	18	100.0	224	ABV97592	Abv97592 Human pan
8	18	100.0	224	ABV98196	Abv98196 Human pan
9	18	100.0	418	ADU12907	Adu12907 Solid tum
10	18	100.0	445	AAC99186	Aac99186 Human pan
11	18	100.0	447	ABK47377	Abk47377 Human Pho
12	18	100.0	447	ADV43454	Adv43454 Human psy
13	18	100.0	496	AAH57324	Aah57324 Human pan
14	18	100.0	562	AAA35100	Aaa35100 Human ade
15	18	100.0	562	AAF21222	Aaf21222 Human low
16	18	100.0	562	ABL64906	Ab164906 Lung canc
17	18	100.0	562	ABL65512	Ab165512 Lung canc
18	18	100.0	562	ABL65915	Ab165915 Lung canc
19	18	100.0	562	ABZ96916	Abz96916 Human nuc

20	18	100.0	562	11	ADI31874	Adi31874 Human CDN
21	18	100.0	562	11	ABD20765	Abd20765 Human pul
22	18	100.0	562	13	ADS83941	Ads83941 Human lym
23	18	100.0	585	12	ADO28598	Ado28598 Human PA2
24	18	100.0	630	3	AAC98824	Aac98824 Human pan
25	18	100.0	644	2	AAZ41391	Aaz41391 Human nor
26	18	100.0	654	4	AAH57532	Aah57532 Human pan
27	18	100.0	654	5	AAS76099	Aas76099 DNA encod
28	18	100.0	742	13	ACN42348	Acn42348 Human dia
29	18	100.0	3375	3	AAA35101	Aaa35101 Human ade
30	18	100.0	3375	3	AAF21223	Aaf21223 Human low
31	18	100.0	3375	10	ABZ96917	Abz96917 Human nuc
32	18	100.0	3375	11	ABD20766	Abd20766 Human pul
33	18	100.0	6771	3	AAA35103	Aaa35103 Human ade
34	18	100.0	6771	3	AAF21225	Aaf21225 Human low
35	18	100.0	6771	10	ABZ96919	Abz96919 Human nuc
36	18	100.0	6771	11	ABD20768	Abd20768 Human pul
37	18	100.0	12174	12	ADI35082	Adi35082 Human PLA
38	18	100.0	12174	12	ADJ09983	Adj09983 Human pho
39	18	100.0	13612	6	ABK47376	Abk47376 Human Pho
40	16	88.9	224	6	ABV95110	Abv95110 Human pan
41	15.4	85.6	611	13	ACN46442	Acn46442 Cotton pr
42	15.4	85.6	1733	13	ADR60118	Adr60118 Cotton CD
43	15.4	85.6	3093	6	ABZ13765	Abz13765 Arabidops
44	15.4	85.6	3093	7	ADZ75114	Adz75114 Arabidops
45	15.4	85.6	3120	10	ADE52630	Ades52630 Caenorhab
46	15.4	85.6	8528	2	AAQ46249	Aaq46249 Construct
47	15.4	85.6	17934	6	ABL33718	Ab133718 Human imm
48	15.4	85.6	110000	11	ACN44150_0	Acn44150 Human gen
49	15.4	85.6	118777	12	ADP44620	Adp44620 Murine al
50	15	83.3	544	6	ABQ28339	Abq28339 Oligonucl
51	15	83.3	544	6	ABQ28338	Abq28338 Oligonucl
52	15	83.3	3951	12	ADQ63331	Adq63331 Novel hum
53	14.8	82.2	362	3	AAA69665	Aaa69665 Pinus rad
54	14.8	82.2	466	6	ABZ08767	Abz08767 Human leu
55	14.8	82.2	506	8	ACC62584	Acc62584 Rice endo
56	14.8	82.2	584	12	ACH91848	Ach91848 Human gen
57	14.8	82.2	591	6	ABQ20739	Abq20739 Oligonucl
58	14.8	82.2	591	6	ABQ20738	Abq20738 Oligonucl
59	14.8	82.2	601	6	ABQ26403	Abq26403 Oligonucl
60	14.8	82.2	601	6	ABQ26402	Abq26402 Oligonucl
61	14.8	82.2	619	6	ABQ46422	Abq46422 Oligonucl
62	14.8	82.2	619	6	ABQ46423	Abq46423 Oligonucl
63	14.8	82.2	621	6	ABQ50029	Abq50029 Oligonucl
64	14.8	82.2	621	6	ABQ50028	Abq50028 Oligonucl
65	14.8	82.2	834	9	ADA28759	Ada28759 DNA encod
66	14.8	82.2	907	6	AAD40514	Aad40514 Human org
67	14.8	82.2	1293	6	ABQ72697	Abq72697 Human MDD
68	14.8	82.2	1597	13	ADX15056	Adx15056 Plant ful
69	14.8	82.2	1719	6	AAD40519	Aad40519 Human org
70	14.8	82.2	1835	11	ADM02866	Adm02866 Human CDN
71	14.8	82.2	2009	4	AAH17000	Aah17000 Human CDN
72	14.8	82.2	2500	14	ADV98063	Adv98063 Bisulfite
73	14.8	82.2	2582	4	ABL23978	Ab123978 Drosophil
74	14.8	82.2	2698	4	ABL16108	Ab116108 Drosophil
75	14.8	82.2	2841	4	ABL23980	Ab123980 Drosophil
76	14.8	82.2	2965	4	AAS26099	Aas26099 Human CDN
77	14.8	82.2	2965	8	ABX73440	Abx73440 Human nov
78	14.8	82.2	2970	4	AAS26029	Aas26029 Human CDN
79	14.8	82.2	2970	8	ABX73370	Abx73370 Human nov
80	14.8	82.2	2984	6	ABA01095	AbA01095 Brevibact
81	14.8	82.2	3237	10	ADB62874	Adb62874 Human CDN
82	14.8	82.2	3692	4	AAC89368	Aac89368 Human org
83	14.8	82.2	3692	14	ADZ49774	Adz49774 Insulin s
84	14.8	82.2	3725	4	AAH17635	Aah17635 Human CDN
85	14.8	82.2	3725	6	ABZ11378	Abz11378 Human pol
86	14.8	82.2	3725	12	ADM43896	Adm43896 Novel hum
87	14.8	82.2	4345	12	ADQ24757	Adq24757 Human sof
88	14.8	82.2	4456	6	ABS73865	Abs73865 Human CDN
89	14.8	82.2	6141	4	ABA07105	AbA07105 Human pan
90	14.8	82.2	6141	4	AAK89317	Aak89317 Human dig
91	14.8	82.2	7500	6	ABL33114	Ab133114 Human imm
92	14.8	82.2	13831	4	ABK42498	Abk42498 Genomic s

c	93	14.8	82.2	13831	9	ADB60654	Adb60654	Connectiv
c	94	14.8	82.2	13832	4	ABK42497	Abk42497	Genomic s
c	95	14.8	82.2	13832	9	ADB60653	Adb60653	Connectiv
c	96	14.8	82.2	15743	6	ABK28395	Abk28395	DNA trans
c	97	14.8	82.2	18001	14	AEb95154	Aeb95154	Mouse eIF
c	98	14.8	82.2	28974	4	AAK69977	Aak69977	Human imm
c	99	14.8	82.2	28974	4	AAS32821	Aas32821	Human gen
	100	14.8	82.2	29360	12	ADQ97189	Adq97189	Human can
	101	14.8	82.2	46765	6	AAS99306	Aas99306	DNA encod
	102	14.8	82.2	70549	12	ADQ97436	Adq97436	Mouse can
c	103	14.8	82.2	85873	10	ADH10008	Adh10008	Human chr
	104	14.8	82.2	99544	14	ADZ13273	Adz13273	Human can
	105	14.8	82.2	99588	11	ACN45034	Acn45034	Human gen
	106	14.8	82.2	110000	11	ACN44582_2	Continuation (3 of	
	107	14.8	82.2	110000	13	ABD32535_2	Continuation (3 of	
	108	14.8	82.2	110000	14	ADZ13035_2	Continuation (3 of	
	109	14.8	82.2	126990	12	ADP13332	Adp13332	Renal cel
c	110	14.8	82.2	140152	12	ADP03002	Adp03002	Human hou
c	111	14.8	82.2	140152	13	ADS88500	Ads88500	Human hou
c	112	14.8	82.2	140152	13	ADU60105	Adu60105	Housekeep
	113	14.8	82.2	158417	13	ADS36461	Ads36461	Human aut
c	114	14.8	82.2	166043	12	ADL08127	Adl08127	Human gen
	115	14.8	82.2	199868	12	ADQ97831	Adq97831	Mouse can
c	116	14.8	82.2	201143	6	ABK83568	Abk83568	Human DNA
c	117	14.8	82.2	227448	13	ABD32841	Abd32841	Mouse can
c	118	14.8	82.2	277616	13	ABD32602	Abd32602	Human can
c	119	14.4	80.0	100	10	ADG70411	Adg70411	CLLD7 SNP
	120	14.4	80.0	204	6	ABS72727	Abs72727	Human gen
c	121	14.4	80.0	317	2	AAT22909	Aat22909	Human gen
	122	14.4	80.0	337	6	ABL78789	Ab178789	Human ova
	123	14.4	80.0	342	6	ABL82353	Ab182353	Human ova
	124	14.4	80.0	377	3	AAF21688	Aaf21688	Human bre
	125	14.4	80.0	377	8	ABZ56640	Abz56640	Aspergill
c	126	14.4	80.0	401	9	ACH31727	Ach31727	Human bon
	127	14.4	80.0	477	6	ABV95161	Abv95161	Human pan
	128	14.4	80.0	549	4	AAH11500	Aah11500	Human pan
c	129	14.4	80.0	628	10	ADF50179	Adf50179	Salmonell
	130	14.4	80.0	640	5	AAH88067	Aah88067	Peppermin
	131	14.4	80.0	739	10	ADF50162	Adf50162	Salmonell
	132	14.4	80.0	825	4	AAL23514	Aal23514	Human bre
	133	14.4	80.0	1428	13	ADS58395	Ads58395	Bacterial
	134	14.4	80.0	1476	5	AAS79679	Aas79679	DNA encod
	135	14.4	80.0	1677	8	ACA44458	Aca44458	Prokaryot
	136	14.4	80.0	1728	10	ADF03105	Adf03105	Bacterial
	137	14.4	80.0	1953	10	ADG77038	Adg77038	Human nuc
c	138	14.4	80.0	2316	10	ADG70165	Adg70165	Human CLL
	139	14.4	80.0	2480	12	ADP56492	Adp56492	Human bre
c	140	14.4	80.0	2902	4	AAH14457	Aah14457	Human cDN
c	141	14.4	80.0	3152	8	ABT17714	Abt17714	Aspergill
c	142	14.4	80.0	3154	10	ADB61996	Adb61996	Human cDN
c	143	14.4	80.0	3790	8	AAD50838	Aad50838	Pig BAC 8
c	144	14.4	80.0	4015	11	ADM02730	Adm02730	Human cDN
c	145	14.4	80.0	4037	6	ABS78715	Abs78715	Human cDN
	146	14.4	80.0	4434	12	ADO60128	Ado60128	Human TFA
c	147	14.4	80.0	4590	8	AAD50839	Aad50839	Pig BAC 9
	148	14.4	80.0	5900	8	ACC50312	Acc50312	Breast ca
	149	14.4	80.0	7179	2	AAZ21006	Aaz21006	Salmonell
c	150	14.4	80.0	7443	13	ADR84285	Adr84285	Aspergill

ALIGNMENTS

RESULT 1
ADI35111
ID ADI35111 standard; DNA; 18 BP.

XX
AC ADI35111;
XX
DT 22-APR-2004 (first entry)
XX Human PLA2G1B fragment hybridising extension oligonucleotide.
DE
XX

KW PLA2G1B; fat deposition; leanness; single nucleotide polymorphism;
KW non-insulin dependent diabetes mellitus; NIDDM; hyperinsulinemia;
KW hypertension; glucose intolerance; dyslipidemia; hypercoagulability;
KW microalbuminuria; ss; SNP.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004002295-A2.
XX
PD 08-JAN-2004.
XX
PF 27-JUN-2003; 2003WO-US020830.
XX
PR 27-JUN-2002; 2002US-0392361P.
XX (SEQU-) SEQUENOM INC.
PA Adam GIR, Langdown ML;
PI WPI; 2004-082843/08.
XX
DR
XX
PT Diagnosing a predisposition to fat deposition or leanness, useful for
PT diagnosing a predisposition to e.g. diabetes or hypertension, comprises
PT detecting the presence of a polymorphism in the PLA2G1B nucleic acid from
the subject.
PS Claim 8; Page 63; 91pp; English.
XX
CC The invention relates to diagnosing a predisposition to fat deposition or
CC leanness in a subject comprising detecting the presence or absence of a
CC polymorphic variation associated with fat deposition at a polymorphic
CC site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a
CC subject, where the presence of the polymorphic variation indicates a
CC predisposition to fat deposition in the subject. The polymorphic
CC variation is a guanine at position 7328 or thymine at position 9182 of
CC the present sequence. The method is useful for diagnosing a
CC predisposition to fat deposition or leanness in a subject, and
CC consequently for diagnosing a predisposition to non-insulin dependent
CC diabetes mellitus (NIDDM) in a subject and conditions such as
CC hyperinsulinemia, hypertension, glucose intolerance, dyslipidemia,
CC hypercoagulability, or microalbuminuria, which can lead to early
CC prescription of preventive measures. Sequences ADI35104-ADI35113
CC represent exemplary extension oligonucleotides that hybridise to a region
CC of the PLA2G1B sequence that is adjacent to the polymorphic variation.
XX
SQ Sequence 18 BP; 5 A; 8 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCACACCTATTTCATACTC 18
| | | | | | | | | | | | | | | |
Db 1 CCACACCTATTTCATACTC 18
RESULT 2
ADJ10012
ID ADJ10012 standard; DNA; 18 BP.
XX
AC ADJ10012;
XX
DT 17-JUN-2004 (first entry)
XX
DE Extension DNA oligo 3 for human phopholipase A2 DNA.
XX
KW ss; human; fat deposition; phospholipase A2; PLA2G1B;
KW appetite suppressant; lipase inhibitor; exercise regimen; obesity;
KW non-insulin dependent diabetes mellitus; NIDDM; cardiovascular disorder;
KW hypertension; antidiabetic; primer; fat reduction.
XX
OS Homo sapiens.

PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
DR WPI; 2002-627435/67.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
PS Claim 1; SEQ ID NO 3941; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 224 BP; 68 A; 68 C; 37 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 5 CCACACCTATTCTACTC 22

RESULT 5
ABV97702
ID ABV97702 standard; cDNA; 224 BP.
XX
AC ABV97702;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 3110.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.

PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
DR WPI; 2002-627435/67.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
PS Claim 1; SEQ ID NO 3110; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 224 BP; 69 A; 67 C; 36 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 5 CCACACCTATTCTACTC 22

RESULT 6
ABV98622
ID ABV98622 standard; cDNA; 224 BP.
XX
AC ABV98622;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 4030.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.

PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0305484P.
PR 27-NOV-2001; 2001US-0313999P.
XX
XX (CORI-) CORIXA CORP.
PA
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI
XX WPI; 2002-627435/67.
DR
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
PT
XX
PS Claim 1; SEQ ID NO 4030; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 224 BP; 68 A; 68 C; 37 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 5 CCACACCTATTCTACTC 22

RESULT 7
ABV97592
ID ABV97592 standard; cDNA; 224 BP.
XX
XX AC ABV97592;
XX
XX 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 3000.
XX
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytotstatic; tumour; gene; ss.
XX
XX Homo sapiens.
OS
XX WO200260317-A2.
PN
XX
PD 08-AUG-2002.
XX
XX 30-JAN-2002; 2002WO-US002781.
PF
XX
XX 30-JAN-2001; 2001US-0265305P.
PR
PR 31-JAN-2001; 2001US-0265682P.
PR
PR 09-FEB-2001; 2001US-0267568P.
PR
PR 21-MAR-2001; 2001US-0278651P.
PR
PR 28-APR-2001; 2001US-0287112P.

PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
XX (CORI-) CORIXA CORP.
PA
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI
XX WPI; 2002-627435/67.
DR
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
PT
XX
PS Claim 1; SEQ ID NO 3000; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 224 BP; 68 A; 69 C; 37 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 5 CCACACCTATTCTACTC 22

RESULT 8
ABV98196
ID ABV98196 standard; cDNA; 224 BP.
XX
XX AC ABV98196;
XX
XX 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 3604.
XX
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytotstatic; tumour; gene; ss.
XX
XX Homo sapiens.
OS
XX WO200260317-A2.
PN
XX
PD 08-AUG-2002.
XX
XX 30-JAN-2002; 2002WO-US002781.
PF
XX
XX 30-JAN-2001; 2001US-0265305P.
PR
PR 31-JAN-2001; 2001US-0265682P.
PR
PR 09-FEB-2001; 2001US-0267568P.
PR
PR 21-MAR-2001; 2001US-0278651P.
PR
PR 28-APR-2001; 2001US-0287112P.
PR
PR 16-MAY-2001; 2001US-0291631P.

PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
DR WPI; 2002-627435/67.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
PS Claim 1; SEQ ID NO 3604; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 224 BP; 68 A; 68 C; 37 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 5 CCACACCTATTTCATCTC 22

RESULT 9
ADU12907
ID ADU12907 standard; DNA; 418 BP.
XX
AC ADU12907;
XX
DT 27-JAN-2005 (first entry)
XX
DE Solid tumour prognosis gene seqid 3346.
XX
KW cytostatic; gene therapy; expression profile; solid tumour;
KW peripheral blood mononuclear cell; PBMC; prognosis; ds.
XX
OS Unidentified.
XX
PN WO2004097052-A2.
XX
PD 11-NOV-2004.
XX
PF 29-APR-2004; 2004WO-US013587.
XX
PR 29-APR-2003; 2003US-0466067P.
PR 23-JAN-2004; 2004US-0538246P.
XX
XX (AMHP) WYETH.
PA (STRA/) STRAHS A.
XX
PI Strahs A, Trepicchio WL, Burczynski ME, Twine NC, Slonim DK;

PI Immerman F, Dorner AJ;
XX
DR WPI; 2004-804779/79.
XX
PT A method, useful for prognosing and treating solid tumor, comprises
PT comparing an expression profile of a gene expressed in peripheral blood
PT mononuclear cells to a reference expression profile of a gene.
XX
PS Disclosure; Page; 111pp; English.
XX
CC The invention describes a method comprising comparing an expression
CC profile of at least one gene in a peripheral blood sample of a patient to
CC at least one reference expression profile of the at least one gene, where
CC the patient has a solid tumour, and each of the gene is differentially
CC expressed in peripheral blood mononuclear cells (PBMCs) of a first class
CC of patients as compared to PBMCs of a second class of patients, where
CC both the first and second classes of patients have the solid tumour, and
CC each of the first and second classes is a subcluster formed by an
CC unsupervised clustering analysis of gene expression profiles in PBMCs of
CC a population of patients who have the solid tumour, and where the
CC majority of the first class of patients has a first clinical outcome, and
CC the majority of the second class of patients has a second clinical
CC outcome. Also described are: a system comprising (i) a memory or a
CC storage medium including data that represent an expression profile of at
CC least one gene in a peripheral blood sample of a patient who has a solid
CC tumour, (ii) at least another storage medium including data that
CC represent at least one reference expression profile of the gene, (iii) a
CC program capable of comparing the expression profile to the reference
CC expression profile, and (iv) a processor capable of executing the
CC program, where expression levels of the gene in peripheral blood
CC mononuclear cells of patients who have the solid tumour correlate with
CC clinical outcomes of the patients; and a nucleic acid or protein array
CC comprising concentrated probes for solid tumour prognosis genes, where
CC each of the solid tumour prognosis genes is differentially expressed in
CC PBMCs of a first class of patients as compared to PBMCs of a second class
CC of patients, where both the first and second classes of patients have a
CC solid tumour, and where the first class of patients has a first clinical
CC outcome, and the second class of patients has a second clinical outcome.
CC The method, system, and array are useful for prognosing and treating
CC solid tumours. This sequence represents a solid tumour prognosis gene of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 418 BP; 105 A; 125 C; 104 G; 84 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 418;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 275 CCACACCTATTTCATCTC 292

RESULT 10
AAC99186
ID AAC99186 standard; cDNA; 445 BP.
XX
AC AAC99186;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:414.
XX
KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;
KW diagnosis; identification; cytostatic; neuroprotective; nootropic;
KW immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic; neural;
KW immune system; muscular; reproductive; gastrointestinal; pulmonary;
KW cardiovascular; renal; proliferative; ss.
XX

OS Homo sapiens.
XX WO200055320-A1.
XX
XX
PD 21-SEP-2000.
XX
XX
PF 08-MAR-2000; 2000WO-US005989.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM;
PI
XX
XX WPI; 2000-579444/54.
DR P-PSDB; AAB54421.
XX
XX
PT New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition.
XX
XX
PS Claim 1; Page 848; 1379pp; English.
XX
CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,
CC neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,
CC gynaecological, cardiant and antiinflammatory activities, and can be used
CC in gene therapy. The polynucleotide and proteins can be used for
CC preventing, treating, or ameliorating a medical condition or in assays
CC for diagnosing a pathological condition or a susceptibility to one in a
CC subject. Binding partners to the proteins and the activity of the
CC proteins can be identified. The pancreatic cancer antigens can be used to
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be used to design nucleic
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC analysis, tissue identification and/or typing and a variety of forensic
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 445 BP; 111 A; 135 C; 94 G; 96 T; 0 U; 9 Other;

Query Match 100.0%; Score 18; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 282 CCACACCTATTCTACTC 299
|||||

RESULT 11
ABK47377
ID ABK47377 standard; cDNA; 447 BP.
XX
AC ABK47377;
XX
DT 18-JUN-2002 (first entry)
XX
XX Human Phospholipase A2, groupIB (PLA2G1B) cDNA.
DE
XX Human; ss; gene; SNP; single nucleotide polymorphism; pancreatitis;
KW pancreatic cancer; Phospholipase A2 groupIB; PLA2G1B; gene therapy;
KW haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT 1..447
FT /*tag= a
FT /product= "Pla2G1B"
FT replace(294,A)
FT /*tag= h
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
FT replace(365,A)
FT /*tag= j
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
XX
XX WO200212562-A2.
PN
XX
XX PD 14-FEB-2002.
XX
XX
PF 06-AUG-2001; 2001WO-US024663.
XX
PR 04-AUG-2000; 2000US-0223179P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Kazemi A, Kliem SE, Koshy B;
XX
DR WPI; 2002-303982/34.
DR P-PSDB; AAU78667.
XX
PT Novel isolated human Phospholipase A2, Group IB pancreas polynucleotide,
PT for therapeutic purposes, for studying expression and function of the
PT polynucleotide and for expressing the phospholipase protein.
XX
PS Claim 27; Fig 2; 51pp; English.
XX
CC The invention relates to an isolated human Phospholipase A2, Group IB
CC (pancreas) (PLA2G1B) polynucleotide comprising a sequence which is a
CC polymorphic variant for a reference sequence for the PLA2G1B gene or its
CC fragment, or a polymorphic variant of a reference sequence for a PLA2G1B
CC cDNA or its fragment. Also included are a reference sequence for a PLA2G1B
CC PLA2G1B gene of an individual, predicting the haplotyping/genotyping the
CC PLA2G1B gene of an individual, identifying an association between a trait
CC and at least one haplotype or haplotype pair of the PLA2G1B gene, an
CC isolated genotyping oligonucleotide for detecting a polymorphism in the
CC PLA2G1B gene, a recombinant non-human organism transformed or transfected
CC with the PLA2G1B sequence, where the organism expresses a PLA2G1B protein
CC encoded by the first nucleotide sequence or by the polymorphic variant
CC sequence, an isolated polypeptide comprising a sequence which is a
CC polymorphic variant of a reference sequence for the PLA2G1B protein or
CC its fragment, an anti-PLA2G1B monoclonal antibody, screening for drugs
CC targeting PLA2G1B, a computer system for storing and analysing
CC polymorphism data for the PLA2G1B gene and a genome anthology for PLA2G1B
CC gene. The PLA2G1B variant is useful in studying the expression and
CC function of PLA2G1B, and in expressing PLA2G1B protein for use in
CC screening for candidate drugs to treat diseases related to PLA2G1B
CC activity (e.g. pancreatitis and pancreatic cancer) and for therapeutic
CC purposes. The transgenic organism is useful for studying expression of
CC the PLA2G1B isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against PLA2G1B protein, and for testing the efficacy of
CC therapeutic agents and compounds in a biological system. The antibody is
CC useful for studying the effect of the variation on the biological
CC activity of PLA2G1B as well as on the binding affinity of candidate drugs
CC targeting PLA2G1B. The PLA2G1B gene is located on chromosome 12q23-q24.1.
CC The present sequence is the cDNA encoding PLA2G1B
XX
SQ Sequence 447 BP; 116 A; 128 C; 112 G; 91 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 447;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 276 CCACACCTATTCTACTC 293
|||||

RESULT 12
ADV43454
ID ADV43454 standard; cDNA; 447 BP.
XX
AC
XX ADV43454;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1082.
XX
KW microarray; psychoneuroendocrinimmune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
XX 04-JUN-2004; 2004WO-US017686.
PF
XX 04-JUN-2003; 2003US-0475915P.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Nicholson A, Vernon SD;
PI
XX WPI; 2005-031682/03.
DR
XX New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
PT
XX Claim 1; SEQ ID NO 1082; 254pp; English.
PS
XX The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX
SQ Sequence 447 BP; 116 A; 128 C; 112 G; 91 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 14; Length 447;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 276 CCACACCTATTCTACTC 293

RESULT 13
AAH57324/c
ID AAH57324 standard; cDNA; 496 BP.
XX
AC
XX AAH57324;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human pancreas specific cDNA sequence SEQ ID NO:164.
XX
KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

XX Homo sapiens.
OS
XX WO200132927-A2.
PN
XX 10-MAY-2001.
PD
XX 02-NOV-2000; 2000WO-US030396.
PF
XX 04-NOV-1999; 99US-0163508P.
PR
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Sornasse T, Seilhamer JJ, Watson GA;
PI WPI; 2001-291057/30.
XX
PT New cell and tissue specific polynucleotides useful for diagnosis,
PT prognosis or monitoring of treatments for disorders where the gene is
PT associated with a cancer, immunopathology or neuropathology.
XX
PS Claim 1; Page 126; 327pp; English.
XX
CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC sequences (I). (I) can have cytostatic, immunomodulatory and
CC neuroprotective activities, and can be used in gene therapy. (I) and
CC proteins (II) encoded by then are used in high throughput screening
CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their
CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
CC agents. Expression of (I) in a sample indicates the differentiation of
CC embryonic stem cells into a tissue selected from brain, heart, kidney,
CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
CC to produce an expression profile that defines a metabolic or
CC developmental process, treatment, condition, disease or disorder. The
CC gene profile can be used for diagnosis, prognosis or monitoring of
CC treatments and for investigating a predisposition to a disorder where the
CC gene is associated with a cancer, immunopathology or neuropathology
XX
SQ Sequence 496 BP; 102 A; 120 C; 142 G; 127 T; 0 U; 5 Other;

Query Match 100.0%; Score 18; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 209 CCACACCTATTCTACTC 192

RESULT 14
AAA35100
ID AAA35100 standard; DNA; 562 BP.
XX
AC AAA35100;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2789.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX

PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 1056; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 562;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 313 CCACACCTATTTCATCTC 330

RESULT 15
AAF21222
ID AAF21222 standard; DNA; 562 BP.
XX
AC AAF21222;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2789.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Disclosure; Page 1135; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 562;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 313 CCACACCTATTTCATCTC 330

RESULT 16
ABL64906
ID ABL64906 standard; DNA; 562 BP.
XX
AC ABL64906;

XX 15-MAY-2002 (first entry)
DT Lung cancer related gene sequence SEQ ID NO:3243.
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
DE stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX Homo sapiens.
OS WO200194629-A2.
XX 13-DEC-2001.
PD 30-MAY-2001; 2001WO-US010838.
XX 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX (AVAL-) AVALON PHARM.
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
DR
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 3243; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 562;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATACTC 18
Db ||||||||||||||||
313 CCACACCTATTTCATACTC 330

RESULT 17
ABL65512
ID ABL65512 standard; DNA; 562 BP.
XX
AC ABL65512;
XX
DT 15-MAY-2002 (first entry)
XX
DE Lung cancer related gene sequence SEQ ID NO:3849.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
DR
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 3243; 44pp; English.

PR	27-SEP-2000; 2000US-0235863P.	DE	Lung cancer related gene sequence SEQ ID NO:4252.
PR	28-SEP-2000; 2000US-0236028P.	XX	
PR	28-SEP-2000; 2000US-0236032P.	KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
PR	28-SEP-2000; 2000US-0236033P.	KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
PR	28-SEP-2000; 2000US-0236034P.	KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
PR	28-SEP-2000; 2000US-0236109P.	KW	gene; ds.
PR	28-SEP-2000; 2000US-0236111P.	XX	
PR	29-SEP-2000; 2000US-0236842P.	OS	Homo sapiens.
PR	29-SEP-2000; 2000US-0236891P.	XX	
PR	02-OCT-2000; 2000US-0237172P.	PN	WO200194629-A2.
PR	02-OCT-2000; 2000US-0237173P.	XX	
PR	02-OCT-2000; 2000US-0237278P.	PD	13-DEC-2001.
PR	02-OCT-2000; 2000US-0237294P.	XX	
PR	02-OCT-2000; 2000US-0237295P.	PF	30-MAY-2001; 2001WO-US010838.
PR	02-OCT-2000; 2000US-0237316P.	XX	
PR	03-OCT-2000; 2000US-0237425P.	PR	05-JUN-2000; 2000US-0209473P.
PR	03-OCT-2000; 2000US-0237604P.	PR	05-JUN-2000; 2000US-0209531P.
PR	03-OCT-2000; 2000US-0237606P.	PR	18-SEP-2000; 2000US-0233133P.
PR	03-OCT-2000; 2000US-0237606P.	PR	18-SEP-2000; 2000US-0233617P.
PR	03-OCT-2000; 2000US-0237608P.	PR	20-SEP-2000; 2000US-0234009P.
PR	01-NOV-2000; 2000US-0244867P.	PR	20-SEP-2000; 2000US-0234034P.
PR	01-NOV-2000; 2000US-0245084P.	PR	20-SEP-2000; 2000US-0234052P.
XX		PR	22-SEP-2000; 2000US-0234509P.
PA	(AVAL-) AVALON PHARM.	PR	22-SEP-2000; 2000US-0234567P.
XX		PR	25-SEP-2000; 2000US-0234923P.
PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;	PR	25-SEP-2000; 2000US-0234924P.
PI	Soppet DR, Weaver Z;	PR	25-SEP-2000; 2000US-0235077P.
XX		PR	25-SEP-2000; 2000US-0235082P.
DR	WPI; 2002-188264/24.	PR	25-SEP-2000; 2000US-0235134P.
XX		PR	25-SEP-2000; 2000US-0235280P.
PT	Screening for anti-neoplastic agent involves exposing cells to a chemical	PR	26-SEP-2000; 2000US-0235637P.
PT	agent to be tested for anti-neoplastic activity, and determining a change	PR	26-SEP-2000; 2000US-0235638P.
PT	in expression of a gene of a signature gene set.	PR	27-SEP-2000; 2000US-0235711P.
XX		PR	27-SEP-2000; 2000US-0235720P.
PS	Claim 1; SEQ ID NO 3849; 44pp; English.	PR	27-SEP-2000; 2000US-0235840P.
XX		PR	27-SEP-2000; 2000US-0235863P.
CC	The present invention describes a method (M1) for screening for an anti-	PR	28-SEP-2000; 2000US-0236028P.
CC	neoplastic agent. The method involves exposing cells to a chemical agent	PR	28-SEP-2000; 2000US-0236032P.
CC	to be tested for anti-neoplastic activity, determining a change in	PR	28-SEP-2000; 2000US-0236033P.
CC	expression of at least one gene (I) of a signature gene set, where (I)	PR	28-SEP-2000; 2000US-0236034P.
CC	comprises a sequence (S) selected from 8447 sequences (given in ABL61664	PR	28-SEP-2000; 2000US-0236109P.
CC	to ABL70110), or is at least 95% identical to (S), where a change in	PR	28-SEP-2000; 2000US-0236111P.
CC	expression is indicative of anti-neoplastic activity. (I) has cytostatic	PR	29-SEP-2000; 2000US-0236842P.
CC	activity and can be used in gene therapy. M1 can be used for screening an	PR	29-SEP-2000; 2000US-0236891P.
CC	anti-neoplastic agent, and can be used for producing a product which is	PR	02-OCT-2000; 2000US-0237172P.
CC	the data collected with respect to the anti-neoplastic agent as a result	PR	02-OCT-2000; 2000US-0237173P.
CC	of M1, and the data is sufficient to convey the chemical structure and/or	PR	02-OCT-2000; 2000US-0237278P.
CC	properties of the agent. M1 can be used in the treatment of cancer such	PR	02-OCT-2000; 2000US-0237294P.
CC	as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,	PR	02-OCT-2000; 2000US-0237295P.
CC	prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell	PR	02-OCT-2000; 2000US-0237316P.
CC	cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous	PR	03-OCT-2000; 2000US-0237598P.
CC	cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's	PR	03-OCT-2000; 2000US-0237604P.
CC	tumour	PR	03-OCT-2000; 2000US-0237606P.
XX		PR	03-OCT-2000; 2000US-0237608P.
SQ	Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;	PR	01-NOV-2000; 2000US-0244867P.
		PR	01-NOV-2000; 2000US-0245084P.
		XX	
		PA	(AVAL-) AVALON PHARM.
		XX	
		PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
		PI	Soppet DR, Weaver Z;
		XX	
		DR	WPI; 2002-188264/24.
		XX	
		PT	Screening for anti-neoplastic agent involves exposing cells to a chemical
		PT	agent to be tested for anti-neoplastic activity, and determining a change
		PT	in expression of a gene of a signature gene set.
		XX	
		PS	Claim 1; SEQ ID NO 3849; 44pp; English.
		XX	
		CC	The present invention describes a method (M1) for screening for an anti-
		CC	neoplastic agent. The method involves exposing cells to a chemical
		CC	agent to be tested for anti-neoplastic activity, and determining a change
		CC	in expression of a gene of a signature gene set.
		XX	
		PA	(AVAL-) AVALON PHARM.
		XX	
		PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
		PI	Soppet DR, Weaver Z;
		XX	
		DR	WPI; 2002-188264/24.
		XX	
		PT	Screening for anti-neoplastic agent involves exposing cells to a chemical
		PT	agent to be tested for anti-neoplastic activity, and determining a change
		PT	in expression of a gene of a signature gene set.
		XX	
		PS	Claim 1; SEQ ID NO 4252; 44pp; English.
		XX	
		CC	The present invention describes a method (M1) for screening for an anti-
		CC	neoplastic agent. The method involves exposing cells to a chemical

CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 562;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||
Db 313 CCACACCTATTTCATCTC 330

RESULT 19
ABZ96916
ID ABZ96916 standard; DNA; 562 BP.

XX

AC ABZ96916;

XX 17-OCT-2003 (first entry)

DT Human nucleic acid sequence.

DE

XX Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

OS WO200285308-A2.

PN 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

PF 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

PA Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

PI WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired

DR respiration, has oligo(s) antisense to specific gene(s) or its

XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX Disclosure; SEQ ID NO 12158; 872pp; English.

PS The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC

CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, increasing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of bronchoconstriction,
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 562;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||
Db 313 CCACACCTATTTCATCTC 330

RESULT 20
ADI31874

ID ADI31874 standard; cDNA; 562 BP.

XX ADI31874;

XX 17-JUN-2004 (first entry)

DT Human cDNA #1200.

DE

XX Human; gene; ss; immunological response; immunopathological condition;

KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;

KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;

KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;

KW osteopathic; antiarthritic; antirheumatic; cytostatic.

XX Homo sapiens.

OS US6607879-B1.

PN 19-AUG-2003.

XX 09-FEB-1998; 98US-00023655.

PF 09-FEB-1998; 98US-00023655.

XX (INCY-) INCYTE CORP.

PA Cocks BG, Stuart SG, Seilhamer JJ;

XX WPI; 2003-895307/82.

PI A composition comprising a plurality of cDNAs, useful for detecting

XX altered expression of genes in an immunological response or for

XX diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma

XX or osteoarthritis.

PS Claim 1; SEQ ID NO 1200; 50pp; English.

XX The invention relates to a composition comprising a plurality of cDNAs

CC for detecting the altered expression of genes in an immunological

CC response. The invention also relates to a method of diagnosing or

CC monitoring the treatment of an immunopathological condition in a sample,

CC comprising obtaining nucleic acids from a sample, contacting the nucleic

CC acids of the sample with an array comprising the plurality of cDNAs under

CC conditions to form one or more hybridisation complexes, detecting the

CC

DR WPI; 2004-387937/36.
XX
PT New compositions having a number of first, second and third
PT polynucleotide probes, useful in research and diagnostic applications in
PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
PT infections.
XX
PS Claim 15; SEQ ID NO 1200; 16pp; English.
XX
CC The invention relates to polynucleotides which are used as probes to
CC detect genes differentially expressed in an immunological response,
CC abundantly expressed in an immunological response and/or coding for a
CC polypeptide known to regulate blood cell biology. The polynucleotides are
CC useful in research and diagnostic applications particularly in cancer and
CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
CC present sequence represents a human lymph node cDNA used to detect blood
CC cell and immunological response gene expression. Note: The present
CC sequence does not appear in the printed specification but was obtained in
CC electronic format from the USPTO web site
CC (seqdata.uspto.gov/sequence.html?DocID=20040077003).
XX
SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 562;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 313 CCACACCTATTCTACTC 330

RESULT 23
ADO28598
ID ADO28598 standard; cDNA; 585 BP.
XX
AC ADO28598;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PA21 encoding cDNA SEQ ID NO:27.
XX
KW high-grade dysplasia; HGD; oesophageal adenocarcinoma;
KW neo-plastic transformation; cancer; cytostatic; gene therapy; human;
KW phospholipase a2 precursor; PA21; chromosome 12; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 40..483
FT /*tag= a
FT /product= "phospholipase a2 precursor (PA21)"
FT /transl_except= (pos:172..177,aa:Tyr)
FT /transl_except= (pos:343..348,aa:Ile)
XX
PN WO2004044178-A2.
XX
PD 27-MAY-2004.
XX
PF 13-NOV-2003; 2003WO-US036260.
XX
PR 13-NOV-2002; 2002US-0425813P.
XX
PA (GETH) GENENTECH INC.
XX
PI Smith V;
XX
DR WPI; 2004-420319/39.
DR P-PSDB; ADO28599.
XX
PT Detecting of high-grade dysplasia in cells of a mammalian tissue sample

PT comprises establishing the level of expression in the test tissue sample
PT of the genes.
XX
PS Claim 1; SEQ ID NO 27; 256pp; English.
XX
CC The present invention describes a method for detecting high-grade
CC dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
CC (1) identifying an oesophageal tissue susceptible to oesophageal
CC adenocarcinoma; (2) determining the predispotion of a mammalian tissue
CC to a neo-plastic transformation by detecting HGD in cells of the tissue;
CC and (3) detecting cancer in a patient. The method can be used in
CC detecting HGD and cancer in cells of a mammalian tissue sample. The
CC methods and compositions of the present invention can be used in treating
CC and preventing HGD and cancer, and in gene therapy. The present sequence
CC encodes human phospholipase a2 precursor (PA21), which is used in the
CC exemplification of the present invention. The human PA21 gene is located
CC on chromosome 12.
XX
SQ Sequence 585 BP; 167 A; 166 C; 125 G; 127 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 312 CCACACCTATTCTACTC 329

RESULT 24
AAC98824
ID AAC98824 standard; cDNA; 630 BP.
XX
AC AAC98824;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:52.
XX
KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;
KW diagnosis; identification; cytostatic; neuroprotective; nootropic;
KW immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic; neural;
KW immune system; muscular; reproductive; gastrointestinal; pulmonary;
KW cardiovascular; renal; proliferative; ss.
XX
OS Homo sapiens.
XX
PN WO200055320-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005989.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-579444/54.
DR P-PSDB; AAB54059.
XX
PT New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition.
XX
PS Claim 1; Page 532; 1379pp; English.
XX
CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,

neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent sequences used in the exemplification of the present invention

Sequence 630 BP; 205 A; 162 C; 136 G; 123 T; 0 U; 4 Other;

Query Match 100.0%; Score 18; DB 3; Length 630;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | | | |
Db 302 CCACACCTATTTCATCTC 319

RESULT 25
AAZ41391
ID AAZ41391 standard; cDNA; 644 BP.

AC AAZ41391;

DT 19-JAN-2000 (first entry)

XX Human normal pancreas tissue derived cDNA 6.

DE Human; pancreas; cancer; treatment; anticancer; cytostatic; gene therapy;
KW EST; expressed sequence tag; ss.

OS Homo sapiens.

XX DE19818598-A1.

PN 21-OCT-1999.

PD 19-APR-1998; 98DE-01018598.

PF 19-APR-1998; 98DE-01018598.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

PI WPI; 1999-592039/51.

DR New nucleic acid sequences expressed in normal pancreatic tissues, and
XX derived polypeptides, for treatment of pancreatic cancer and
PT identification of therapeutic agents.

XX Claim 3; Page 50; 92pp; German.

PS This invention describes novel cDNA sequences (A) that are highly
XX expressed in normal human pancreatic tissue and which have anticancer and
CC cytostatic activity. (A) are used (i) for recombinant expression of
CC polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to
CC identify agents suitable for treatment of pancreatic cancer; (ii)
CC directly for treating this form of cancer (including expression from gene
CC therapy vectors) and (iii) for generation of specific antibodies. (A) are

CC identified by assembling ESTs (expressed sequence tags) from a particular
CC tissue type before comparison of expression patterns. This allows a
CC significantly longer fragment of the gene to be revealed, so should
CC reduce the number of failures associated with the fact that ESTs from
CC different libraries may represent different parts of the same unknown
CC gene, distorting the estimated frequency of occurrence in a particular
CC tissue. AAZ41386-241423 represent human normal pancreatic tissue derived
CC cDNA fragments which encode the protein fragments represented in AAY59893
CC -Y59920

XX Sequence 644 BP; 195 A; 171 C; 145 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 644;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | | | |
Db 337 CCACACCTATTTCATCTC 354

RESULT 26
AAH57532
ID AAH57532 standard; cDNA; 654 BP.

XX AAH57532;

DT 10-SEP-2001 (first entry)

XX Human pancreas cell specific cDNA sequence SEQ ID NO:372.

DE Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

XX Homo sapiens.

XX WO200132927-A2.

XX 10-MAY-2001.

PF 02-NOV-2000; 2000WO-US030396.

XX 04-NOV-1999; 99US-0163508P.

XX (INCY-) INCYTE GENOMICS INC.

XX Sornasse T, Seilhamer JJ, Watson GA;

DR WPI; 2001-291057/30.

XX New cell and tissue specific polynucleotides useful for diagnosis,
PT prognosis or monitoring of treatments for disorders where the gene is
PT associated with a cancer, immunopathology or neuropathology.

PS Claim 1; Page 288; 327pp; English.

XX AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC sequences (I). (I) can have cytostatic, immunomodulatory and
CC neuroprotective activities, and can be used in gene therapy. (I) and
CC proteins (II) encoded by then are used in high throughput screening
CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their
CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
CC agents. Expression of (I) in a sample indicates the differentiation of
CC embryonic stem cells into a tissue selected from brain, heart, kidney,
CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
CC to produce an expression profile that defines a metabolic or
CC developmental process, treatment, condition, disease or disorder. The
CC gene profile can be used for diagnosis, prognosis or monitoring of
CC treatments and for investigating a predisposition to a disorder where the
CC gene is associated with a cancer, immunopathology or neuropathology

XX SQ Sequence 654 BP; 165 A; 193 C; 145 G; 143 T; 0 U; 8 Other;
Query Match 100.0%; Score 18; DB 4; Length 654;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCACACCTATTTCATCTC 18
Db 428 CCACACCTATTTCATCTC 445
RESULT 27
AAS76099
ID AAS76099 standard; cDNA; 654 BP.
XX AC AAS76099;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #11903.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR P-PSDB; ABG11912.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX Claim 1; SEQ ID NO 11903; 103pp; English.
PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 654 BP; 190 A; 174 C; 170 G; 120 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 5; Length 654;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCACACCTATTTCATCTC 18
Db 483 CCACACCTATTTCATCTC 500
RESULT 28
ACN42348
ID ACN42348 standard; cDNA; 742 BP.
XX AC ACN42348;
XX DT 18-NOV-2004 (first entry)
XX DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1223.
XX KW ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
XX KW dithp.
XX OS Homo sapiens.
XX PN WO2004023973-A2.
XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-US028227.
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.
XX PA (INCY-) INCYTE CORP.
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
DR P-PSDB; ABM83696.
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX Claim 1; Page; 190pp; English.
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp polynucleotide of
CC the invention. Note: The sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX SQ Sequence 742 BP; 182 A; 204 C; 191 G; 165 T; 0 U; 0 Other;

CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 3375;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 3304 CCACACCTATTCTACTC 3321

RESULT 31
ABZ96917
ID ABZ96917 standard; DNA; 3375 BP.
XX
AC ABZ96917;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human nucleic acid sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Disclosure; SEQ ID NO 12159; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of ubiqunone or
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 3375;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 3304 CCACACCTATTCTACTC 3321

RESULT 32
ABD20766
ID ABD20766 standard; DNA; 3375 BP.
XX
AC ABD20766;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human pulmonary and inflammatory target DNA #377.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 12159; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating

PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
XX WPI; 2000-679539/66.
DR
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Disclosure; Page 1137-1139; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 6771;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 313 CCACACCTATTTCATCTC 330

RESULT 35
ABZ96919
ID ABZ96919 standard; DNA; 6771 BP.

XX
AC ABZ96919;

XX 17-OCT-2003 (first entry)

XX Human nucleic acid sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; de.

XX Homo sapiens.

PN WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

PR 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 12161; 872pp; English.

PS The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, a
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 6771;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 313 CCACACCTATTTCATCTC 330

RESULT 36
ABD20768
ID ABD20768 standard; DNA; 6771 BP.

XX
AC ABD20768;

XX 29-JUL-2004 (first entry)

XX Human pulmonary and inflammatory target DNA #379.

XX Human; antisense; bronchoconstriction; allergy; hyoposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;

KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds.

XX Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and bronchodilating agent.

PS Claim 15; SEQ ID NO 12161; 763pp; English.

XX This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it

XX

SQ Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 11; Length 6771;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 313 CCACACCTATTTCATCTC 330

RESULT 37

ADI35082

ID ADI35082 standard; DNA; 12174 BP.

XX ADI35082;

XX 22-APR-2004 (first entry)

XX Human PLA2G1B nucleotide sequence.

DE PLA2G1B ; fat deposition; leanness; polymorphism; non-insulin dependent diabetes mellitus; NIDDM; hyperinsulinemia; hypertension; glucose intolerance; dyslipidemia; hypercoagulability; microalbuminuria; human; gene; ds.

XX Homo sapiens.

XX WO2004002295-A2.

PN 08-JAN-2004.

XX 27-JUN-2003; 2003WO-US020830.

XX 27-JUN-2002; 2002US-0392361P.

XX (SEQU-) SEQUENOM INC.

PI Adam GIR, Langdown ML;

XX WPI; 2004-082843/08.

DR P-PSDB; ADI35083.

XX Diagnosing a predisposition to fat deposition or leanness, useful for diagnosing a predisposition to e.g. diabetes or hypertension, comprises detecting the presence of a polymorphism in the PLA2G1B nucleic acid from the subject.

XX Claim 1; SEQ ID NO 1; 91pp; English.

XX The invention relates to diagnosing a predisposition to fat deposition or leanness in a subject comprising detecting the presence or absence of a polymorphic variation associated with fat deposition at a polymorphic site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a subject, where the presence of the polymorphic variation indicates a predisposition to fat deposition in the subject. The polymorphic variation is a guanine at position 7328 or thymine at position 9182 of the present sequence. The method is useful for diagnosing a predisposition to fat deposition or leanness in a subject, and consequently for diagnosing a predisposition to non-insulin dependent diabetes mellitus (NIDDM) in a subject and conditions such as hyperinsulinemia, hypertension, glucose intolerance, dyslipidemia, hypercoagulability, or microalbuminuria, which can lead to early prescription of preventive measures. The present sequence represents a human PLA2G1B nucleotide sequence.

XX

SQ Sequence 12174 BP; 3217 A; 2992 C; 2738 G; 3215 T; 0 U; 12 Other;

Query Match 100.0%; Score 18; DB 12; Length 12174;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 7310 CCACACCTATTTCATCTC 7327

RESULT 38

ADJ09983

ID ADJ09983 standard; DNA; 12174 BP.

XX ADJ09983;

XX 17-JUN-2004 (first entry)

XX Human phospholipase A2 (PLA2G1B) DNA SegID 1.

KW human; gene; ds; fat reduction; fat deposition; phospholipase A2;
KW PLA2G1B; chromosome 12q24; single nucleotide polymorphism; SNP;
KW appetite suppressant; lipase inhibitor; exercise regimen; obesity;
KW non-insulin dependent diabetes mellitus; NIDDM; cardiovascular disorder;
XX hypertension; antidiabetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT variation replace(436,c)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(839,a)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(4050,a)
FT /*tag= c
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(4689,t)
FT /*tag= d
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(6282,a)
FT /*tag= e
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(6358,c)
FT /*tag= f
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(6653,t)
FT /*tag= g
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(7256,t)
FT /*tag= h
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(7300,a)
FT /*tag= i
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(7301,c)
FT /*tag= j
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(7328,g)
FT /*tag= k
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(8062,c)
FT /*tag= l
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(9182,t)
FT /*tag= m
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(11649,c)
FT /*tag= n
FT /standard_name= "Single nucleotide polymorphisms"
XX
XX WO2004002296-A2.
XX
XX
PD 08-JAN-2004.
XX
PF 27-JUN-2003; 2003WO-US020831.
XX
PR 27-JUN-2002; 2002US-03923362P.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Adam GIR, Langdown ML, Denissenko MF, Dennis E, Cantor C;
PI Rubin B;
XX WPI; 2004-071944/07.
DR P-PSDB; ADJ09984.
XX
PT Identifying a candidate therapeutic for fat reduction, useful for
PT treating diabetes, by introducing a test molecule to a system comprising
PT PLA2G1B protein or nucleic acid, and determining the presence of
PT interaction between the compounds.
XX

PS Claim 1; SEQ ID NO 1; 116pp; English.
XX
CC This invention relates to a novel candidate therapeutic agent useful for
CC fat reduction and disorders related to fat depositions. Specifically, it
CC refers to polymorphic variations in the phospholipase A2 (PLA2G1B) DNA,
CC which is located on chromosome 12q24 and has been associated with central
CC fat deposition. The present invention describes methods to detect the
CC presence or absence of these single nucleotide polymorphisms of PLA2G1B,
CC in particular G7328A and T9182G, and subsequently provide treatment that
CC reduces fat deposition. This treatment may consist of an appetite
CC suppressant, a lipase inhibitor, a phospholipase inhibitor, an exercise
CC regimen, a dietary regimen, psychological counselling, psychotherapy or a
CC psychotherapeutic. Accordingly, PLA2G1B is a target for reducing fat
CC deposition and it can be used to treat both obesity and non-insulin
CC dependent diabetes mellitus (NIDDM), as well as cardiovascular disorders
CC such as hypertension. As such, it exhibits antidiabetic activity. This
CC polynucleotide sequence is the human PLA2G1B DNA of the invention.
XX
SQ Sequence 12174 BP; 3220 A; 2996 C; 2739 G; 3219 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 12174;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 7310 CCACACCTATTTCATCTC 7327

RESULT 39
ABK47376
ID ABK47376 standard; DNA; 13612 BP.
XX
AC ABK47376;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Phospholipase A2, groupIB (PLA2G1B) gene.
XX
KW Human; ds; gene; SNP; single nucleotide polymorphism; pancreatitis;
KW pancreatic cancer; Phospholipase A2 groupIB; PLA2G1B; gene therapy;
KW haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(3845,A)
FT /*tag= a
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
FT variation replace(3968,A)
FT /*tag= b
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
FT CDS 4053. .9613
FT /*tag= c
FT /product= "Pla2G1B"
FT exon 4053. .4086
FT /*tag= d
FT /number= 1
FT intron 4087. .5785
FT /*tag= e
FT /number= 1
FT exon 5786. .5945
FT /*tag= f
FT /number= 2
FT intron 5946. .6744
FT /*tag= g
FT /number= 2
FT variation replace(6060,A)
FT /*tag= h
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
FT

FT exon 6745. .6873
FT /*tag= i
FT /number= 3
FT replace(6844,A)
FT /*tag= j
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
FT intron 6874. .9489
FT /*tag= k
FT /number= 3
FT 9490. .9613
FT /*tag= l
FT /number= 4
FT replace(9531,A)
FT /*tag= m
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
XX
PN WO200212562-A2.
XX
PD 14-FEB-2002.
XX
PF 06-AUG-2001; 2001WO-US024663.
XX
PR 04-AUG-2000; 2000US-0223179P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
XX Kazemi A, Kliem SE, Koshy B;
PI WPI; 2002-303982/34.
XX P-PSDB; AAU78667.
DR
XX
PT Novel isolated human Phospholipase A2, Group IB pancreas polynucleotide,
PT for therapeutic purposes, for studying expression and function of the
PT polynucleotide and for expressing the phospholipase protein.
XX
PS Claim 1; Fig 1; 51pp; English.
XX
CC The invention relates to an isolated human Phospholipase A2, Group IB
CC (pancreas) (PLA2G1B) polynucleotide comprising a sequence which is a
CC polymorphic variant for a reference sequence for the PLA2G1B gene or its
CC fragment, or a polymorphic variant of a reference sequence for a PLA2G1B
CC cDNA or its fragment. Also included are haplotyping/genotyping the
CC PLA2G1B gene of an individual, predicting the haplotype pair for the
CC PLA2G1B gene of an individual, identifying an association between a trait
CC and at least one haplotype or haplotype pair of the PLA2G1B gene, an
CC isolated genotyping oligonucleotide for detecting a polymorphism in the
CC PLA2G1B gene, a recombinant non-human organism transformed or transfected
CC with the PLA2G1B sequence, where the organism expresses a PLA2G1B protein
CC encoded by the first nucleotide sequence or by the polymorphic variant
CC sequence, an isolated polypeptide comprising a sequence which is a
CC polymorphic variant of a reference sequence for the PLA2G1B protein or
CC its fragment, an anti-PLA2G1B monoclonal antibody, screening for drugs
CC targeting PLA2G1B, a computer system for storing and analysing
CC polymorphism data for the PLA2G1B gene and a genome anthology for PLA2G1B
CC gene. The PLA2G1B variant is useful in studying the expression and
CC function of PLA2G1B, and in expressing PLA2G1B protein for use in
CC screening for candidate drugs to treat diseases related to PLA2G1B
CC activity (e.g. pancreatitis and pancreatic cancer) and for therapeutic
CC purposes. The transgenic organism is useful for studying expression of
CC the PLA2G1B isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against PLA2G1B protein, and for testing the efficacy of
CC therapeutic agents and compounds in a biological system. The antibody is
CC useful for studying the effect of the variation on the biological
CC activity of PLA2G1B as well as on the binding affinity of candidate drugs
CC targeting PLA2G1B. The present sequence is the PLA2G1B gene which is
CC located on chromosome 12q23-q24.1
XX
SQ Sequence 13612 BP; 3637 A; 3290 C; 3070 G; 3615 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 13612;
Best Local Similarity 100.0%; Pred. No. 19;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCACACCTATTTCATACTC 18
| | | | | | | | | | | | | | | |
Db 6826 CCACACCTATTTCATACTC 6843

RESULT 40
ABV95110
ID ABV95110 standard; cDNA; 224 BP.
XX
AC ABV95110;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 518.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
DR
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
PS Claim 1; SEQ ID NO 518; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 224 BP; 66 A; 63 C; 37 G; 53 T; 0 U; 5 Other;

Query Match 88.9%; Score 16; DB 6; Length 224;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 17
| | | | | | | | | | | |
Db 5 CCACACCTATTTCATANT 21

RESULT 41
ACN46442
ID ACN46442 standard; cDNA; 611 BP.
XX
AC ACN46442;
XX
DT 02-DEC-2004 (first entry)
XX
DE Cotton primed seed EST Clone ID: LIB3825-020-Q1-K6-B2, SEQ:1223.
XX

KW Cotton; plant; EST; expressed sequence tag; transgenic plant; seed;
KW variety DP50B; library LIB3825; molecular tag; molecular marker;
KW genetic mapping; molecular mapping; seed germination; plant growth;
KW plant quality; plant yield; plant breeding; tissue printing; ss.
XX
OS Gossypium hirsutum.

XX US2004123340-A1.
XX
PD 24-JUN-2004.
XX
PF 12-DEC-2001; 2001US-00021323.
XX
PR 14-DEC-2000; 2000US-0255619P.

XX (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.

PI Deikman J, Feng PCC, Fincher KL, Ziegler TE;
XX
XX WPI; 2004-479808/45.
DR
XX

PT New isolated nucleic acid molecule that encodes a plant protein or its
PT fragment, useful for isolating a variety of agronomically significant
PT genes associated with plant growth, quality or yield, and as molecular
PT tags to map genes.
XX

PS Claim 1; SEQ ID NO 1223; 34pp; English.

XX
CC The invention relates to 17880 cotton expressed sequence tags (ESTs;
CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
CC from primed or non-primed seeds from variety DP50B, mature seeds from
CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
CC tissue, developing fibres, carpel walls and septa from variety
CC Nucotton33B. The invention also relates to substantially purified
CC proteins or their fragments encoded by nucleic acid molecules of the
CC invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC molecular tags to isolate genetic regions, to isolate genes, to map
CC genes, to determine gene function and to determining whether genes are
CC members of a particular gene family. The nucleic acid molecules may be
CC used for isolating a variety of agronomically significant genes
CC associated with plant growth, quality, yield, and could also serve as
CC links in metabolic and catabolic pathways. The nucleic acid molecules are
CC also useful for identifying genes important in initiating and maintaining
CC seed germination or that may be used to mitigate stresses encountered
CC during seed germination. The ESTs additionally enable the acquisition of
CC promoters and cis-regulatory elements which will be useful to express
CC agronomically significant genes in these tissues and/or other tissues,
CC and also permits the acquisition of molecular markers useful in breeding
CC schemes, genetic and molecular mapping, and in cloning of agronomically
CC significant genes. The nucleic acid molecules are further useful for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the presence or quantity of a protein by tissue printing. The
CC present sequence represents a specifically claimed EST isolated from a

CC cotton variety DP50B primed seed cDNA library (LIB3825). The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20040123340

SQ Sequence 611 BP; 134 A; 131 C; 145 G; 201 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 13; Length 611;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
| | | | | | | | | | | |
Db 340 CACACCTATTTCATCTC 356

RESULT 42
ADR60118
ID ADR60118 standard; cDNA; 1733 BP.
XX
AC ADR60118;
XX
DT 02-DEC-2004 (first entry)
XX
DE Cotton cDNA sequence, SEQ ID 899.
XX

KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
KW drought tolerance; plant disease resistance; galactomannan; lignin;
KW plant growth regulator; heat tolerance; herbicide tolerance;
KW homologous recombination; extreme osmotic condition tolerance;
KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
KW stress resistance.

XX Gossypium hirsutum.
OS
XX US2004181830-A1.
PN
XX

PD 16-SEP-2004.

XX 29-JAN-2004; 2004US-00767795.

XX 07-MAY-2001; 2001US-00849529.

PR 12-DEC-2001; 2001US-00021323.

XX (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.

XX Kovalic DK, Zhou Y, Cao Y;

DR WPI; 2004-667718/65.

XX New recombinant nucleic acid molecules and polypeptides from Gossypium
PT hirsutum, useful for producing plants with improved biological
PT characteristics (e.g. improved plant cold or drought tolerance).

XX Claim 1; SEQ ID NO 899; 14pp; English.

PS
XX The invention relates to a recombinant polynucleotide comprising any of
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
CC Also a recombinant polypeptide comprising any of the 58798 amino acid
CC sequences mentioned in the specification and producing a plant having an
CC improved property. Producing a plant having an improved property
CC comprises transforming a plant with a recombinant construct comprising a
CC promoter region functional in a plant cell operably joined to a
CC polynucleotide comprising a coding sequence for a polypeptide associated
CC with the property, and growing the transformed plant. The polypeptide is
CC useful for improving plant cold tolerance, manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, improving plant
CC drought tolerance, providing increased resistance to plant disease,
CC producing galactomannan (or lignin or plant growth regulators), improving
CC plant heat tolerance, improving plant tolerance to herbicides, increasing
CC the rate of homologous recombination in plants, improving plant tolerance

CC encoded by an Arabidopsis gene having a promoter selected from one of
CC ADZ75177-AD275257, a recombinant vector comprising N1-N3, an expression
CC cassette comprising N1-N3 operatively linked to an open reading frame, a
CC recombinant vector comprising the above expression cassette, a host cell
CC comprising the expression cassette, a plant cell containing the
CC expression cassette, a transformed plant (the genome of which is
CC augmented with the expression cassette), a transformed plant comprising
CC transformed plant cells (where the cells contain the expression
CC cassette), a method (M1) for augmenting a plant genome, a method (M2) to
CC identify a gene having a promoter (the expression of which is altered in
CC root), a method (M3) to identify a gene having a promoter (the expression
CC of which is constitutive in a plant cell), a method (M4) to identify a
CC gene having a promoter (the expression of which is altered in leaves of a
CC plant), and a method to alter the phenotype of a plant cell comprising
CC introducing the expression cassette. for the expression cassette, the
CC open reading frame is from an insect resistance gene, a bacterial disease
CC resistance gene, a fungal disease resistance gene, a viral disease
CC resistance gene, a nematode disease resistance gene, a herbicide
CC resistance gene, a stress resistance gene, a gene affecting grain
CC composition or quality, a nutrient utilization gene, a mycotoxin
CC reduction gene, a male sterility gene, a selectable marker gene, a
CC screenable marker gene, a negative selectable marker, a gene affecting
CC plant agronomic characteristics, or an environment or stress resistance
CC gene. The stress resistance gene confers resistance or tolerance to
CC drought, heat, chilling, freezing, excessive moisture, excessive salt, or
CC excessive oxidative stress. The promoters are useful for regulating the
CC expression of selected transgenes in economically important plants. For
CC example, root-specific promoters may be useful for expressing defense-
CC related genes, including those conferring insecticidal resistance and
CC stress tolerance genes, e.g., salt, cold or drought tolerance, and genes
CC for altering nutrient uptake, and leaf-specific promoters may be useful
CC for producing large quantities of protein, for expressing oils or
CC proteins of interest, and genes for increasing the nutritional value of a
CC plant. Constitutive promoters are useful for expressing a wide variety of
CC genes including those which alter metabolic pathways, confer disease
CC resistance, for protein production, e.g., antibody production, or to
CC improve nutrient uptake. The present sequence is an open reading frame
CC from an Arabidopsis leaf specific promoter gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 3093 BP; 866 A; 592 C; 790 G; 845 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 7; Length 3093;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCT 17
Db 553 CCACACCTATTGATACT 537

RESULT 45
ADE52630/c
ID ADE52630 standard; DNA; 3120 BP.

XX ADE52630;
AC ADE52630;
XX 29-JAN-2004 (first entry)

XX Caenorhabditis elegans SQV DNA sequence #1.

XX SQV protein; SQV-1; SQV-2; SQV-4; SQV-5; SQV-6;
KW glycosaminoglycan biosynthetic activity; connective tissue disease;
KW Ehlers-Danlos syndrome; progeroid disorder;
KW aging related cellular damage; ds.

XX Caenorhabditis elegans.

XX WO2003062448-A2.

XX 31-JUL-2003.

XX 17-JAN-2003; 2003WO-US001558.
XX 18-JAN-2002; 2002US-0349630P.
PR 24-JUN-2002; 2002US-0390930P.
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX Horvitz HR, Hwang HY;
PI WPI; 2003-627462/59.

XX New SQV polypeptides and nucleic acids having a glycosaminoglycan
PT biosynthetic biological activity, useful for diagnosing and treating a
PT connective tissue disease, progeroid disorder, or cellular damage related
PT to aging.

XX Disclosure; SEQ ID NO 1; 247pp; English.

XX The invention comprises the amino acid and coding sequences of SQV
CC proteins (i.e. SQV-1, SQV-2, SQV-4, SQV-5 and SQV-6), having a
CC glycosaminoglycan biosynthetic biological activity. The SQV DNA and
CC protein sequences are useful for diagnosing and treating connective
CC tissue disease, such as: Ehlers-Danlos syndrome, progeroid disorder, or
CC cellular damage related to aging. The SQV DNA and protein sequences may
CC also be used to identify compounds that modulate a glycosaminoglycan
CC biosynthetic biological activity. The present nucleic acid represents an
CC SQV DNA sequence of the invention.

XX Sequence 3120 BP; 1004 A; 580 C; 551 G; 985 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 10; Length 3120;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CACACCTATTTCATCTC 18
Db 3067 CACACCTATTTCCTACTC 3051

RESULT 46
AAQ46249
ID AAQ46249 standard; DNA; 8528 BP.

XX AAQ46249;

XX 25-MAR-2003 (revised)
DT 17-MAR-1994 (first entry)

XX Construct EC2L (Contains catR and pyrG codingsequences) .

XX Aspergillus niger; catalase; catR; hydrogen peroxide; ss.

XX Synthetic.

XX Key Location/Qualifiers
FH misc_feature 1..8
FT /*tag= a
FT /label= Linker sequence.
FT 5'UTR 9..1957
FT /*tag= b
FT /function= "GlaA promoter."
FT CDS 1958..4370
FT /*tag= c
FT /label= catR coding region.
FT 3'UTR 4371..4432
FT /*tag= d
FT misc_feature 4433..4440
FT /*tag= e
FT /label= Linker sequence.
FT polyA_site 4441..6093
FT /*tag= f
FT /label= glaA polyadenylation and termination signals

```
FT CDS 6094..8510
FT FT /*tag= g
FT FT /label= pyrG gene.
FT misc_feature 8511..8528
FT FT /*tag= h
FT FT /label= Linker sequence.
XX
PN WO9318166-A2.
XX
PD 16-SEP-1993.
XX
XX 04-MAR-1993; 93WO-US002020.
PF 04-MAR-1992; 92US-00845989.
PR 04-MAR-1992; 92US-00846181.
XX
PA (GEMV ) GENENCOR INT INC.
XX
XX Berka RM, Fowler T, Rey MW;
XX WPI; 1993-303480/38.
XX
PT Aspergillus niger catR gene sequence - from which catR promoter has been
PT deleted and Aspergillus glucoamylase promoter gene has been inserted.
XX
PS Disclosure; Fig 3; 43pp; English.
XX
CC The Aspergillus niger catR gene was identified and isolated. The native
CC promoter of the gene was removed and replaced with the Aspergillus
CC glucoamylase promoter gene. This modification allows increased expression
CC of the catR gene without the need to supply hydrogen peroxide to induce
CC expression. Cells into which this construct is inserted preferably have
CC the glucose oxidase gene (goxΔ) deleted. This deletion minimises the
CC generation of gluconate waste material and the use of waste treatment
CC processes. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8528 BP; 1951 A; 2321 C; 2209 G; 2047 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 2; Length 8528;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATACT 17
Db 5916 CCACACCTATTCTCTACT 5932

RESULT 47
ABL33718/c
ID ABL33718 standard; DNA; 17934 BP.
XX
AC ABL33718;
XX
XX 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 1691.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.
XX
OS Homo sapiens.
XX
XX WO200200928-A2.
PN
XX 03-JAN-2002.
PD
XX 02-JUL-2001; 2001WO-EP007537.
PF

XX 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI WPI; 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
PS Claim 1; SEQ ID NO 1691; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 17934 BP; 4443 A; 283 C; 4663 G; 8545 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 17934;
Best Local Similarity 94.1%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATACTC 18
Db 14397 CACACCTATACATACTC 14381

RESULT 48
ACN44150_0
WP Sequence split into 5 fragments LOCUS ACN44150 Accession Acn44150
WP Fragment Name Begin End
WP ACN44150_0 1 110000
WP ACN44150_1 100001 210000
WP ACN44150_2 200001 310000
WP ACN44150_3 300001 410000
WP ACN44150_4 400001 439892
ID ACN44150 standard; DNA; 439892 BP.
XX
AC ACN44150;
XX
XX 18-NOV-2004 (first entry)
DT
XX Human genomic sequence HCG27278.
DE
XX Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
KW
XX Homo sapiens.
OS
XX WO2003073826-A2.
PN
XX 12-SEP-2003.
PD
XX 28-FEB-2003; 2003WO-US006235.
PF
XX 01-MAR-2002; 2002US-00087192.
PR
XX (SAGR-) SAGRES DISCOVERY.
PA
XX Morris DW;
PI
XX WPI; 2003-328604/31.
XX
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
XX comprises a nucleotide sequence.
PT
```


XX
PS Claim 1; SEQ ID NO 454; Opp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
SQ Sequence 439892 BP; 100791A; 104435C; 106090G; 116168T; OU; 124080Other;

Query Match 85.6%; Score 15.4; DB 11; Length 110000;
Best Local Similarity 94.1%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CACACCTATTTCATCTC 18
Db 54190 CACACCTTTTCATCTC 54206

RESULT 49
ADP44620/C
ID ADP44620 standard; DNA; 118777 BP.
XX
AC ADP44620;
XX
DT 26-AUG-2004 (first entry)
XX
DE Murine alpha-synuclein (SNCA) DNA - SEQ ID 10.
XX
KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;
KW Huntington's; spinocerebellar ataxia type 1;
KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
KW dentatorubral-pallidoluysian atrophy; DRPLA; alpha-synuclein; SNCA; ds;
KW murine; house mouse.
XX
OS Mus musculus.
XX
PN WO2004047872-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US037650.
XX
PR 26-NOV-2002; 2002US-0429387P.
PR 03-FEB-2003; 2003US-0444614P.
XX
PA (MEDT) MEDTRONIC INC.
XX
PI Kaemmerer WF;
XX
DR WPI; 2004-441106/41.
XX
PT New medical system comprising an intracranial access device, a mapping
PT means, a small interfering RNA or vector encoding the RNA, and a delivery
PT means, useful for treating a neurodegenerative disorder.
XX
PS Claim 23; SEQ ID NO 10; 228pp; English.
XX
CC The invention relates to a novel medical system for treating a
CC neurodegenerative disorder comprising an intracranial access device, a
CC mapping means for locating a predetermined location in the brain, a
CC deliverable amount of a small interfering RNA (siRNA), or vector encoding
CC the siRNA, and a delivery means. The system of the invention has

CC applications related to the CNS and may be useful for treating a
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).
CC The current sequence is that of the murine alpha-synuclein (SNCA) DNA
CC (SEQ ID 10) of the invention.
XX
SQ Sequence 118777 BP; 35967 A; 22351 C; 22620 G; 37839 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 12; Length 118777;
Best Local Similarity 94.1%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 17
Db 77795 CCACACATATTTCATCT 77779

RESULT 50
ABQ28339
ID ABQ28339 standard; DNA; 544 BP.
XX
AC ABQ28339;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 14930.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-

CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention

XX SQ Sequence 544 BP; 247 A; 145 C; 42 G; 110 T; 0 U; 0 Other;
Query Match 83.3%; Score 15; DB 6; Length 544;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATCTC 18
Db 13 CACCTATTTCATCTC 27

RESULT 51
ABQ28338/c
ID ABQ28338 standard; DNA; 544 BP.
XX
AC ABQ28338;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 14929.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention

XX SQ Sequence 544 BP; 110 A; 42 C; 145 G; 247 T; 0 U; 0 Other;
Query Match 83.3%; Score 15; DB 6; Length 544;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATCTC 18
Db 532 CACCTATTTCATCTC 518

RESULT 52
ADQ63331
ID ADQ63331 standard; cDNA; 3951 BP.
XX
AC ADQ63331;
XX
DT 07-OCT-2004 (first entry)
XX
DE Novel human cDNA sequence #492.
XX
KW ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX
OS Homo sapiens.
XX
PN EP1440981-A2.
XX
PD 28-JUL-2004.
XX
PF 21-JAN-2004; 2004EP-00001196.
XX
PR 21-JAN-2003; 2003JP-00102206.
PR 09-MAY-2003; 2003JP-00131392.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX
DR WPI; 2004-535376/52.
DR P-PSDB; ADQ65519.
XX
PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 492; 2449pp; English.
XX
CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a nucleotide
CC sequence of the invention.
XX
SQ Sequence 3951 BP; 992 A; 1043 C; 1111 G; 805 T; 0 U; 0 Other;
Query Match 83.3%; Score 15; DB 12; Length 3951;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15
Db 3820 CCACACCTATTTCATA 3834

RESULT 53

AAA69665
ID AAA69665 standard; cDNA; 362 BP.
XX
AC AAA69665;
XX
DT 08-NOV-2000 (first entry)
XX
DE Pinus radiata methyl sterol oxidase cDNA SEQ ID NO:139.
XX
KW Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant;
KW metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid;
KW genome mapping; physical mapping; positional cloning; forestry;
KW agriculture; medicine; fermentation; plant development; pest resistance;
KW pinene; myrcene; Monterey pine; ss.
XX
OS Pinus radiata.
XX
PN WO200036081-A2.
XX
PD 22-JUN-2000.
XX
PF 16-DEC-1999; 99WO-NZ000219.
XX
PR 17-DEC-1998; 98US-00215504.
PR 29-JUL-1999; 99US-0146441P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Havukkala IJ;
XX
DR WPI; 2000-431575/37.
DR P-PSDB; AAB18065.
XX
PT New plant polynucleotides encoding polypeptides involved in the
PT production and modification of isoprenoids, useful in forestry and
PT agriculture for manipulation of isoprenoid metabolism.
XX
PS Claim 1; Page 95; 164pp; English.
XX
CC The present invention describes plant polynucleotides encoding
CC polypeptides involved in the production and modification of isoprenoids,
CC such as terpenoid and steroid compounds. The polynucleotides are used in
CC genome mapping, in physical mapping and in positional cloning of genes.
CC The polynucleotides and polypeptides are useful in forestry and
CC agriculture for manipulation of isoprenoid metabolism, in medicine for
CC therapeutic effects, including direct application in diseased organisms
CC or indirect application by transgenic organisms and in fermentation and
CC chemical processing industries involving isoprenoids. In plant
CC applications, manipulating isoprenoid pathways or isoprenoid composition
CC may, for example, affect plant development, pest resistance, and the
CC value of extractives (e.g. pinene and myrcene). The ubiquitous and varied
CC roles of isoprenoids make the polynucleotides attractive targets for
CC biotechnical applications in a variety of fields. AAA69527 to AAA69690
CC and AAB18004 to AAB18143 represent Eucalyptus grandis and Pinus radiata
CC polynucleotides and proteins used in the exemplification of the present
CC invention
XX
SQ Sequence 362 BP; 101 A; 69 C; 86 G; 106 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 3; Length 362;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
||| ||||| |||||
Db 5 CCTCACCTATTTCACACTC 22

RESULT 54
ABZ08767/c
ID ABZ08767 standard; cDNA; 466 BP.
XX

AC ABZ08767;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte derived cDNA SEQ ID NO 8758.
XX
KW Human; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quertermous T, Johnson F;
XX
DR WPI; 2002-636525/68.
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 26; Page 2011; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection. The
CC present sequence is that of a human leukocyte expressed cDNA of the
CC invention
XX
SQ Sequence 466 BP; 135 A; 74 C; 131 G; 110 T; 0 U; 16 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 466;
Best Local Similarity 88.9%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
||| ||||| |||||
Db 298 CCACTCCTATCCATCTC 281

RESULT 55
ACC62584/c
ID ACC62584 standard; cDNA; 506 BP.
XX
AC ACC62584;
XX
DT 27-JUN-2003 (first entry)
XX
DE Rice endosperm EST #3.
XX
KW rice; endosperm; expressed sequence tag; biochip; EST; ss.
XX

OS Oryza sativa.
XX
PN CN1366079-A.
XX
XX
PD 28-AUG-2002.
XX
PF 31-OCT-2001; 2001CN-00137670.
XX
PR 31-OCT-2001; 2001CN-00137670.
XX
PA (UYZH-) UNIV ZHEJIANG.
XX
PI Dong H, Li D;
XX
DR WPI; 2003-269237/27.
XX
PT New rice endosperm specific expression sequence label for use in a
PT biochip and for DNA sequencing to configure a rice endosperm cDNA
PT library.
XX
PS Claim 1; Page 11-12; 30pp; Chinese.
XX
CC The invention relates to a novel rice endosperm specific expressed
CC sequence tag (EST) and its constituted biochip. The cDNA sequence has one
CC of 50 sequences. The EST technique is used for DNA sequencing to
CC configure a rice endosperm cDNA library. The obtained expression sequence
CC label goes through removing redundant sequences, indexing Internet
CC database, sorting and collecting non-redundant sequences to obtain 50 new
CC expression sequence labels. The biochip is prepared from them by the
CC microarray technique and has broad-spectrum application. The sequences
CC shown in ACC62582-ACC62631 represent the EST's of the invention
XX
SQ Sequence 506 BP; 119 A; 122 C; 124 G; 141 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 8; Length 506;
Best Local Similarity 88.9%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 255 CAACACCAATTTCATCTC 238

RESULT 56
ACH91848
ID ACH91848 standard; DNA; 584 BP.
XX
AC ACH91848;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon probe #25043.
XX
KW Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
DR WPI; 2004-119264/12.

XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
PS Claim 1; SEQ ID NO 25043; 80pp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above- mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ Sequence 584 BP; 145 A; 166 C; 66 G; 204 T; 0 U; 3 Other;

Query Match 82.2%; Score 14.8; DB 12; Length 584;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 364 CCACACTTATTCCTACTC 381

RESULT 57
ABQ20739
ID ABQ20739 standard; DNA; 591 BP.
XX
AC ABQ20739;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 7330.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.

XX 07-MAR-2002.
XX
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
XX 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
PS
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 591 BP; 230 A; 175 C; 52 G; 134 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 591;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 566 CAACACCTATTTCATAATC 583

RESULT 58
ABQ20738/c
ID ABQ20738 standard; DNA; 591 BP.
XX
XX ABQ20738;
AC
XX 12-JUL-2002 (first entry)
DT
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 7329.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
OS
XX WO200218632-A2.
PN
XX 07-MAR-2002.
XX
PD 07-MAR-2002.
XX
XX 07-MAR-2002.

PF 01-SEP-2001; 2001WO-EP010074.
XX
XX 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
PS
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 591 BP; 134 A; 52 C; 175 G; 230 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 591;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 26 CAACACCTATTTCATAATC 9

RESULT 59
ABQ26403
ID ABQ26403 standard; DNA; 601 BP.
XX
XX ABQ26403;
AC
XX 12-JUL-2002 (first entry)
DT
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12994.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
OS
XX WO200218632-A2.
PN
XX 07-MAR-2002.
PD
XX 01-SEP-2001; 2001WO-EP010074.
PF
XX 01-SEP-2000; 2000DE-01043826.
PR

```
PR 05-SEP-2000; 2000DE-01044543.
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful for
DR diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
PT
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
PS
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 601 BP; 183 A; 266 C; 70 G; 82 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 601;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 164 CCACCCCTACTCATCTC 181

RESULT 60
ABQ26402/c
ID ABQ26402 standard; DNA; 601 BP.
XX
AC ABQ26402;
XX
XX 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12993.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
XX WO200218632-A2.
PN
XX
XX 07-MAR-2002.
PD
XX
XX 01-SEP-2001; 2001WO-EP010074.
PF
XX
XX 01-SEP-2000; 2000DE-01043826.
PR
XX 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIG-) EPIGENOMICS AG.
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XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
PS
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX
SQ Sequence 601 BP; 82 A; 70 C; 266 G; 183 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 601;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 438 CCACCCCTACTCATCTC 421

Search completed: May 10, 2006, 04:14:04
Job time : 682 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 18:53:06 ; Search time 3760 Seconds
(without alignments)
223.981 Million cell updates/sec

Title: US-10-608-296-38
Perfect score: 18
Sequence: 1 ccacacctattcatactc 18
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length DB	ID	Description
C 1	18	100.0	263	1	AW873835
C 2	18	100.0	267	1	AA921407
C 3	18	100.0	270	1	AA921386
4	18	100.0	287	1	AA366418
C 5	18	100.0	289	1	AA844966
6	18	100.0	309	11	DQ047208
C 7	18	100.0	330	1	AA983889
C 8	18	100.0	349	3	BI791451
9	18	100.0	352	2	BG192232
10	18	100.0	356	6	CA867922
11	18	100.0	369	5	BU786585
12	18	100.0	380	5	BX113838
C 13	18	100.0	405	6	CA943648
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21	18	100.0	443	5	BU071934
22	18	100.0	444	3	BQ126651

C 23	18	100.0	448	5	BU949152
C 24	18	100.0	449	1	AA835575
C 25	18	100.0	449	5	BU949187
C 26	18	100.0	455	5	BU075990
C 27	18	100.0	459	1	AA845006
28	18	100.0	459	5	BU949393
C 29	18	100.0	465	3	BM504818
30	18	100.0	466	5	BU071991
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C 37	18	100.0	501	1	AA844755
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42	18	100.0	523	5	BU949426
C 43	18	100.0	523	5	BU952506
C 44	18	100.0	525	2	BE047053
C 45	18	100.0	526	3	BQ126412
C 46	18	100.0	526	3	BQ271518
47	18	100.0	526	5	BU951064
C 48	18	100.0	529	1	AA835293
49	18	100.0	529	3	BQ101169
C 50	18	100.0	532	1	AA835315
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C 52	18	100.0	539	1	AA844927
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54	18	100.0	552	3	BM264109
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58	18	100.0	577	4	BC013384
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63	18	100.0	581	3	BP324960
64	18	100.0	582	3	BP323989
65	18	100.0	582	3	BP324302
66	18	100.0	582	3	BP325524
67	18	100.0	583	3	BP323356
68	18	100.0	584	3	BP322177
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70	18	100.0	584	3	BP322827
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C 86	16.4	91.1	415	1	AA835121
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88	16.4	91.1	453	6	CF705448
C 89	16.4	91.1	482	1	AA536183
90	16.4	91.1	578	6	CF691710
91	16.4	91.1	589	6	CB230127
92	16.4	91.1	594	9	AQ725293
93	16.4	91.1	597	2	CF721282
94	16.4	91.1	608	2	BG907012
95	16.4	91.1	630	6	CF718422

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BU949187	in67b10.x
BU075990	im52h05.x
AA845006	ak61f09.s
BU949393	in66f07.y
BM504818	ig90h06.x
BU071991	im52h05.y
AA921338	ak56a06.s
BM505143	ig90h06.y
BG142111	ia49b01.y
AA835294	ak66b10.s
CK902774	in68e07.x
A1985509	ws08d11.x
AA844755	ak59b12.s
BQ631720	il21c12.y
BU949263	in68e07.x
BU952425	io74d05.x
AW583679	ia03a06.y
BU949426	in67b10.y
BU952506	io75d05.x
BE047053	hq55g05.x
BQ126412	il17e08.x
BQ271518	ik15a01.x
BU951064	io75d05.y
AA835293	ak66b09.s
BQ101169	ij24h05.y
AA835315	ak66e08.s
BU950978	io74d05.y
AA844927	ak61a06.s
BQ632018	il21c12.x
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CK902775	in68e07.y
A1925956	whl2g03.x
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BP324031	BP324031
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BP324960	BP324960
BP323989	BP323989
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BP323356	BP323356
BP322177	BP322177
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BP322827	BP322827
BP322937	BP322937
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DQ047209	Pan trogl
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BG185996	RST4952.A
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BZ835788	CH240.236
AA835121	ak63e02.s
BQ171759	WHE1659-1
CF705448	CCAFR13TO
AA536183	nf96c06.s
CF691710	CCAGK20TF
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AQ725293	HS.5404.A
CF721282	CCAFQ13TO
BG907012	TaLr1156E
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103 16.4 91.1 739 6 CF695153
c 104 16.4 91.1 756 10 AG125573
c 105 16.4 91.1 764 9 CC526286
c 106 16.4 91.1 769 11 CR079365
107 16.4 91.1 772 10 AG426024
108 16.4 91.1 781 6 CF702140
109 16.4 91.1 785 6 CF690792
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112 16.4 91.1 821 6 CF699771
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117 16.4 91.1 902 10 CL067667
118 16.4 91.1 912 6 CF684468
119 16.4 91.1 1038 9 CC303390
120 16.4 91.1 1065 10 CL069301
121 16.4 91.1 2358 4 AK082210
122 16 88.9 162 2 BE816984
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145 15.4 85.6 337 3 BP687159
c 146 15.4 85.6 357 10 BX121953
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ALIGNMENTS

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sequence.
ACCESSION AW873835
VERSION AW873835.1 GI:8007888
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
```

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Hominidae; Homo.
REFERENCE 1 (bases 1 to 263)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 231.
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Average insert size 1.1 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 100.0%; Score 18; DB 1; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
|||
Db 262 CCACACCTATTTCATCTC 245
RESULT 2
AA921407/c 267 bp mRNA linear EST 20-APR-1998
LOCUS ak56h08.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
DEFINITION IMAGE:1411935 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION AA921407
VERSION AA921407.1 GI:3068186
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 267)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
FEATURES
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1..267
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1st strand cDNA was primed with a Not I - oligo(dT) primer
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TGTTACGAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT
3'] ; double-stranded cDNA was ligated to Eco RI adaptors
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Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead. "

ORIGIN

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 253 CCACACCTATTCACTC 236

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LOCUS
DEFINITION
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IMAGE:1411907 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN) ;, mRNA sequence.

ACCESSION
AA921386
VERSION
AA921386.1 GI:3068165
KEYWORDS
EST.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 270)
AUTHORS
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham.

TITLE
JOURNAL
COMMENT
Location/Qualifiers
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/lab_host="DH10B"
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1st strand cDNA was primed with a Not I - oligo(dT) primer
[5,
TGTTACGAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT

3'] ; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead. "

ORIGIN

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 262 CCACACCTATTCACTC 245

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LOCUS
DEFINITION
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EST77396 Pancreas tumor III Homo sapiens cDNA 5' end similar to
phospholipase A2 (GB:M21054), mRNA sequence.

ACCESSION
AA366418
VERSION
AA366418.1 GI:2018768
KEYWORDS
EST.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 287)
AUTHORS
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
7566098
Other_ESTs: THCL65995
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1. .287
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||

Db 261 CCACACCTATTTCATCTC 278

RESULT 5
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LOCUS
DEFINITION
ak57el2.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1412014 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION
AA844966
VERSION
AA844966.1 GI:2931417
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 289)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES
source
1. .289
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1412014"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACGAATCTGAAGTGGGAGCGGCCCTTTTtttttttttttttttttt
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead."

ORIGIN
Query Match 100.0%; Score 18; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||

Db 200 CCACACCTATTTCATCTC 183

RESULT 6
DQ047208
, LOCUS

DEFINITION
Homo sapiens PLA2G1B gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
DQ047208
VERSION
DQ047208.1 GI:66900407
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 309)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)

JOURNAL
PUBMED
15869325
REFERENCE
2 (bases 1 to 309)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES
Location/Qualifiers
1. .309
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
<1. .>309
/gene="PLA2G1B"
/locus_tag="HC15100"

ORIGIN
Query Match 100.0%; Score 18; DB 11; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCATCTC 18
|||||

Db 82 CCACACCTATTCATCTC 99

RESULT 7
AA983889/c
LOCUS
DEFINITION
AA983889 330 bp mRNA linear EST 07-JUL-1998
op63d03.s1 Soares NFL T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1581509 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION
AA983889
VERSION
AA983889.1 GI:3162414
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 330)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2522 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES	source	Location/Qualifiers											
		1. .330											
		/organism="Homo sapiens"											
		/mol_type="mRNA"											
		/db_xref="taxon:9606"											
		/clone="IMAGE:1581509"											
		/lab_host="DH10B"											
		/clone_lib="Soares_NFL_T_GBC_S1"											
		/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."											
		ORIGIN											
Query Match 100.0%; Score 18; DB 1; Length 330;													
Best Local Similarity 100.0%; Pred. No. 1.8e+02;													
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;													
QY	1	CCACACCTATTTCATACTC 18											
Db	250	CCACACCTATTTCATACTC 233											
RESULT 8	BI791451/c	LOCUS											
		BI791451 349 bp mRNA linear EST 11-MAR-2002											
		id98b09.x1 HR85 islet Homo sapiens cDNA clone IMAGE:5085640 3' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.											
		ACCESSION											
		VERSION											
		KEYWORDS											
		SOURCE											
		ORGANISM											
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.											
		1 (bases 1 to 349)											
REFERENCE	AUTHORS	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.											
		Endocrine Pancreas Consortium											
		Unpublished (2000)											
		Other_ESTs: id98b09.y1											
		Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue											
		Endocrine Pancreas Consortium											
		Harvard University, Howard Hughes Medical Institute											
		Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138											
		Tel: 617-495-1812											
		Fax: 617-495-8557											
Email: dmelton@biohp.harvard.edu													
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)													
Seq primer: -40UP from Gibco.													
Location/Qualifiers													
1. .349													
/organism="Homo sapiens"													
/mol_type="mRNA"													
/db_xref="taxon:9606"													
FEATURES	source	ORIGIN											
		Query Match 100.0%; Score 18; DB 1; Length 330;											
		Best Local Similarity 100.0%; Pred. No. 1.8e+02;											
		Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
		QY	1	CCACACCTATTTCATACTC 18									
		Db	250	CCACACCTATTTCATACTC 233									
		RESULT 9	BG192232	LOCUS									
				BG192232 352 bp mRNA linear EST 21-APR-2001									
				RST11340 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.									
				ACCESSION									
VERSION													
KEYWORDS													
SOURCE													
ORGANISM													
Homo sapiens (human)													
Homo sapiens													
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.													
1 (bases 1 to 352)													
REFERENCE	AUTHORS	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.											
		Creation of genome-wide protein expression libraries using random activation of gene expression											
		Nat. Biotechnol. 19 (5), 440-445 (2001)											
		PUBMED											
		COMMENT											
		Contact: Scott J. Cain											
		Athersys, Inc.											
		3201 Carnegie Ave, Cleveland, OH 44115, USA											
		Tel: 216 431 9900											
		Fax: 216 361 9596											
Email: scain@athersys.com													
High quality sequence stop: 352.													
Location/Qualifiers													
1. .352													
/organism="Homo sapiens"													
/mol_type="mRNA"													
/db_xref="taxon:9606"													
/cell_line="HT1080"													
/clone_lib="Athersys RAGE Library"													
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."													
ORIGIN													
Query Match 100.0%; Score 18; DB 2; Length 352;													
Best Local Similarity 100.0%; Pred. No. 1.8e+02;													
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;													
QY	1	CCACACCTATTTCATACTC 18											

Db 88 CCACACCTATTTCATCTC 105
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CA867922 356 bp mRNA linear EST 20-DEC-2002
ir83a11.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6608758 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
CA867922 GI:27319471
CA867922.1 GI:27319471
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 356)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 357
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .356
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6608758"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 356;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCACACCTATTTCATCTC 18
|||||
Db 95 CCACACCTATTTCATCTC 112
RESULT 11
BU786585

LOCUS BU786585 369 bp mRNA linear EST 11-OCT-2002
DEFINITION in56905.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6126153 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
BU786585
BU786585.1 GI:238333402
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 369)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 257.
Location/Qualifiers
1. .369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6126153"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
ORIGIN
Query Match 100.0%; Score 18; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCACACCTATTTCATCTC 18
|||||
Db 201 CCACACCTATTTCATCTC 218
RESULT 12
BX113838
LOCUS BX113838 380 bp mRNA linear EST 07-FEB-2003
DEFINITION BX113838 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE998E093695; IMAGE:1461104, mRNA sequence.
BX113838
BX113838.1 GI:27879441
EST.
Homo sapiens (human)
SOURCE

ORGANISM	Homo sapiens	Hitllier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
REFERENCE	1 (bases 1 to 380)	Endocrine Pancreas Consortium
AUTHORS	Ebert,L., Heil,O., Hennig,S., Neubert.P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.	Unpublished (2000)
TITLE	Human Unigeneset - RZPD3	Other_ESTs: ir83a11.y1
JOURNAL	Unpublished (2003)	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
COMMENT	Contact: Ina Rolfs	Endocrine Pancreas Consortium
	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH	Harvard University, Howard Hughes Medical Institute
	Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany	Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
	RZPD; IMAGp998E093695.	Tel: 617-495-1812
	RZPDLIB; I.M.A.G.E. CDNA Clone Collection;	Fax: 617-495-8557
	Human Unigeneset - RZPD3 (RZPDLIB No.972)	Email: dmelton@biohp.harvard.edu
	http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972	Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH	Seq primer: -40RP from Gibco.
	Heubnerweg 6, D-14059 Berlin, Germany	
	Tel: +49 30 32639 101	
	Fax: +49 30 32639 111	
	www.rzpd.de	
FEATURES	This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.	
source	Location/Qualifiers	
	1. .380	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="IMAGp998E093695 ; IMAGE:1461104"	
	/lab_host="DH10B"	
	/clone_lib="Soares_NFL_T_GBC_S1"	
	/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "	
ORIGIN		
	Query Match 100.0%; Score 18; DB 5; Length 380;	
	Best Local Similarity 100.0%; Pred. No. 1.8e+02;	
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CCACACCTATTTCATCTC 18	
Db		
	116 CCACACCTATTTCATCTC 133	
RESULT 13		
CA943648/c		
LOCUS	CA943648	
DEFINITION	ir83a11.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6608758 3'	
	similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.	
ACCESSION	CA943648.1 GI:27432128	
VERSION	EST.	
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 405)	
AUTHORS	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,	

TITLE	JOURNAL	Hitllier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
COMMENT	Unpublished (2000)	Endocrine Pancreas Consortium
	Other_ESTs: ir83a11.y1	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
	Endocrine Pancreas Consortium	Harvard University, Howard Hughes Medical Institute
	Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138	Tel: 617-495-1812
	Fax: 617-495-8557	Email: dmelton@biohp.harvard.edu
	Email: dmelton@biohp.harvard.edu	Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
FEATURES	Seq primer: -40RP from Gibco.	
source	Location/Qualifiers	
	1. .405	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:6608758"	
	/tissue_type="Purified pancreatic islet"	
	/lab_host="DH10B"	
	/clone_lib="HR85 islet"	
	/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."	
ORIGIN		
	Query Match 100.0%; Score 18; DB 6; Length 405;	
	Best Local Similarity 100.0%; Pred. No. 1.8e+02;	
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CCACACCTATTTCATCTC 18	
Db		
	249 CCACACCTATTTCATCTC 232	
RESULT 14		
CA943649/c		
LOCUS	CA943649	
DEFINITION	ir83a12.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6608760 3'	
	similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.	
ACCESSION	CA943649.1 GI:27432129	
VERSION	EST.	
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 405)	
AUTHORS	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,	

TITLE	JOURNAL	Hitllier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
COMMENT	Unpublished (2000)	Endocrine Pancreas Consortium
	Other_ESTs: ir83a12.y1	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
	Endocrine Pancreas Consortium	Harvard University, Howard Hughes Medical Institute
	Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138	Tel: 617-495-1812
	Fax: 617-495-8557	Email: dmelton@biohp.harvard.edu
	Email: dmelton@biohp.harvard.edu	Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
FEATURES	Seq primer: -40RP from Gibco.	
source	Location/Qualifiers	
	1. .405	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:6608758"	
	/tissue_type="Purified pancreatic islet"	
	/lab_host="DH10B"	
	/clone_lib="HR85 islet"	
	/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."	
ORIGIN		
	Query Match 100.0%; Score 18; DB 6; Length 405;	
	Best Local Similarity 100.0%; Pred. No. 1.8e+02;	
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CCACACCTATTTCATCTC 18	
Db		
	249 CCACACCTATTTCATCTC 232	
RESULT 14		
CA943649/c		
LOCUS	CA943649	
DEFINITION	ir83a12.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6608760 3'	
	similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.	
ACCESSION	CA943649.1 GI:27432129	
VERSION	EST.	
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 405)	
AUTHORS	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,	

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)

Seq primer: -40RP from Gibco.

Location/Qualifiers

FEATURES

source

1. .405
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6608760"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
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Db 249 CCACACCTATTTCATCTC 232

RESULT 15

BI712863

LOCUS

DEFINITION BI712863 409 bp mRNA linear EST 11-MAR-2002
id98b09.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5085640 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.

BI712863 1 GI:15688558

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 409)

REFERENCE

AUTHORS

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)

Trace considered overall poor quality

Seq primer: -40RP from Gibco

High quality sequence stop: 1.

FEATURES

source

1. .409
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5085640"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
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Db 241 CCACACCTATTTCATCTC 258

RESULT 16

CA867923

LOCUS

DEFINITION CA867923 416 bp mRNA linear EST 20-DEC-2002
ir83a12.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6608760 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.

CA867923

CA867923.1 GI:27319472

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 416)

REFERENCE

AUTHORS

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)

Putative full length read

vector to vector length is

FEATURES	Seq primer: -40UP from Gibco.	
	Location/Qualifiers	
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	/tissue_type="Purified pancreatic islet"	
	/lab_host="DH10B"	
	/clone_lib="HR85 islet"	
	/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."	
	ORIGIN	
	Query Match	100.0%; Score 18; DB 6; Length 416;
Best Local Similarity	100.0%; Pred. No. 1.8e+02;	
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	CCACACCTATTTCATCTC 18
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	Db	
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	BU949507	
	LOCUS	
	DEFINITION	
	ACCESSION	
	VERSION	
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	SOURCE	
	ORGANISM	
REFERENCE	AUTHORS	
	COMMENT	
	TITLE	
	AUTHORS	
	REFERENCE	
	ORGANISM	
	SOURCE	
	KEYWORDS	
	VERSION	
	ACCESSION	
	DEFINITION	
	LOCUS	
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FEATURES	Seq primer: -40RP from Gibco.	
	Putative full length read	
	Vector to vector length is 470	
	obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)	
	Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on	
	Email: dmelton@biohp.harvard.edu	
	Fax: 617-495-8557	
	Tel: 617-495-1812	
	MA 02138	
	Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,	
	Harvard University, Howard Hughes Medical Institute	
	Endocrine Pancreas Consortium	
	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue	
	Other ESTs: in68e07.x1	
FEATURES	Unpublished (2000)	
	Endocrine Pancreas Consortium	
	Williams, T., Jackson, Y. and Bowers, Y.	
	Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,	
	Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,	
	Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,	
	Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,	
	Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,	
	1 (bases 1 to 423)	
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
FEATURES	EST.	
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	similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA	
	in68e07.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6127213 5'	
	BU949507	
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	BU949507	
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	DEFINITION	
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FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
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FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
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FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
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FEATURES	Unpublished (1997)	
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	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
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FEATURES	Unpublished (1997)	
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	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
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	Homo sapiens (human)	
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FEATURES	Unpublished (1997)	
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	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
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	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
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FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
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FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
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FEATURES	Unpublished (1997)	
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	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
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FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
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FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
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FEATURES	Unpublished (1997)	
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	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
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FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
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	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
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FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	
	Tumor Gene Index	
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
	1 (bases 1 to 425)	
	Hominidae; Homo.	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Homo sapiens	
	Homo sapiens (human)	
	AW139696	
	AW139696.1 GI:6144414	
	EST.	
	AW139696	
FEATURES	Unpublished (1997)	

NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6, NCI_CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI_CGAP_Pt22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351). Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_TISSUE=lung
TAG_LIB=NCI_CGAP_Lu5
TAG_SEQ=CAAC"

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 265 CCACACCTATTTCATCTC 248

RESULT 19
BQ271823

LOCUS BQ271823 426 bp mRNA linear EST 15-JUL-2003
DEFINITION ik15a01.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5781000 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.

ACCESSION BQ271823
VERSION BQ271823.1 GI:20496890
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 426)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE
JOURNAL
COMMENT

Other ESTs: ik15a01.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Putative full length read

FEATURES
source

vector to vector length is 465
Seq primer: -40RP from Gibco
High quality sequence stop: 403.
Location/Qualifiers
1..426
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5781000"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 201 CCACACCTATTTCATCTC 218

RESULT 20
BQ100865/c

LOCUS

DEFINITION

BQ100865 442 bp mRNA linear EST 29-APR-2002
ij24h05.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:6135800 3' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 442)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Other_ESTs: ij24h05.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center This clone is available royalty-free through LLNL; please contact the IMAGE consortium (info@image.llnl.gov) for further information
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..442

FEATURES

source

<pre>/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6135800" /sex="Both" /tissue_type="Islets of Langerhans" /dev_stage="Adult" /lab_host="DH10B" /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1" /note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1; Site 2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."</pre>		<pre>Location/Qualifiers 1. .443 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6038726" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /clone_lib="HR85 islet" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: Not1; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."</pre>	
ORIGIN		ORIGIN	
<pre>Query Match 100.0%; Score 18; DB 3; Length 442; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>		<pre>Query Match 100.0%; Score 18; DB 5; Length 443; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	
QY	1 CCACACCTATTTCATCTC 18	QY	1 CCACACCTATTTCATCTC 18
Db	167 CCACACCTATTTCATCTC 150	Db	202 CCACACCTATTTCATCTC 219
<pre>RESULT 21 BU071934 LOCUS DEFINITION BU071934.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6038726 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.</pre>		<pre>RESULT 22 BQ126651 LOCUS DEFINITION BQ126651.y1 Melton Amplified Mouse El6 5 Pancreas 3 M16S1 A Mus musculus cDNA clone IMAGE:5942102 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.</pre>	
<pre>ACCESSION VERSION KEYWORDS SOURCE ORGANISM Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 443) Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y. Endocrine Pancreas Consortium Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Putative full length read vector to vector length is 463 Seq primer: -40RP from Gibco High quality sequence stop: 404.</pre>		<pre>ACCESSION VERSION KEYWORDS SOURCE ORGANISM Mus musculus (house mouse) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus. 1 (bases 1 to 444) Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y. Endocrine Pancreas Consortium Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center This clone is available royalty-free through LNL; please contact the IMAGE consortium (info@image.llnl.gov) for further information Putative full length read vector to vector length is 526 Seq primer: -40RP from Gibco. Location/Qualifiers 1. .444 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:5942102"</pre>	
FEATURES		FEATURES	
source		source	

/sex="Both"
/tissue_type="pancreas"
/dev_stage="Embryonic day E16.5"
/lab_host="DH10B"
/clone_lib="Melton Amplified Mouse E16 5 Pancreas 3 M16S1 A"
/note="Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1;
Library constructed using SuperScript Plasmid Library kit
(Life Technologies). cDNA made by oligo-dT priming.
Size-selected by column fractionation; average insert size
0.97 kb. Amplified once on solid support. cDNA library
Preparation: Guolin Chen."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 267 CCACACCTATTTCATCTC 284

RESULT 23

BU949152/c
LOCUS BU949152 448 bp mRNA linear EST 21-OCT-2002
DEFINITION in66f07.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6127237 3' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
ACCESSION BU949152
VERSION BU949152.1 GI:24200503
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 448)

REFERENCE AUTHORS

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE JOURNAL COMMENT

Other ESTs: in66f07.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohpc.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .448

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6127237"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: Not1; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning.

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 248 CCACACCTATTTCATCTC 231

RESULT 24

AA835575/c
LOCUS AA835575 449 bp mRNA linear EST 23-FEB-1998
DEFINITION ak68h10.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone IMAGE:1413091 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AA835575
VERSION AA835575.1 GI:2909303
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)

REFERENCE AUTHORS

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)

TITLE JOURNAL COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .449

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1413091"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACGAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead."

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 459)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 377.
Location/Qualifiers
1. .459
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1412393"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACGAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead."

FEATURES
source

1. .459
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1412393"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACGAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead."

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 263 CCACACCTATTTCATCTC 246

RESULT 28
BU949393
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BU949393 459 bp mRNA linear EST 21-OCT-2002
in66f07.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6127237 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
BU949393
BU949393.1 GI:24200744
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 459)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

REFERENCE
AUTHORS
TITLE
JOURNAL

BU949393 459 bp mRNA linear EST 21-OCT-2002
in66f07.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6127237 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
BU949393
BU949393.1 GI:24200744
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 459)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 523
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .459
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6127237"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 262 CCACACCTATTTCATCTC 279

RESULT 29
BM504818/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM504818 465 bp mRNA linear EST 14-FEB-2002
ig90h06.x1 HR85 islet Homo sapiens cDNA 3' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
BM504818
BM504818.1 GI:18667671
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 465)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM504818 465 bp mRNA linear EST 14-FEB-2002
ig90h06.x1 HR85 islet Homo sapiens cDNA 3' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
BM504818
BM504818.1 GI:18667671
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 465)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM504818 465 bp mRNA linear EST 14-FEB-2002
ig90h06.x1 HR85 islet Homo sapiens cDNA 3' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
BM504818
BM504818.1 GI:18667671
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 465)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM504818 465 bp mRNA linear EST 14-FEB-2002
ig90h06.x1 HR85 islet Homo sapiens cDNA 3' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
BM504818
BM504818.1 GI:18667671
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 465)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 375.
Location/Qualifiers
1. .465
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

FEATURES
source

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 465;
Best Local Similarity 100.0%; Pred. NO. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
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Db 253 CCACACCTATTCTACTC 236

RESULT 30

BU071991

LOCUS

DEFINITION BU071991 466 bp mRNA linear EST 27-AUG-2002
im52h05.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6039008 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 466)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Other ESTs: im52h05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 541

FEATURES
source

Seq primer: -40RP from Gibco.
Location/Qualifiers
1. .466
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6039008"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 466;
Best Local Similarity 100.0%; Pred. NO. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
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Db 281 CCACACCTATTCTACTC 298

RESULT 31

AA921338/c

LOCUS

DEFINITION

AA921338 474 bp mRNA linear EST 20-APR-1998
ak56a06.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1411858 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 474)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

TITLE

JOURNAL

COMMENT

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1411858"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)

FEATURES

source

REFERENCE 1 (bases 1 to 497)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 386.
Location/Qualifiers
1. .497
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2496597"
/lab host="DH10B"
/clone lib="NCI CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "

FEATURES
source
1. .497
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2496597"
/lab host="DH10B"
/clone lib="NCI CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "

ORIGIN
Query Match 100.0%; Score 18; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||

Db 253 CCACACCTATTCTACTC 236

RESULT 37
AA844755/c
LOCUS
DEFINITION
AA844755 501 bp mRNA linear EST 04-MAR-1998
ak59b12.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1412159 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.
AA844755
AA844755.1 GI:2931206
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 501)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

AA844755 501 bp mRNA linear EST 04-MAR-1998
ak59b12.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1412159 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.
AA844755
AA844755.1 GI:2931206
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 501)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 53.
Location/Qualifiers
1. .501
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1412159"
/sex="female"
/dev stage="adult, 34 years"
/lab_host="DH10B"
/clone lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACGAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead. "

ORIGIN
Query Match 100.0%; Score 18; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||

Db 268 CCACACCTATTCTACTC 251

RESULT 38
BQ631720
LOCUS
DEFINITION
BQ631720 517 bp mRNA linear EST 02-JUL-2002
il21c12.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6030718 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
BQ631720
BQ631720.1 GI:21683238
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 517)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
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Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 520
Seq primer: -40RP from Gibco
High quality sequence stop: 461.

FEATURES	Location/Qualifiers		
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ORIGIN			
Query Match 100.0%; Score 18; DB 5; Length 517;			
Best Local Similarity 100.0%; Pred. No. 1.9e+02;			
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	261	CCACACCTATTTCATCTC 278	
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LOCUS			
DEFINITION			
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sequence.			
ACCESSION			
BU949263			
VERSION	520 bp	mRNA	
KEYWORDS			
EST.			
SOURCE	Homo sapiens (human)	linear	
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
REFERENCE	1 (bases 1 to 520)		
AUTHORS			
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.			
Endocrine Pancreas Consortium			
Unpublished (2000)			
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Endocrine Pancreas Consortium			
Harvard University, Howard Hughes Medical Institute			
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/note="Organ			

Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||

Db 245 CCACACCTATTTCATCTC 228

RESULT 41
AW583679
LOCUS
DEFINITION
ia03a06.y1 Human Pancreatic Islets Homo sapiens cDNA clone
IMAGE:5637202 5' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION
AW583679.1 GI:7260653
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 522)
Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
Wyllie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
Bowers,Y.
WashU-Harvard Pancreas EST Project
Unpublished (2000)
Other_ESTs: ia03a06.x3

TITLE
JOURNAL
COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Libraries were constructed by Dr. Douglas Melton
DNA sequencing by: Washington University Genome Sequencing Center
For information on obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
This sequence now available from the IMAGE consortium, for clone
orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 397.

FEATURES
source
1. .522
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5637202"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Human Pancreatic Islets"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Library constructed using SuperScript
Plasmid Library kit (Life Technologies). cDNA made by
oligo-dT priming. Size-selected by column fractionation;
average insert size 1.08 kb. Primary library,
unamplified."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 18; DB 1; Length 522;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||

Db 282 CCACACCTATTTCATCTC 299

RESULT 42
BU949426
LOCUS
DEFINITION
BU949426 523 bp mRNA linear EST 21-OCT-2002
in67b10.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6127074 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.

ACCESSION
BU949426
VERSION
BU949426.1 GI:24200777
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 523)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: in67b10.x1

TITLE
JOURNAL
COMMENT
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 524
Seq primer: -40RP from Gibco
High quality sequence stop: 467.

FEATURES
source
1. .523
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6127074"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 CCACACCTATTCACTC 18
Db 263 CCACACCTATTCACTC 280

RESULT 43
BU952506/c
LOCUS
DEFINITION
BU952506 523 bp mRNA linear EST 21-OCT-2002
io75d05.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6132152 3'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
BU952506
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 523)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Email: dmelton@biohp.harvard.edu
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 409.
Location/Qualifiers
1 .523
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6132152"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match 100.0%; Score 18; DB 5; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTCACTC 18
Db 248 CCACACCTATTCACTC 231

RESULT 44
BU952506/c
LOCUS
DEFINITION
BU952506 523 bp mRNA linear EST 19-APR-2002
ii17e08.x1 Melton Amplified Mouse E16 5 Pancreas 3 M16S1 A Mus
musculus cDNA clone IMAGE:5942102 3' similar to SW:PA21_HUMAN
P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
BU952506
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 526)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,

```

Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: i117e08.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LLNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Seq primer: -40UP from Gibco
High quality sequence stop: 443.

TITLE
JOURNAL
COMMENT

FEATURES
source
1. .526
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5942102"
/sex="Both"
/tissue_type="pancreas"
/dev_stage="Embryonic day E16.5"
/lab_host="DH10B"
/clone_lib="Melton Amplified Mouse E16 5 Pancreas 3 M16S1
A"
/note="Vector: pSPORT1; Site 1: Not 1; Site 2: Sal 1;
Library constructed using SuperScript Plasmid Library kit
(Life Technologies). cDNA made by oligo-dT priming.
Size-selected by column fractionation; average insert size
0.97 kb. Amplified once on solid support. cDNA Library
Preparation: Guolin Chen."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
|||||
Db 248 CCACACCTATTTCATCTC 231

RESULT 46
BQ271518/c
LOCUS
DEFINITION
BQ271518 526 bp mRNA linear EST 15-JUL-2003
ik15a01.x1 HR85 islet Homo sapiens cDNA clone IMAGE:5781000 3'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BQ271518 1 GI:20496584
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 526)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute

TITLE
JOURNAL
COMMENT

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 410.

FEATURES
source
1. .526
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5781000"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
|||||
Db 251 CCACACCTATTTCATCTC 234

RESULT 47
BU951064

LOCUS
DEFINITION
BU951064 526 bp mRNA linear EST 21-OCT-2002
io75d05.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6132152 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BU951064 1 GI:24202816
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 526)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

TITLE
JOURNAL
COMMENT

Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 484.
Location/Qualifiers

FEATURES

source
1. .526
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6132152"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 300 CCACACCTATTTCATCTC 317

RESULT 48

AA835293/c
LOCUS
DEFINITION
AA835293
ak66b09.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1412825 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

TITLE

JOURNAL
COMMENT
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 478.

FEATURES

source
1. .529
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1412825"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"

/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoRI; Site 2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACGAATCTGAAGTGGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead. "

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 529;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 252 CCACACCTATTTCATCTC 235

RESULT 49

BQ101169
LOCUS
DEFINITION
BQ101169
ij24h05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6135800 5' similar to SW:PA21_HUMAN P04054
PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.

TITLE

JOURNAL
COMMENT
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: ij24h05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LLNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Putative full length read

vector to vector length is 572

Seq primer: -40RP from Gibco

High quality sequence stop: 475.

FEATURES

source
Location/Qualifiers
1. .529
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6135800"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;

Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 529;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACTATTTCATACTC 18
|||||
Db 280 CCACACTATTTCATACTC 297

RESULT 50

AA835315/c

LOCUS

DEFINITION AA835315 532 bp mRNA linear EST 23-FEB-1998
ak66e08.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1412870 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION

AA835315

VERSION

AA835315.1 GI:2909043

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 532)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 458.

FEATURES

source

Location/Qualifiers
1..532
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1412870"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
15'
TGTTACGAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.

ORIGIN

Library constructed by Bob Barstead. "

Query Match 100.0%; Score 18; DB 1; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATACTC 18
|||||
Db 254 CCACACCTATTTCATACTC 237

RESULT 51

BU950978

LOCUS

DEFINITION BU950978 537 bp mRNA linear EST 21-OCT-2002
io74d05.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6132129 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.

ACCESSION

BU950978

VERSION

BU950978.1 GI:24202730

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 537)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 572
Seq primer: -40RP from Gibco
High quality sequence stop: 480.

FEATURES

source

Location/Qualifiers
1..537
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6132129"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||

Db 313 CCACACCTATTTCATCTC 330

RESULT 52
AA844927/c
LOCUS
DEFINITION
IMAGE:1412338 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 423.

FEATURES
source
1..539
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1412338"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoRI; Site 2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5,
TGTTACGAATCTGAAGTGGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGGATCCCTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead."

ORIGIN
Query Match 100.0%; Score 18; DB 1; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||

Db 260 CCACACCTATTTCATCTC 243

RESULT 53
BQ632018/c
LOCUS
DEFINITION
il21c12.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6030718 3'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA

sequence.
BQ632018
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Other_ESTs: il21c12.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 455.

FEATURES
source
1..544
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6030718"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match 100.0%; Score 18; DB 5; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||

Db 249 CCACACCTATTTCATCTC 232

RESULT 54
BM264109
LOCUS
DEFINITION
ig31a01.y1 HR85 islet Homo sapiens cDNA 5' similar to SW:PA21_HUMAN
P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 552)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 473.
Location/Qualifiers
1. .552
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

FEATURES
source

Query Match 100.0%; Score 18; DB 3; Length 552;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
|||||
Db 291 CCACACCTATTTCATCTC 308

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 552;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
|||||
Db 291 CCACACCTATTTCATCTC 308

RESULT 55
CK902775/c
LOCUS

DEFINITION

CK902775 553 bp mRNA linear EST 11-MAR-2004 in68e07.y5 HR85 islet Homo sapiens cDNA clone IMAGE:6127213 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CK902775 553 bp mRNA linear EST 11-MAR-2004 in68e07.y5 HR85 islet Homo sapiens cDNA clone IMAGE:6127213 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
CK902775
CK902775.1 GI:45364306
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 553)
Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.

REFERENCE
AUTHORS

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 552)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 473.
Location/Qualifiers
1. .552
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

FEATURES
source

Query Match 100.0%; Score 18; DB 3; Length 552;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
|||||
Db 291 CCACACCTATTTCATCTC 308

ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
|||||
Db 268 CCACACCTATTTCATCTC 251

RESULT 56
AI925956/c
LOCUS

DEFINITION

AI925956 562 bp mRNA linear EST 07-MAR-2000 wh12g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380564 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AI925956 562 bp mRNA linear EST 07-MAR-2000 wh12g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380564 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR (HUMAN);, mRNA sequence.
AI925956
AI925956.1 GI:5661920
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 562)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

REFERENCE
AUTHORS

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 562)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

TITLE
JOURNAL
COMMENT

WashU-Harvard Pancreas EST Project
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
This read is a 5' RESEQUENCE of a previously sequenced pancreas clone
Good hit to opposite strand read. .wrong orientation BUT PASSED FOR MOUSE-PANCREAS VERIFICATION
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .553
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6127213"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 7; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
|||||
Db 268 CCACACCTATTTCATCTC 251

RESULT 56
AI925956/c
LOCUS

DEFINITION

AI925956 562 bp mRNA linear EST 07-MAR-2000 wh12g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380564 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AI925956 562 bp mRNA linear EST 07-MAR-2000 wh12g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380564 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR (HUMAN);, mRNA sequence.
AI925956
AI925956.1 GI:5661920
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 562)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

REFERENCE
AUTHORS

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 562)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 672 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 462.
Location/Qualifiers
1. .562
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2380564"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 132376-132391, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "
ORIGIN
Query Match 100.0%; Score 18; DB 1; Length 562;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTCATCTC 18
|||||
Db 248 CCACACCTATTCATCTC 231
RESULT 57
BP323152
LOCUS
DEFINITION BP323152 Sugano cDNA library, pancreas Homo sapiens cDNA clone
PNC03992, mRNA sequence.
ACCESSION BP323152
VERSION BP323152.1 GI:52252127
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 572)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1. .572
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PNC03992"
/tissue type="pancreas"
/clone_lib="Sugano cDNA library, pancreas"
ORIGIN
Query Match 100.0%; Score 18; DB 3; Length 572;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTCATCTC 18

|||||
Db 302 CCACACCTATTCATCTC 319
RESULT 58
BC013384
LOCUS
DEFINITION BC013384 Homo sapiens, phospholipase A2, group IB (pancreas), clone
IMAGE:3950037, mRNA.
ACCESSION BC013384
VERSION BC013384.1 GI:15426542
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 577)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kettman and Anuradha Madan
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 31 Row: h Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4505846
This clone has the following problem: frame shifted.
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/db_xref="taxon:9606"
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/tissue type="pancreas"
/clone_lib="NIH_MGC_78"
/lab_host="DH10B"
/note="Vector: pDNR-LIB"
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTCATCTC 18
|||||
Db 306 CCACACCTATTCATCTC 323
RESULT 59
BP322008
LOCUS
DEFINITION BP322008 Sugano cDNA library, pancreas Homo sapiens cDNA clone
PNC01231, mRNA sequence.
ACCESSION BP322008
VERSION BP322008.1 GI:52250983
KEYWORDS EST.
SOURCE Homo sapiens (human)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 02:36:42 ; Search time 188 Seconds
(without alignments)
170.192 Million cell updates/sec

Title: US-10-608-296-38

Perfect score: 18
Sequence: 1 ccacacctattcatactc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	15.4	85.6	601	3	US-09-949-016-140490 Sequence 140490, Ap
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4	15.4	85.6	8533	2	US-07-845-989-6 Sequence 6, Appli
5	15.4	85.6	30172	3	US-09-949-002-660 Sequence 660, App
6	15.4	85.6	49487	3	US-09-949-016-15721 Sequence 15721, A
7	14.8	82.2	466	3	US-10-131-827-8758 Sequence 8758, Ap
8	14.8	82.2	482	3	US-09-270-767-29684 Sequence 29684, A
9	14.8	82.2	601	3	US-09-949-016-132353 Sequence 132353, Ap
10	14.8	82.2	601	3	US-09-949-016-140957 Sequence 140957, Ap
11	14.8	82.2	834	3	US-09-328-352-46 Sequence 46, Appli
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c 136 13.8 76.7 107750 3 US-09-949-016-12662 Sequence 12662, A
c 137 13.8 76.7 107751 3 US-09-949-016-15412 Sequence 15412, A
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ALIGNMENTS

RESULT 1
US-09-023-655-1200
; Sequence 1200, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO

Query Match 85.6%; Score 15.4; DB 3; Length 601;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACACCTATTCTACT 17

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1200:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g190012
US-09-023-655-1200

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Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 140490, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140490
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-140490

Db 307 CCACACCTATTGATACT 323
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US-07-846-181-6
; Sequence 6, Application US/07846181
; Patent No. 5360732
; GENERAL INFORMATION:
; APPLICANT: BERKA, RANDY M
; APPLICANT: FOWLER, TIMOTHY
; APPLICANT: REY, MICHAEL W
; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
; TITLE OF INVENTION: CATALASE-R
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
; STREET: 180 KIMBALL WAY
; CITY: SOUTH SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/846,181
; FILING DATE: 19920304
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HORN MS, MARGARET A
; REGISTRATION NUMBER: 33401
; REFERENCE/DOCKET NUMBER: GC204-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-742-7536
; TELEFAX: 415-742-7217
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-846-181-6
Query Match 85.6%; Score 15.4; DB 2; Length 8533;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATACT 17
Db 5921 CCACACCTATTTCCTACT 5937
RESULT 4
US-07-845-989-6
; Sequence 6, Application US/07845989
; Patent No. 5360901
; GENERAL INFORMATION:
; APPLICANT: BERKA, RANDY M
; APPLICANT: FOWLER, TIMOTHY
; APPLICANT: REY, MICHAEL W
; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
; TITLE OF INVENTION: CATALASE-R
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
; STREET: 180 KIMBALL WAY
; CITY: SOUTH SAN FRANCISCO
; STATE: CA
; COUNTRY: USA

; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/845,989
; FILING DATE: 19920304
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HORN MS, MARGARET A
; REGISTRATION NUMBER: 33401
; REFERENCE/DOCKET NUMBER: GC208-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-742-7536
; TELEFAX: 415-742-7217
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-845-989-6
Query Match 85.6%; Score 15.4; DB 2; Length 8533;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
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RESULT 5
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; Sequence 660, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-660
Query Match 85.6%; Score 15.4; DB 3; Length 30172;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATACT 17
Db 28366 CCACACCTATTGATACT 28350
RESULT 6
US-09-949-016-15721
; Sequence 15721, Application US/09949016

```
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15721
; LENGTH: 49487
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(49487)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15721
```

```
Query Match      85.6%;   Score 15.4;   DB 3;   Length 49487;
Best Local Similarity 94.1%;   Pred. No. 1.5e+02;
Matches 16;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;
```

```
QY      1 CCACACCTATTTCATACT 17
      |||||
Db      22985 CCACACCTATTGATACT 23001
```

```
RESULT 7
US-10-131-827-8758/c
; Sequence 8758, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: LY, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8758
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(466)
; OTHER INFORMATION: n = A, C, T or G
US-10-131-827-8758
```

```
Query Match      82.2%;   Score 14.8;   DB 3;   Length 466;
Best Local Similarity 88.9%;   Pred. No. 2.1e+02;
Matches 16;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;
```

```
QY      1 CCACACCTATTTCATACT 18
      |||||
Db      298 CCACCTCTATCCATACT 281
```

```
RESULT 8
US-09-270-767-29684
; Sequence 29684, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29684
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-29684
```

```
Query Match      82.2%;   Score 14.8;   DB 3;   Length 482;
Best Local Similarity 88.9%;   Pred. No. 2.1e+02;
Matches 16;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;
```

```
QY      1 CCACACCTATTTCATACT 18
      |||||
Db      210 CCACATCTTTCATACT 227
```

```
RESULT 9
US-09-949-016-132353
; Sequence 132353, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132353
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; OTHER INFORMATION:
US-09-949-016-132353
```

```
Query Match      82.2%;   Score 14.8;   DB 3;   Length 601;
Best Local Similarity 88.9%;   Pred. No. 2.1e+02;
Matches 16;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;
```

```
QY      1 CCACACCTATTTCATACT 18
      |||||
Db      423 CCACACCTATTTCACAC 440
```

```
RESULT 10
US-09-949-016-140957
; Sequence 140957, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```



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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140957
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-140957

Query Match      82.2%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTCTACTC 18
      ||||| ||||| |||
Db      141 CCACACCTATTCTACTC 158

RESULT 11
US-09-328-352-46
; Sequence 46, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 46
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-46

Query Match      82.2%; Score 14.8; DB 3; Length 834;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTCTACTC 18
      ||||| ||||| |||||
Db      468 CCAGACATATTCTACTC 485

RESULT 12
US-09-270-767-13670
; Sequence 13670, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13670
; LENGTH: 1298
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-13670

Query Match      82.2%; Score 14.8; DB 3; Length 1298;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTCTACTC 18
      ||||| ||||| |||||
Db      1026 CCACATCTTCTACTC 1043

RESULT 13
US-10-104-047-1028
; Sequence 1028, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1028
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1028

Query Match      82.2%; Score 14.8; DB 3; Length 3237;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTCTACTC 18
      ||||| ||||| |||||
Db      1669 CCACACCTATTCTACTC 1686

RESULT 14
US-09-575-081B-7
; Sequence 7, Application US/09575081B
; Patent No. 6692934
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: NOVEL ORGANIC ANION TRANSPORT PROTEINS
; FILE REFERENCE: DB23
; CURRENT APPLICATION NUMBER: US/09/575,081B
; CURRENT FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 60/135,081
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (713)..(713)
; OTHER INFORMATION: y = c or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2397)..(2397)
; OTHER INFORMATION: k = g or t
US-09-575-081B-7

Query Match      82.2%; Score 14.8; DB 3; Length 3692;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTCTACTC 18
      ||||| ||||| |||||
Db      1449 CCACACCTATTCTACTC 1466
```

```
RESULT 15
US-09-799-451-260
; Sequence 260, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 260
; LENGTH: 3725
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (718)..(2778)
US-09-799-451-260

Query Match      82.2%; Score 14.8; DB 3; Length 3725;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCACTC 18
Db      1550 CCACACCTATTATACCC 1567

RESULT 16
US-09-949-016-15540/c
; Sequence 15540, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15540
; LENGTH: 14673
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15540
```

```
Query Match      82.2%; Score 14.8; DB 3; Length 14673;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCACTC 18
Db      1622 CCACACCTTTTCACACTC 1605

RESULT 17
US-09-949-016-15491
; Sequence 15491, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15491
; LENGTH: 86877
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15491

Query Match      82.2%; Score 14.8; DB 3; Length 86877;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCACTC 18
Db      29326 CTACACATATTCACTC 29343

RESULT 18
US-09-949-016-15492
; Sequence 15492, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15492
; LENGTH: 86877
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15492

Query Match      82.2%; Score 14.8; DB 3; Length 86877;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | | |
Db 29326 CTACACATATTCTACTC 29343

RESULT 19
US-09-949-016-15729
; Sequence 15729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15729
; LENGTH: 148783
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(148783)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15729

Query Match 82.2%; Score 14.8; DB 3; Length 148783;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | | |
Db 140850 CCACACCTATTCTACTC 140867

RESULT 20
US-09-949-016-15830/c
; Sequence 15830, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15830
; LENGTH: 192506
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15830

Query Match 82.2%; Score 14.8; DB 3; Length 192506;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | | |

Db 129567 CCACACCTATTCTACAC 129550
| | | | | | | | | | | | | | | |

RESULT 21
US-09-949-016-13358/c
; Sequence 13358, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13358
; LENGTH: 260247
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13358

Query Match 82.2%; Score 14.8; DB 3; Length 260247;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | | |
Db 74550 CCACACCTATTCTGTACAC 74533

RESULT 22
US-09-949-016-17371
; Sequence 17371, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17371
; LENGTH: 373182
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(373182)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17371

Query Match 82.2%; Score 14.8; DB 3; Length 373182;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | | |

Db 274013 CCACACCTCTTCAGACTC 274030

RESULT 23

US-09-949-016-12062

; Sequence 12062, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12062

; LENGTH: 373694

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(373694)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12062

Query Match 82.2%; Score 14.8; DB 3; Length 373694;

Best Local Similarity 88.9%; Pred. No. 3.7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18

|||||

Db 274068 CCACACCTCTTCAGACTC 274085

RESULT 24

US-09-949-016-15473

; Sequence 15473, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15473

; LENGTH: 450395

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(450395)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15473

Query Match 82.2%; Score 14.8; DB 3; Length 450395;

Best Local Similarity 88.9%; Pred. No. 3.8e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18

|||||

Db 95949 CCACACCTATTCTACAC 95966

RESULT 25

US-09-949-016-49992

; Sequence 49992, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49992

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-49992

Query Match 80.0%; Score 14.4; DB 3; Length 601;

Best Local Similarity 93.8%; Pred. No. 3.4e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 16

|||||

Db 461 CCACACCTATTCTATCC 476

RESULT 26

US-09-949-016-49993

; Sequence 49993, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49993

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-49993

Query Match 80.0%; Score 14.4; DB 3; Length 601;

Best Local Similarity 93.8%; Pred. No. 3.4e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 16

|||||

Db 354 CCACACCTATTCTATCC 369


```
RESULT 27
US-09-543-681A-3390
; Sequence 3390, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3390
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3390

Query Match      80.0%; Score 14.4; DB 3; Length 1728;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACACCTATTTCATCT 17
Db      1152 CACACCTATTTCATCCT 1167

RESULT 28
US-10-104-047-150/c
; Sequence 150, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
; LENGTH: 3154
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-150

Query Match      80.0%; Score 14.4; DB 3; Length 3154;
Best Local Similarity 93.8%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATAC 16
Db      2863 CCACACATATTTCATAC 2848

RESULT 29
US-09-762-311-1
; Sequence 1, Application US/09762311
; Patent No. 6825004
; GENERAL INFORMATION:
; APPLICANT: BLUMENFELD, Marta
; APPLICANT: BOUGUELERET, Lydie
; APPLICANT: CHUMAKOV, Ilya
; TITLE OF INVENTION: Nucleic Acids Encoding Human TBC-1 Protein And Polymorphic Markers
; TITLE OF INVENTION: Thereof.
; FILE REFERENCE: 46.US2.PCT
; CURRENT APPLICATION NUMBER: US/09/762,311
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/095,653
```

```
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 17590
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..2000
; OTHER INFORMATION: 5' regulatory region
; NAME/KEY: exon
; LOCATION: 2001..2077
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 12292..12373
; OTHER INFORMATION: exon 1b
; NAME/KEY: exon
; LOCATION: 12740..13249
; OTHER INFORMATION: exon 2
; NAME/KEY: allele
; LOCATION: 9494
; OTHER INFORMATION: 99-430-352 : polymorphic base A or G
; NAME/KEY: primer_bind
; LOCATION: 9391..9408
; OTHER INFORMATION: 99-430.rp
; NAME/KEY: primer_bind
; LOCATION: 9828..9845
; OTHER INFORMATION: 99-430.pu complement
; NAME/KEY: primer_bind
; LOCATION: 9475..9493
; OTHER INFORMATION: 99-430-352.mis
; NAME/KEY: primer_bind
; LOCATION: 9495..9513
; OTHER INFORMATION: 99-430-352.mis complement
; NAME/KEY: primer_bind
; LOCATION: 9482..9506
; OTHER INFORMATION: 99-430-352.probe
; NAME/KEY: misc feature
; LOCATION: 3953,4056,4167,4739,6217,6245,6860,9998..9999,10006,10012,10104
; LOCATION: 10477,10822,10825,11095,11256,11273,11857..11858,11895..11896
; LOCATION: 14057,15912..15913,16217..16218,16329..16330,17504
; OTHER INFORMATION: n=a, g, c or t
US-09-762-311-1

Query Match      80.0%; Score 14.4; DB 3; Length 17590;
Best Local Similarity 93.8%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ACACCTATTTCATCT 18
Db      8958 ACACCTATTTCAACTC 8973

RESULT 30
US-09-949-016-13200
; Sequence 13200, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 13200
; LENGTH: 28494
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13200

Query Match      80.0%; Score 14.4; DB 3; Length 28494;
Best Local Similarity 93.8%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATAC 16
Db      5232 CCACACCTATTTCATCC 5247

RESULT 31
US-09-949-016-17285/c
; Sequence 17285, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17285
; LENGTH: 33353
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17285

Query Match      80.0%; Score 14.4; DB 3; Length 33353;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATAC 16
Db      4322 CCACACCTTTTCATAC 4307

RESULT 32
US-09-780-049-18/c
; Sequence 18, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-049-18

Query Match      80.0%; Score 14.4; DB 3; Length 40000;
Best Local Similarity 93.8%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATAC 16
```

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Qy      1 CCACACCTATTTCATAC 16
Db      3791 CCACACCTTTTCATAC 3776

RESULT 33
US-09-949-016-17192/c
; Sequence 17192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17192
; LENGTH: 107937
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(107937)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17192

Query Match      80.0%; Score 14.4; DB 3; Length 107937;
Best Local Similarity 93.8%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ACACCTATTTCATCTC 18
Db      59479 AGACCTATTTCATCTC 59464

RESULT 34
US-09-949-016-15393/c
; Sequence 15393, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15393
; LENGTH: 194790
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15393

Query Match      80.0%; Score 14.4; DB 3; Length 194790;
Best Local Similarity 93.8%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATAC 16
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Db      139221 CCACACCTATTCATTC 139206
|||||
RESULT 35
US-09-949-016-13840/c
; Sequence 13840, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13840
; LENGTH: 276687
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(276687)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13840
Query Match      80.0%; Score 14.4; DB 3; Length 276687;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACACCTATTCATAC 16
|||||
Db      181287 CCACACCTATTCATCC 181272

RESULT 36
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
Query Match      80.0%; Score 14.4; DB 3; Length 640681;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ACACCTATTCATCTC 18
|||||
Db      10623 ACACCTATTCATACAC 10608
```

```
RESULT 37
US-09-304-232-737
; Sequence 737, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; TITLE OF INVENTION: Hypertension
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304,232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084,641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 737
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PLA2AEX3 131
US-09-304-232-737
Query Match      77.8%; Score 14; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 ACCTATTCATCTC 18
|||||
Db      1 ACCTATTCATCTC 14

RESULT 38
US-09-513-999C-34796
; Sequence 34796, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 34796
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 47
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 63
; OTHER INFORMATION: v=a or c or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 130
; OTHER INFORMATION: d=a or g or t
US-09-513-999C-34796
Query Match      77.8%; Score 14; DB 3; Length 162;
```

Best Local Similarity 83.3%; Pred. No. 4.9e+02; Indels 0; Gaps 0; Mismatches 2; Conservative 15; Matches 15;

Qy 1 CCACACCTATTTCATCTC 18
| | | | | : | | | |
Db 51 CAACACCAATTCVTACTC 68

RESULT 39
US-09-949-016-168810/c
; Sequence 168810, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 168810
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-168810

Query Match 77.8%; Score 14; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCAT 14
| | | | | | | | | |
Db 400 CCACACCTATTTCAT 387

RESULT 40
US-09-533-559-293
; Sequence 293, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 293
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(636)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-293

Query Match 77.8%; Score 14; DB 3; Length 636;

Best Local Similarity 100.0%; Pred. No. 5.6e+02; Indels 0; Gaps 0; Mismatches 0; Conservative 14; Matches 14;

Qy 2 CACACCTATTTCATA 15
| | | | | | | | | |
Db 454 CACACCTATTTCATA 467

RESULT 41
US-09-328-352-321
; Sequence 321, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 321
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-321

Query Match 77.8%; Score 14; DB 3; Length 1020;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CACCTATTTCATACT 17
| | | | | | | | | |
Db 569 CACCTATTTCATACT 582

RESULT 42
US-09-949-016-17511/c
; Sequence 17511, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17511
; LENGTH: 44676
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17511

Query Match 77.8%; Score 14; DB 3; Length 44676;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CACCTATTTCATACT 17
| | | | | | | | | |
Db 18115 CACCTATTTCATACT 18102

RESULT 43
US-09-949-016-16502
; Sequence 16502, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16502
; LENGTH: 157032
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(157032)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16502

Query Match 77.8%; Score 14; DB 3; Length 157032;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCAT 14
|||||
Db 91068 CCACACCTATTTCAT 91081

RESULT 44
US-09-363-939A-153/c
; Sequence 153, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 65
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified base
; LOCATION: (1)..(65)
; OTHER INFORMATION: All pyrimidines are 2'F.

US-09-363-939A-153
Query Match 76.7%; Score 13.8; DB 3; Length 65;
Best Local Similarity 88.2%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CACACCTATTTCATCTC 18
|||||
Db 45 CACAGCTATACATCTC 29
RESULT 45
US-09-791-301-153/c
; Sequence 153, Application US/09791301
; Patent No. 6713616
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFBeta Nucleic Acid Ligands and
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX 87/C
; CURRENT APPLICATION NUMBER: US/09/791,301
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 65
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
; NAME/KEY: modified base
; LOCATION: (1)..(65)
; OTHER INFORMATION: All pyrimidines are 2'F.

US-09-791-301-153
Query Match 76.7%; Score 13.8; DB 3; Length 65;
Best Local Similarity 88.2%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CACACCTATTTCATCTC 18
|||||
Db 45 CACAGCTATACATCTC 29
RESULT 46
US-09-270-767-30909/c
; Sequence 30909, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30909
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-30909

Query Match 76.7%; Score 13.8; DB 3; Length 273;
Best Local Similarity 88.2%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATACT 17
|||||
Db 81 CCACACCTATCCATATT 65

RESULT 47
US-09-621-976-15284
; Sequence 15284, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15284
; LENGTH: 295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15284

Query Match 76.7%; Score 13.8; DB 3; Length 295;
Best Local Similarity 88.2%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATACT 17
|||||
Db 27 CCACAGCTATTCAGACT 43

RESULT 48
US-10-131-827-8755/c
; Sequence 8755, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8755
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8755

Query Match 76.7%; Score 13.8; DB 3; Length 496;

Best Local Similarity 88.2%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CACACCTATTTCATACTC 18
|||||
Db 262 CACTCCTATCCATACTC 246

RESULT 49
US-10-131-827-8885
; Sequence 8885, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8885
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(524)
; OTHER INFORMATION: n =A, C, T or G
US-10-131-827-8885

Query Match 76.7%; Score 13.8; DB 3; Length 524;
Best Local Similarity 88.2%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CACACCTATTTCATACTC 18
|||||
Db 462 CACTCCTATCCATACTC 478

RESULT 50
US-09-949-016-21757
; Sequence 21757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21757
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-21757

Query Match 76.7%; Score 13.8; DB 3; Length 601;

Best Local Similarity 88.2%; Pred. No. 7.1e+02; Indels 0; Gaps 0; Matches 15; Conservative 0; Mismatches 2;

QY 2 CACACCTATTCACTC 18
||| ||||| |||||
Db 21 CAGACCTATTCAAAC 37

RESULT 51
US-09-949-016-21758
; Sequence 21758, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21758
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-21758

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02; Indels 0; Gaps 0; Matches 15; Conservative 0; Mismatches 2;

QY 2 CACACCTATTCACTC 18
||| ||||| |||||
Db 112 CAGACCTATTCAAAC 128

RESULT 52
US-09-949-016-21759
; Sequence 21759, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21759
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-21759

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02; Indels 0; Gaps 0; Matches 15; Conservative 0; Mismatches 2;

QY 2 CACACCTATTCACTC 18
||| ||||| |||||

Db 426 CAGACCTATTCAAAC 442

RESULT 53
US-09-949-016-23388/c
; Sequence 23388, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23388
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-23388

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02; Indels 0; Gaps 0; Matches 15; Conservative 0; Mismatches 2;

QY 1 CCACACCTATTCACT 17
||| ||||| |||||
Db 234 CCACACCTATGCAC 218

RESULT 54
US-09-949-016-36971/c
; Sequence 36971, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36971
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-36971

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02; Indels 0; Gaps 0; Matches 15; Conservative 0; Mismatches 2;

QY 2 CACACCTATTCACTC 18
||| ||||| |||||
Db 184 CACAGCTATTCAAC 168

RESULT 55
US-09-949-016-67685/c

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; Sequence 67685, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67685
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-67685
```

```
Query Match          76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 CACACCTATTTCATCTC 18
        ||||| ||| |||||
Db      41 CACACCTGTTCTCTACTC 25
```

RESULT 56

```
US-09-949-016-67686/c
; Sequence 67686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67686
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-67686
```

```
Query Match          76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 CACACCTATTTCATCTC 18
        ||||| ||| |||||
Db      297 CACACCTGTTCTCTACTC 281
```

RESULT 57

```
US-09-949-016-86494/c
; Sequence 86494, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86494
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-86494
```

```
Query Match          76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 CACACCTATTTCATCTC 18
        ||||| ||| |||||
Db      62 CACACCTCTTTTACTC 46
```

RESULT 58

```
US-09-949-016-105324/c
; Sequence 105324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 105324
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105324
```

```
Query Match          76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 CACACCTATTTCATCTC 18
        ||||| ||| |||||
Db      306 CACACCTATACATACAC 290
```

RESULT 59

```
US-09-949-016-144569
; Sequence 144569, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
```


; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144569
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-144569

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACT 17
Db 417 CCACACCTAATCATATT 433

RESULT 60

US-09-949-016-153387
; Sequence 153387, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153387
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-153387

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACCTATTCTACTC 18
Db 128 CACACCTTTTCCTACTC 144

Search completed: May 10, 2006, 04:17:17
Job time : 197 secs

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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 19:12:50 ; Search time 425 Seconds
(without alignments)
350.232 Million cell updates/sec

Title: US-10-608-296-38

Perfect score: 18

Sequence: 1 ccaacacctattcatactc 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications_NA_Main.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-607-806-38	Sequence 38, Appl
2	18	100.0	224	US-10-060-036-3000	Sequence 3000, Ap
3	18	100.0	224	US-10-060-036-3110	Sequence 3110, Ap
4	18	100.0	224	US-10-060-036-3600	Sequence 3600, Ap
5	18	100.0	224	US-10-060-036-3604	Sequence 3604, Ap
6	18	100.0	224	US-10-060-036-3941	Sequence 3941, Ap
7	18	100.0	224	US-10-060-036-4030	Sequence 4030, Ap
8	18	100.0	427	US-10-425-115-153893	Sequence 153893,
9	18	100.0	445	US-09-925-297-414	Sequence 414, App
10	18	100.0	562	US-09-954-456-216	Sequence 216, App
11	18	100.0	562	US-09-954-456-822	Sequence 822, App
12	18	100.0	562	US-09-954-456-1225	Sequence 1225, Ap
13	18	100.0	562	US-10-641-643-1200	Sequence 1200, Ap
14	18	100.0	562	US-10-607-806-3	Sequence 3, Appli
15	18	100.0	562	US-10-843-641A-3243	Sequence 3243, Ap
16	18	100.0	562	US-10-843-641A-3849	Sequence 3849, Ap
17	18	100.0	562	US-10-843-641A-4252	Sequence 4252, Ap
18	18	100.0	585	US-10-712-124-27	Sequence 27, Appl
19	18	100.0	630	US-09-925-297-52	Sequence 52, Appl
20	18	100.0	644	US-10-330-051A-6	Sequence 6, Appli
21	18	100.0	654	US-10-450-763-11903	Sequence 11903, A
22	18	100.0	12174	US-10-607-806-1	Sequence 1, Appli
23	16.4	91.1	586	US-09-925-065A-935053	Sequence 935053,

24	16.4	91.1	586	4	US-09-925-065A-935054	Sequence 935054,
25	16.4	91.1	586	4	US-09-925-065A-952779	Sequence 952779,
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30	15.4	85.6	533	8	US-10-425-115-33674	Sequence 33674, A
c 31	15.4	85.6	567	4	US-09-925-065A-459786	Sequence 459786,
32	15.4	85.6	603	4	US-09-925-065A-366085	Sequence 366085,
33	15.4	85.6	611	7	US-10-021-323-1223	Sequence 1223, Ap
34	15.4	85.6	1202	5	US-10-027-632-122849	Sequence 122849,
35	15.4	85.6	1202	5	US-10-027-632-122850	Sequence 122850,
36	15.4	85.6	1202	6	US-10-027-632-122849	Sequence 122849,
37	15.4	85.6	1202	6	US-10-027-632-122850	Sequence 122850,
38	15.4	85.6	1733	8	US-10-767-795-899	Sequence 899, App
c 39	15.4	85.6	3093	3	US-09-938-842A-1570	Sequence 1570, Ap
c 40	15.4	85.6	3093	3	US-09-938-842A-1570	Sequence 1570, Ap
c 41	15.4	85.6	3120	6	US-10-347-470A-1	Sequence 1, Appli
c 42	15.4	85.6	17934	6	US-10-311-455-1691	Sequence 1691, Ap
c 43	15.4	85.6	118777	7	US-10-721-693-10	Sequence 10, Appl
c 44	15.4	85.6	118777	8	US-10-852-997-10	Sequence 10, Appl
45	15.4	85.6	439892	5	US-10-087-192-454	Sequence 454, App
c 46	15	83.3	136	7	US-10-242-535A-27057	Sequence 27057, A
c 47	15	83.3	136	7	US-10-085-783A-27057	Sequence 27057, A
c 48	15	83.3	446	8	US-10-425-115-78961	Sequence 78961, A
c 49	15	83.3	478	4	US-09-925-065A-817638	Sequence 817638,
c 50	15	83.3	478	4	US-09-925-065A-817639	Sequence 817639,
c 51	15	83.3	544	8	US-10-363-345A-14929	Sequence 14929, A
52	15	83.3	544	8	US-10-363-345A-14930	Sequence 14930, A
c 53	15	83.3	544	9	US-10-363-483A-14929	Sequence 14929, A
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55	14.8	82.2	203	7	US-10-424-599-127043	Sequence 127043,
56	14.8	82.2	241	8	US-10-425-115-104465	Sequence 104465,
57	14.8	82.2	323	7	US-10-424-599-72836	Sequence 72836, A
58	14.8	82.2	392	4	US-09-925-065A-614775	Sequence 614775,
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c 68	14.8	82.2	538	4	US-09-925-065A-523202	Sequence 523202,
c 69	14.8	82.2	538	4	US-09-925-065A-523203	Sequence 523203,
70	14.8	82.2	562	7	US-10-424-599-12484	Sequence 12484, A
c 71	14.8	82.2	565	4	US-09-925-065A-143110	Sequence 143110,
c 72	14.8	82.2	565	4	US-09-925-065A-143111	Sequence 143111,
c 73	14.8	82.2	568	4	US-09-925-065A-523201	Sequence 523201,
c 74	14.8	82.2	568	4	US-09-925-065A-523204	Sequence 523204,
c 75	14.8	82.2	584	4	US-09-925-065A-630983	Sequence 630983,
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c 79	14.8	82.2	587	5	US-10-027-632-134872	Sequence 134872,
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c 82	14.8	82.2	591	8	US-10-363-345A-7329	Sequence 7329, Ap
83	14.8	82.2	591	8	US-10-363-345A-7330	Sequence 7330, Ap
c 84	14.8	82.2	591	9	US-10-363-483A-7329	Sequence 7329, Ap
85	14.8	82.2	591	9	US-10-363-483A-7330	Sequence 7330, Ap
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c 88	14.8	82.2	601	9	US-10-363-483A-12993	Sequence 12993, A
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93	14.8	82.2	608	4	US-09-925-065A-858127	Sequence 858127,
c 94	14.8	82.2	611	4	US-09-925-065A-790417	Sequence 790417,
95	14.8	82.2	614	4	US-09-925-065A-832759	Sequence 832759,
96	14.8	82.2	616	4	US-09-925-065A-753972	Sequence 753972,


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RESULT 8
US-10-425-115-153893
; Sequence 153893, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 153893
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_7192C.1
US-10-425-115-153893

Query Match      100.0%; Score 18; DB 8; Length 427;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTCACTC 18
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Db      288 CCACACCTATTCACTC 305

RESULT 9
US-09-925-297-414
; Sequence 414, Application US/09925297
; Patent No. US2002081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 414
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (243)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (256)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (341)
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; NAME/KEY: misc feature
; LOCATION: (344)
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; NAME/KEY: misc feature
; LOCATION: (356)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (370)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: misc feature
; LOCATION: (416)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (442)
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US-09-925-297-414

Query Match      100.0%; Score 18; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      282 CCACACCTATTCACTC 299

RESULT 10
US-09-954-456-216
; Sequence 216, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 216
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-216

Query Match      100.0%; Score 18; DB 3; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTCACTC 18
      |||||
Db      313 CCACACCTATTCACTC 330

RESULT 11
US-09-954-456-822
; Sequence 822, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
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APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 822
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-822

Query Match 100.0%; Score 18; DB 3; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 313 CCACACCTATTCTACTC 330

RESULT 12
US-09-954-456-1225
; Sequence 1225, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863

PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1225
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1225
Query Match 100.0%; Score 18; DB 3; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 313 CCACACCTATTCTACTC 330

RESULT 13
US-10-641-643-1200
; Sequence 1200, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g190012
; SEQUENCE DESCRIPTION: SEQ ID NO: 1200 :
US-10-641-643-1200
Query Match 100.0%; Score 18; DB 7; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 313 CCACACCTATTCTACTC 330

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Db          313 CCACACCTATTCACTC 330

RESULT 14
US-10-607-806-3
; Sequence 3, Application US/10607806
; Publication No. US20050014158A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Gail Isabel Reid
; APPLICANT: Langdown, Maria L.
; APPLICANT: Denissenko, Mikhaili F.
; APPLICANT: Dennis, Edward
; APPLICANT: Cantor, Charles
; APPLICANT: Rubin, Byron
; TITLE OF INVENTION: THERAPEUTIC METHODS FOR REDUCING FAT
; TITLE OF INVENTION: DEPOSITION AND TREATING ASSOCIATED CONDITIONS
; FILE REFERENCE: 524592003200
; CURRENT APPLICATION NUMBER: US/10/607,806
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392,362
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-806-3

Query Match          100.0%; Score 18; DB 8; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 CCACACCTATTCACTC 18
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Db          313 CCACACCTATTCACTC 330

RESULT 15
US-10-607-806-3
; Sequence 3243, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3243

QY          1 CCACACCTATTCACTC 18
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Db          313 CCACACCTATTCACTC 330

RESULT 16
US-10-843-641A-3849
; Sequence 3849, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3849
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-3849

Query Match          100.0%; Score 18; DB 9; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 CCACACCTATTCACTC 18
           |||||
Db          313 CCACACCTATTCACTC 330

RESULT 17
US-10-843-641A-4252
; Sequence 4252, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
```

```
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-3243

Query Match          100.0%; Score 18; DB 9; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 CCACACCTATTCACTC 18
           |||||
Db          313 CCACACCTATTCACTC 330

RESULT 16
US-10-843-641A-3849
; Sequence 3849, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3849
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-3849

Query Match          100.0%; Score 18; DB 9; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 CCACACCTATTCACTC 18
           |||||
Db          313 CCACACCTATTCACTC 330

RESULT 17
US-10-843-641A-4252
; Sequence 4252, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
```


; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4252
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-4252

Query Match 100.0%; Score 18; DB 9; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||
Db 313 CCACACCTATTTCATCTC 330

RESULT 18
US-10-712-124-27
; Sequence 27, Application US/10712124
; Publication No. US20040146907A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, VICTORIA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
; FILE REFERENCE: P2000R1
; CURRENT APPLICATION NUMBER: US/10/712,124
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/425,813
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 27
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-712-124-27

Query Match 100.0%; Score 18; DB 7; Length 585;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||
Db 312 CCACACCTATTTCATCTC 329

RESULT 19
US-09-925-297-52
; Sequence 52, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (628)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-52

Query Match 100.0%; Score 18; DB 3; Length 630;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||
Db 302 CCACACCTATTTCATCTC 319

RESULT 20
US-10-330-051A-6
; Sequence 6, Application US/10330051A
; Publication No. US20040002471A1
; GENERAL INFORMATION:
; APPLICANT: Specht, Thomas
; APPLICANT: Hinzmann, Bernd
; APPLICANT: Schmitt, Armin
; APPLICANT: Pilarsky, Christian
; APPLICANT: Dahl, Edgar
; APPLICANT: Rosenthal, Andre
; TITLE OF INVENTION: Human Nucleic Acid Sequences Which Are Overexpressed In No. US2004
; TITLE OF INVENTION: Tissue
; FILE REFERENCE: ALBRE-2D1
; CURRENT APPLICATION NUMBER: US/10/330,051A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/647,801
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 6
; LENGTH: 644
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-330-051A-6

Query Match 100.0%; Score 18; DB 6; Length 644;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||
Db 337 CCACACCTATTTCATCTC 354

RESULT 21
US-10-450-763-11903
; Sequence 11903, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

```
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 11903
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(711)
; OTHER INFORMATION: 87% homologous to Homo sapiens syntaxin 8,accession number
; OTHER INFORMATION: AF036715,Smith-Waterman Score=1008.
US-10-450-763-11903

Query Match          100.0%; Score 18; DB 9; Length 654;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCACTC 18
      |||||||
Db      483 CCACACCTATTCACTC 500

RESULT 22
US-10-607-806-1
; Sequence 1, Application US/10607806
; Publication No. US20050014158A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Gail Isabel Reid
; APPLICANT: Langdown, Maria L.
; APPLICANT: Denissenko, Mikhaili F.
; APPLICANT: Dennis, Edward
; APPLICANT: Cantor, Charles
; APPLICANT: Rubin, Byron
; TITLE OF INVENTION: THERAPEUTIC METHODS FOR REDUCING FAT
; TITLE OF INVENTION: DEPOSITION AND TREATING ASSOCIATED CONDITIONS
; FILE REFERENCE: 524592003200
; CURRENT APPLICATION NUMBER: US/10/607,806
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392,362
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 436
; OTHER INFORMATION: y = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4050)...(4050)
; OTHER INFORMATION: m = A or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4689
; OTHER INFORMATION: w = A or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6282
; OTHER INFORMATION: m = A or C
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: 6358
; OTHER INFORMATION: y = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7256
; OTHER INFORMATION: y = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7300
; OTHER INFORMATION: m = A or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7301)...(7301)
; OTHER INFORMATION: m = A or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7328)...(7328)
; OTHER INFORMATION: r = A or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8062)...(8062)
; OTHER INFORMATION: y = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9182)...(9182)
; OTHER INFORMATION: k = G or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11649)...(11649)
; OTHER INFORMATION: m = A or C
US-10-607-806-1

Query Match          100.0%; Score 18; DB 8; Length 12174;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCACTC 18
      |||||||
Db      7310 CCACACCTATTCACTC 7327

RESULT 23
US-09-925-065A-935053
; Sequence 935053, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 935053
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935053

Query Match          91.1%; Score 16.4; DB 4; Length 586;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



```
RESULT 28
US-10-060-036-518
; Sequence 518, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 518
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 20, 53, 56, 58, 59
; OTHER INFORMATION: n = A,T,C or G
US-10-060-036-518

Query Match      88.9%; Score 16; DB 5; Length 224;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATACT 17
      |||||
Db      5 CCACACCTATTTCATANT 21

RESULT 29
US-10-424-599-127447
; Sequence 127447, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 127447
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8608C.1
US-10-424-599-127447

Query Match      85.6%; Score 15.4; DB 7; Length 321;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACACCTATTTCATACTC 18
      |||||
Db     152 CACACCTATTCCTACTC 168

RESULT 30
US-10-425-115-33674
; Sequence 33674, Application US/10425115
```

```
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 33674
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_130716C.1
US-10-425-115-33674
```

```
Query Match      85.6%; Score 15.4; DB 8; Length 533;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CACACCTATTTCATACTC 18
      |||||
Db     136 CACACCTATCCATACTC 152
```

```
RESULT 31
US-09-925-065A-459786/c
; Sequence 459786, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 459786
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-459786
```

```
Query Match      85.6%; Score 15.4; DB 4; Length 567;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CACACCTATTTCATACTC 18
      |||||
Db     66 CACACCCATTTCATACTC 50
```

```
RESULT 32
US-09-925-065A-366085
; Sequence 366085, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```


; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366085
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-366085

Query Match 85.6%; Score 15.4; DB 4; Length 603;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATACT 17
|||||
Db 197 CCACACCTATCCATACT 213

RESULT 33

US-10-021-323-1223
; Sequence 1223, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 1223
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3825-020-Q1-K6-B2
US-10-021-323-1223

Query Match 85.6%; Score 15.4; DB 7; Length 611;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATACTC 18
|||||
Db 340 CACACCTATTTCATTC 356

RESULT 34

US-10-027-632-122849
; Sequence 122849, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122849
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-122849

Query Match 85.6%; Score 15.4; DB 5; Length 1202;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATACTC 18
|||||
Db 468 CACACCTATACATACTC 484

RESULT 35

US-10-027-632-122850
; Sequence 122850, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122850
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-122850

Query Match 85.6%; Score 15.4; DB 5; Length 1202;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATACTC 18

```
Db          468 CACACCTATACATACTC 484
|||||
RESULT 36
US-10-027-632-122849
; Sequence 122849, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122849
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-122849

Query Match      85.6%; Score 15.4; DB 6; Length 1202;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          2 CACACCTATTTCATACTC 18
|||||
Db          468 CACACCTATACATACTC 484

RESULT 37
US-10-027-632-122850
; Sequence 122850, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122850
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-122850
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; SEQ ID NO 122850
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-122850

Query Match      85.6%; Score 15.4; DB 6; Length 1202;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          2 CACACCTATTTCATACTC 18
|||||
Db          468 CACACCTATACATACTC 484

RESULT 38
US-10-767-795-899
; Sequence 899, Application US/10767795
; Publication No. US20040181830A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53534)B
; CURRENT APPLICATION NUMBER: US/10/767,795
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 899
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C13173_1
US-10-767-795-899

Query Match      85.6%; Score 15.4; DB 8; Length 1733;
Best Local Similarity 94.1%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          2 CACACCTATTTCATACTC 18
|||||
Db          805 CACACCTATTTCATTCTC 821

RESULT 39
US-09-938-842A-1570/c
; Sequence 1570, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1570
; LENGTH: 3093
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1570
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Query Match 85.6%; Score 15.4; DB 3; Length 3093;
Best Local Similarity 94.1%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 17
Db 553 CCACACCTATTGATCT 537

RESULT 40
US-09-938-842A-1570/c
; Sequence 1570, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1570
; LENGTH: 3093
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1570

Query Match 85.6%; Score 15.4; DB 3; Length 3093;
Best Local Similarity 94.1%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 17
Db 553 CCACACCTATTGATCT 537

RESULT 41
US-10-347-470A-1/c
; Sequence 1, Application US/10347470A
; Publication No. US20040002054A1
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hwang, Ho Yon
; TITLE OF INVENTION: SQV NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 01997/542003
; CURRENT APPLICATION NUMBER: US/10/347,470A
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 60/349,630
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/390,930
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3120
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-10-347-470A-1

Query Match 85.6%; Score 15.4; DB 6; Length 3120;
Best Local Similarity 94.1%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCT 18

Db 3067 CACACCTATTTCCTACTC 3051

RESULT 42
US-10-311-455-1691/c
; Sequence 1691, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Methylation of Cytosine
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1691
; LENGTH: 17934
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1691

Query Match 85.6%; Score 15.4; DB 6; Length 17934;
Best Local Similarity 94.1%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCT 18
Db 14397 CACACCTATACATCTC 14381

RESULT 43
US-10-721-693-10/c
; Sequence 10, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery of siRNA
; TITLE OF INVENTION: siRNA
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 118777
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(118777)
; OTHER INFORMATION: LOCUS AF163865
; OTHER INFORMATION: OD 24-JAN-2001
; OTHER INFORMATION: DEFINITION Mus musculus alpha-synuclein (Snca) gene, complete cds
; OTHER INFORMATION: s.
; OTHER INFORMATION: ACCESSION AF163865
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF163865
; DATABASE ENTRY DATE: 2001-01-24
; RELEVANT RESIDUES: (1)..(118777)
US-10-721-693-10

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Query Match      85.6%; Score 15.4; DB 7; Length 118777;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATACT 17
      ||||| ||||| |||||
Db      77795 CCACACATATTTCATACT 77779

RESULT 44
US-10-852-997-10/c
; Sequence 10, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Deliv
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 118777
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(118777)
; OTHER INFORMATION: LOCUS AF163865 118777 bp DNA linear R
; OTHER INFORMATION: OD 24-JAN-2001
; OTHER INFORMATION: DEFINITION Mus musculus alpha-synuclein (Snca) gene, complete cd
; OTHER INFORMATION: s.
; OTHER INFORMATION: ACCESSION AF163865
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF163865
; DATABASE ENTRY DATE: 2001-01-24
; RELEVANT RESIDUES: (1)..(118777)
US-10-852-997-10

Query Match      85.6%; Score 15.4; DB 8; Length 118777;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATACT 17
      ||||| ||||| |||||
Db      77795 CCACACATATTTCATACT 77779

RESULT 45
US-10-087-192-454
; Sequence 454, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 454
; LENGTH: 439892
,
```

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(439892)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-454

Query Match      85.6%; Score 15.4; DB 5; Length 439892;
Best Local Similarity 94.1%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CACACCTATTTCATACTC 18
      ||||| ||||| |||||
Db      54190 CACACCTTTTCATACTC 54206

RESULT 46
US-10-242-535A-27057/c
; Sequence 27057, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27057
; LENGTH: 136
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-27057

Query Match      83.3%; Score 15; DB 7; Length 136;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CACCTATTTCATACTC 18
      ||||| ||||| |||||
Db      63 CACCTATTTCATACTC 49

RESULT 47
US-10-085-783A-27057/c
; Sequence 27057, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27057
,
```



```

; LENGTH: 136
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-27057

Query Match      83.3%; Score 15; DB 7; Length 136;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CACCTATTTCATC 18
      |||||
Db      63 CACCTATTTCATC 49

RESULT 48
US-10-425-115-78961/c
; Sequence 78961, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 78961
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172037C.1
US-10-425-115-78961

Query Match      83.3%; Score 15; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATA 15
      |||||
Db      100 CCACACCTATTTCATA 86

RESULT 49
US-09-925-065A-817638/c
; Sequence 817638, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 817638
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-817638

Query Match      83.3%; Score 15; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATA 15
      |||||
Db      100 CCACACCTATTTCATA 86

RESULT 49
US-09-925-065A-817638/c
; Sequence 817638, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 817638
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-817638
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US-09-925-065A-817638

Query Match      83.3%; Score 15; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATA 15
      |||||
Db      258 CCACACCTATTTCATA 244

RESULT 50
US-09-925-065A-817639/c
; Sequence 817639, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 817639
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-817639

Query Match      83.3%; Score 15; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATA 15
      |||||
Db      258 CCACACCTATTTCATA 244

RESULT 51
US-10-363-345A-14929/c
; Sequence 14929, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 14929
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 14929
US-10-363-345A-14929

Query Match      83.3%; Score 15; DB 8; Length 544;
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Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;
QY 4 CACCTATTCATCTC 18
| | | | | | | | | |
Db 532 CACCTATTCATCTC 518
RESULT 52
US-10-363-345A-14930
; Sequence 14930, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 14930
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 14930
US-10-363-345A-14930

Query Match 83.3%; Score 15; DB 8; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CACCTATTCATCTC 18
| | | | | | | | | |
Db 13 CACCTATTCATCTC 27

RESULT 53
US-10-363-483A-14929/c
; Sequence 14929, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 14929
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 14929
US-10-363-483A-14929

Query Match 83.3%; Score 15; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CACCTATTCATCTC 18
| | | | | | | | | |
Db 532 CACCTATTCATCTC 518

RESULT 54

US-10-363-483A-14930
; Sequence 14930, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 14930
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 14930
US-10-363-483A-14930

Query Match 83.3%; Score 15; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CACCTATTCATCTC 18
| | | | | | | | | |
Db 13 CACCTATTCATCTC 27

RESULT 55
US-10-424-599-127043
; Sequence 127043, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 127043
; LENGTH: 203
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(203)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_85726C.1
US-10-424-599-127043

Query Match 82.2%; Score 14.8; DB 7; Length 203;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCACACCTATTCATCTC 18
| | | | | | | | | |
Db 93 CCACACTTATTCATGCTC 110

RESULT 56
US-10-425-115-104465
; Sequence 104465, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 104465
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(241)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_26775C.1
;
US-10-425-115-104465

Query Match 82.2%; Score 14.8; DB 8; Length 241;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
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Db 5 CCACACTACTCTCTACTC 22

RESULT 57
US-10-424-599-72836
; Sequence 72836, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 72836
; LENGTH: 323
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(323)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36786C.1
;
US-10-424-599-72836

Query Match 82.2%; Score 14.8; DB 7; Length 323;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||
Db 102 CCAACCTATTCAAACCTC 119

RESULT 58
US-09-925-065A-614775
; Sequence 614775, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614775
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-925-065A-614775

Query Match 82.2%; Score 14.8; DB 4; Length 392;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 133 CCACACCTATTTCACACAC 150

RESULT 59
US-09-925-065A-614776
; Sequence 614776, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614776
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-925-065A-614776

Query Match 82.2%; Score 14.8; DB 4; Length 392;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 133 CCACACCTATTTCACACAC 150

RESULT 60
US-09-925-065A-614778
; Sequence 614778, Application US/09925065A
; Publication No. US20050228172A9

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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614778
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614778

Query Match      82.2%; Score 14.8; DB 4; Length 392;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTCTACTC 18
        |||||
Db      133 CCACACCTATTCTACACAC 150
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Search completed: May 10, 2006, 19:48:29
Job time : 428 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 19:26:26 ; Search time 681 Seconds
(without alignments)
107.802 Million cell updates/sec

Title: US-10-608-296-38
Perfect score: 18
Sequence: 1 ccaacacctattcatactc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9312410 seqs, 2039259788 residues

Total number of hits satisfying chosen parameters: 18624820

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications NA_New:*
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2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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18: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq5:*
19: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	16.4	91.1	586	7	US-09-925-065A-935053 Sequence 935053,
2	16.4	91.1	586	7	US-09-925-065A-935054 Sequence 935054,
3	16.4	91.1	586	7	US-09-925-065A-952779 Sequence 952779,
C 4	16.4	91.1	770	7	US-09-925-065A-919397 Sequence 919397,
5	16.4	91.1	156544	17	US-11-121-086-81 Sequence 81, App1
6	16	88.9	25	17	US-11-121-849-134677 Sequence 134677,
C 7	15.4	85.6	566	12	US-10-301-480-517106 Sequence 517106,
C 8	15.4	85.6	566	12	US-10-301-480-1130515 Sequence 1130515,
C 9	15.4	85.6	567	7	US-09-925-065A-459786 Sequence 459786,
10	15.4	85.6	589	12	US-10-301-480-436566 Sequence 436566,
11	15.4	85.6	589	12	US-10-301-480-1049975 Sequence 1049975,
12	15.4	85.6	603	7	US-09-925-065A-366085 Sequence 366085,
C 13	15.4	85.6	990	12	US-10-301-480-556079 Sequence 556079,
C 14	15.4	85.6	990	12	US-10-301-480-1169488 Sequence 1169488,

15	15.4	85.6	1201	10	US-10-750-185-59851	Sequence 59851, A
16	15.4	85.6	1201	10	US-10-750-623-59851	Sequence 59851, A
17	15.4	85.6	34116	17	US-11-124-367A-5020	Sequence 5020, Ap
18	15	83.3	19	15	US-11-101-244-376219	Sequence 376219,
19	15	83.3	19	16	US-11-083-784-376219	Sequence 376219,
C 20	15	83.3	478	7	US-09-925-065A-817638	Sequence 817638,
C 21	15	83.3	478	7	US-09-925-065A-817639	Sequence 817639,
22	14.8	82.2	201	10	US-10-995-561-74454	Sequence 74454, A
23	14.8	82.2	201	10	US-10-995-561-75240	Sequence 75240, A
24	14.8	82.2	392	7	US-09-925-065A-614775	Sequence 614775,
25	14.8	82.2	392	7	US-09-925-065A-614776	Sequence 614776,
26	14.8	82.2	392	7	US-09-925-065A-614778	Sequence 614778,
27	14.8	82.2	470	12	US-10-301-480-461153	Sequence 461153,
28	14.8	82.2	470	12	US-10-301-480-1074562	Sequence 1074562,
29	14.8	82.2	477	7	US-09-925-065A-393035	Sequence 393035,
C 30	14.8	82.2	484	12	US-10-301-480-326616	Sequence 326616,
C 31	14.8	82.2	484	12	US-10-301-480-940025	Sequence 940025,
C 32	14.8	82.2	489	7	US-09-925-065A-246390	Sequence 246390,
33	14.8	82.2	503	17	US-11-128-061-1580	Sequence 1580, Ap
34	14.8	82.2	503	17	US-11-128-061-5222	Sequence 5222, Ap
35	14.8	82.2	503	17	US-11-128-049-1580	Sequence 1580, Ap
36	14.8	82.2	503	17	US-11-128-049-5222	Sequence 5222, Ap
37	14.8	82.2	533	12	US-10-301-480-370251	Sequence 370251,
38	14.8	82.2	533	12	US-10-301-480-370252	Sequence 370252,
39	14.8	82.2	533	12	US-10-301-480-983660	Sequence 983660,
40	14.8	82.2	533	12	US-10-301-480-983661	Sequence 983661,
41	14.8	82.2	535	7	US-09-925-065A-293390	Sequence 293390,
42	14.8	82.2	535	7	US-09-925-065A-293391	Sequence 293391,
C 43	14.8	82.2	538	7	US-09-925-065A-523202	Sequence 523202,
C 44	14.8	82.2	538	7	US-09-925-065A-523203	Sequence 523203,
C 45	14.8	82.2	565	7	US-09-925-065A-143110	Sequence 143110,
C 46	14.8	82.2	565	7	US-09-925-065A-143111	Sequence 143111,
C 47	14.8	82.2	566	11	US-10-301-480-59147	Sequence 59147, A
C 48	14.8	82.2	566	12	US-10-301-480-672556	Sequence 672556,
C 49	14.8	82.2	568	7	US-09-925-065A-523201	Sequence 523201,
C 50	14.8	82.2	568	7	US-09-925-065A-523204	Sequence 523204,
C 51	14.8	82.2	570	12	US-10-301-480-237818	Sequence 237818,
C 52	14.8	82.2	570	12	US-10-301-480-237819	Sequence 237819,
C 53	14.8	82.2	570	12	US-10-301-480-851227	Sequence 851227,
C 54	14.8	82.2	570	12	US-10-301-480-851228	Sequence 851228,
C 55	14.8	82.2	584	7	US-09-925-065A-630983	Sequence 630983,
C 56	14.8	82.2	589	7	US-09-925-065A-305234	Sequence 305234,
C 57	14.8	82.2	599	12	US-10-301-480-381253	Sequence 381253,
C 58	14.8	82.2	599	12	US-10-301-480-994662	Sequence 994662,
C 59	14.8	82.2	606	7	US-09-925-065A-614773	Sequence 614773,
60	14.8	82.2	606	7	US-09-925-065A-614777	Sequence 614777,
C 61	14.8	82.2	606	11	US-10-301-480-76260	Sequence 76260, A
C 62	14.8	82.2	606	12	US-10-301-480-689669	Sequence 689669,
C 63	14.8	82.2	608	7	US-09-925-065A-634274	Sequence 634274,
64	14.8	82.2	608	7	US-09-925-065A-858127	Sequence 858127,
C 65	14.8	82.2	611	7	US-09-925-065A-790417	Sequence 790417,
66	14.8	82.2	614	7	US-09-925-065A-832759	Sequence 832759,
67	14.8	82.2	616	7	US-09-925-065A-753972	Sequence 753972,
68	14.8	82.2	619	7	US-09-925-065A-825175	Sequence 825175,
C 69	14.8	82.2	629	7	US-09-925-065A-943020	Sequence 943020,
70	14.8	82.2	630	12	US-10-301-480-545243	Sequence 545243,
71	14.8	82.2	630	12	US-10-301-480-1158652	Sequence 1158652,
72	14.8	82.2	633	7	US-09-925-065A-246509	Sequence 246509,
73	14.8	82.2	633	7	US-09-925-065A-246510	Sequence 246510,
74	14.8	82.2	636	7	US-09-925-065A-766178	Sequence 766178,
75	14.8	82.2	636	7	US-09-925-065A-870338	Sequence 870338,
76	14.8	82.2	637	7	US-09-925-065A-758685	Sequence 758685,
C 77	14.8	82.2	675	7	US-09-925-065A-870153	Sequence 870153,
78	14.8	82.2	677	7	US-09-925-065A-873079	Sequence 873079,
79	14.8	82.2	677	7	US-09-925-065A-873080	Sequence 873080,
80	14.8	82.2	679	7	US-09-925-065A-852313	Sequence 852313,
81	14.8	82.2	861	11	US-10-301-480-95013	Sequence 95013, A
82	14.8	82.2	861	12	US-10-301-480-708422	Sequence 708422,
C 83	14.8	82.2	910	7	US-09-925-065A-919331	Sequence 919331,
C 84	14.8	82.2	910	7	US-09-925-065A-919332	Sequence 919332,
C 85	14.8	82.2	1109	7	US-09-925-065A-693989	Sequence 693989,
86	14.8	82.2	1413	7	US-09-925-065A-80878	Sequence 80878, A
87	14.8	82.2	1413	11	US-10-301-480-182117	Sequence 182117,

88	14.8	82.2	1413	12	US-10-301-480-795526	Sequence 795526,
C 89	14.8	82.2	1724	11	US-10-301-480-165982	Sequence 165982,
C 90	14.8	82.2	1727	7	US-09-925-065A-64744	Sequence 64744, A
C 91	14.8	82.2	1727	7	US-09-925-065A-64745	Sequence 64745, A
C 92	14.8	82.2	1727	11	US-10-301-480-165983	Sequence 165983,
C 93	14.8	82.2	1727	12	US-10-301-480-779391	Sequence 779391,
C 94	14.8	82.2	1727	12	US-10-301-480-779392	Sequence 779392,
C 95	14.8	82.2	2167	7	US-09-925-065A-59143	Sequence 59143, A
C 96	14.8	82.2	2167	7	US-09-925-065A-59144	Sequence 59144, A
C 97	14.8	82.2	2167	11	US-10-301-480-160381	Sequence 160381,
C 98	14.8	82.2	2167	11	US-10-301-480-160382	Sequence 160382,
C 99	14.8	82.2	2167	12	US-10-301-480-773790	Sequence 773790,
C 100	14.8	82.2	2167	12	US-10-301-480-773791	Sequence 773791,
101	14.8	82.2	2261	11	US-10-301-480-83615	Sequence 83615, A
102	14.8	82.2	2261	11	US-10-301-480-83616	Sequence 83616, A
103	14.8	82.2	2261	11	US-10-301-480-83617	Sequence 83617, A
104	14.8	82.2	2261	11	US-10-301-480-83618	Sequence 83618, A
105	14.8	82.2	2261	12	US-10-301-480-697024	Sequence 697024,
106	14.8	82.2	2261	12	US-10-301-480-697025	Sequence 697025,
107	14.8	82.2	2261	12	US-10-301-480-697026	Sequence 697026,
108	14.8	82.2	2261	12	US-10-301-480-697027	Sequence 697027,
C 109	14.8	82.2	2462	7	US-09-925-065A-678154	Sequence 678154,
C 110	14.8	82.2	2462	7	US-09-925-065A-678155	Sequence 678155,
C 111	14.8	82.2	2462	7	US-09-925-065A-678156	Sequence 678156,
C 112	14.8	82.2	2462	7	US-09-925-065A-678157	Sequence 678157,
113	14.8	82.2	3237	18	US-11-072-512-1028	Sequence 1028, Ap
114	14.8	82.2	20945	10	US-10-995-561-13463	Sequence 13463, A
115	14.8	82.2	23082	10	US-10-995-561-13457	Sequence 13457, A
116	14.8	82.2	29360	11	US-10-330-773-165	Sequence 165, App
117	14.8	82.2	70549	11	US-10-330-773-413	Sequence 413, App
C 118	14.8	82.2	98862	17	US-11-121-086-76	Sequence 76, Appl
C 119	14.8	82.2	172756	18	US-11-114-798-48	Sequence 48, Appl
120	14.8	82.2	175100	17	US-11-121-086-21	Sequence 21, Appl
C 121	14.8	82.2	197241	18	US-11-114-798-47	Sequence 47, Appl
122	14.8	82.2	199868	11	US-10-330-773-808	Sequence 808, App
123	14.8	82.2	380749	10	US-10-995-561-13216	Sequence 13216, A
124	14.6	81.1	446	7	US-09-824-575A-3	Sequence 3, Appli
125	14.6	81.1	446	7	US-09-925-065A-730125	Sequence 730125,
126	14.6	81.1	456	7	US-09-925-065A-808879	Sequence 808879,
127	14.4	80.0	379	7	US-09-925-065A-599197	Sequence 599197,
128	14.4	80.0	392	7	US-09-925-065A-614774	Sequence 614774,
129	14.4	80.0	490	7	US-09-925-065A-649037	Sequence 649037,
130	14.4	80.0	490	7	US-09-925-065A-649038	Sequence 649038,
C 131	14.4	80.0	497	7	US-09-925-065A-439259	Sequence 439259,
C 132	14.4	80.0	509	7	US-09-925-065A-259014	Sequence 259014,
C 133	14.4	80.0	522	7	US-09-925-065A-316303	Sequence 316303,
C 134	14.4	80.0	527	12	US-10-301-480-391279	Sequence 391279,
C 135	14.4	80.0	527	12	US-10-301-480-1004688	Sequence 1004688,
136	14.4	80.0	529	12	US-10-301-480-431996	Sequence 431996,
137	14.4	80.0	529	12	US-10-301-480-1045405	Sequence 1045405,
138	14.4	80.0	532	12	US-10-301-480-431997	Sequence 431997,
C 139	14.4	80.0	532	12	US-10-301-480-500419	Sequence 500419,
140	14.4	80.0	532	12	US-10-301-480-1045406	Sequence 1045406,
C 141	14.4	80.0	532	12	US-10-301-480-1113828	Sequence 1113828,
142	14.4	80.0	534	12	US-10-301-480-337583	Sequence 337583,
143	14.4	80.0	534	12	US-10-301-480-950992	Sequence 950992,
C 144	14.4	80.0	536	11	US-10-301-480-19086	Sequence 19086, A
C 145	14.4	80.0	536	11	US-10-301-480-19087	Sequence 19087, A
C 146	14.4	80.0	536	12	US-10-301-480-632495	Sequence 632495,
C 147	14.4	80.0	536	12	US-10-301-480-632496	Sequence 632496,
C 148	14.4	80.0	537	11	US-10-301-480-19084	Sequence 19084, A
C 149	14.4	80.0	537	12	US-10-301-480-632493	Sequence 632493,
150	14.4	80.0	539	7	US-09-925-065A-360917	Sequence 360917,

ALIGNMENTS

RESULT 1
US-09-925-065A-935053
; Sequence 935053, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 935053
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935053

Query Match 91.1%; Score 16.4; DB 7; Length 586;
Best Local Similarity 94.4%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 320 CCACACCTATTCTATACAC 337

RESULT 2
US-09-925-065A-935054
; Sequence 935054, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 935054
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935054

Query Match 91.1%; Score 16.4; DB 7; Length 586;
Best Local Similarity 94.4%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 320 CCACACCTATTCTATACAC 337

RESULT 3
US-09-925-065A-952779

; Sequence 952779, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 952779
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-952779

Query Match 91.1%; Score 16.4; DB 7; Length 586;
Best Local Similarity 94.4%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 320 CCACACCTATTTCATCAC 337

RESULT 4
US-09-925-065A-919397/c
; Sequence 919397, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 919397
; LENGTH: 770
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-919397

Query Match 91.1%; Score 16.4; DB 7; Length 770;
Best Local Similarity 94.4%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 158 CCACACCTATTTCATCAC 141

RESULT 5
US-11-121-086-81
; Sequence 81, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 156544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-81

Query Match 91.1%; Score 16.4; DB 17; Length 156544;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 92675 CCACACCTATTTCATCAC 92692

RESULT 6
US-11-121-849-134677
; Sequence 134677, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 134677
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-134677

Query Match 88.9%; Score 16; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | |
Db 1 ACACCTATTTCATCTC 16

RESULT 7
US-10-301-480-517106/c
; Sequence 517106, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598

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; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 517106
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-517106

Query Match      85.6%; Score 15.4; DB 12; Length 566;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CACACCTATTCACTC 18
      ||||| ||||| |||||
Db      65 CACACCCATTCATACTC 49

RESULT 8
US-10-301-480-1130515/c
; Sequence 1130515, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1130515
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1130515

Query Match      85.6%; Score 15.4; DB 12; Length 566;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CACACCTATTCACTC 18
      ||||| ||||| |||||
Db      65 CACACCCATTCATACTC 49

RESULT 9
US-09-925-065A-459786/c
; Sequence 459786, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
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; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 459786
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-459786

Query Match      85.6%; Score 15.4; DB 7; Length 567;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CACACCTATTCACTC 18
      ||||| ||||| |||||
Db      66 CACACCCATTCATACTC 50

RESULT 10
US-10-301-480-436566
; Sequence 436566, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 436566
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-436566

Query Match      85.6%; Score 15.4; DB 12; Length 589;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCACTC 17
      ||||| ||||| |||||
Db      183 CCACACCTATCCATACT 199

RESULT 11
US-10-301-480-1049975
; Sequence 1049975, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1049975
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1049975

Query Match      85.6%; Score 15.4; DB 12; Length 589;
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Best Local Similarity 94.1%; Pred. No. 1.6e+02; DB 1; Indels 0; Gaps 0; Matches 16; Conservative 0; Mismatches 1;

QY 1 CCACACCTATTTCATACT 17
Db 183 CCACACCTATCCATACT 199

RESULT 12
US-09-925-065A-366085
; Sequence 366085, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 366085
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-366085

Query Match 85.6%; Score 15.4; DB 7; Length 603;
Best Local Similarity 94.1%; Pred. No. 1.6e+02; DB 1; Indels 0; Gaps 0; Matches 16; Conservative 0; Mismatches 1;

QY 1 CCACACCTATTTCATACT 17
Db 197 CCACACCTATCCATACT 213

RESULT 13
US-10-301-480-556079/c
; Sequence 556079, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 556079
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-556079

Query Match 85.6%; Score 15.4; DB 12; Length 990;
Best Local Similarity 94.1%; Pred. No. 1.8e+02; DB 1; Indels 0; Gaps 0; Matches 16; Conservative 0; Mismatches 1;

QY 2 CACACCTATTTCATACTC 18
Db 977 CACACCTGTTCATACTC 961

RESULT 14
US-10-301-480-1169488/c
; Sequence 1169488, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1169488
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1169488

Query Match 85.6%; Score 15.4; DB 12; Length 990;
Best Local Similarity 94.1%; Pred. No. 1.8e+02; DB 1; Indels 0; Gaps 0; Matches 16; Conservative 0; Mismatches 1;

QY 2 CACACCTATTTCATACTC 18
Db 977 CACACCTGTTCATACTC 961

RESULT 15
US-10-750-185-59851
; Sequence 59851, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 59851
; LENGTH: 1201
; TYPE: DNA
; ORGANISM: Bovine 19866881032028
US-10-750-185-59851

Query Match 85.6%; Score 15.4; DB 10; Length 1201;
Best Local Similarity 94.1%; Pred. No. 1.8e+02; DB 1; Indels 0; Gaps 0; Matches 16; Conservative 0; Mismatches 1;

QY 2 CACACCTATTTCATACTC 18
Db 560 CACACCCATTTCATACTC 576

RESULT 16

RESULT 19
US-11-083-784-376219
; Sequence 376219, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 376219
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-376219

Query Match 83.3%; Score 15; DB 16; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15
|||||:|:|:|
Db 5 CCACACCUAUUCAUA 19

RESULT 20
US-09-925-065A-817638/c
; Sequence 817638, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 817638
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-817638

Query Match 83.3%; Score 15; DB 7; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15

Db 258 CCACACCTATTTCATA 244
|||
RESULT 21
US-09-925-065A-817639/c
; Sequence 817639, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 817639
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-817639

Query Match 83.3%; Score 15; DB 7; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15
|||||
Db 258 CCACACCTATTTCATA 244

RESULT 22
US-10-995-561-74454
; Sequence 74454, Application US/109955561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74454
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-74454

Query Match 82.2%; Score 14.8; DB 10; Length 201;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 156 CCACACCTATCCATACAC 173

RESULT 23
US-10-995-561-75240

```
; Sequence 75240, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75240
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-75240

Query Match      82.2%; Score 14.8; DB 10; Length 201;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      156 CCACACCTATCCATACAC 173

RESULT 24
US-09-925-065A-614775
; Sequence 614775, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 614775
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614775

Query Match      82.2%; Score 14.8; DB 7; Length 392;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      133 CCACACCTATTTCACAC 150

RESULT 25
US-09-925-065A-614776
; Sequence 614776, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
,; 
```

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; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 614776
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614776

Query Match      82.2%; Score 14.8; DB 7; Length 392;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      133 CCACACCTATTTCACAC 150

RESULT 26
US-09-925-065A-614778
; Sequence 614778, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 614778
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614778

Query Match      82.2%; Score 14.8; DB 7; Length 392;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      133 CCACACCTATTTCACAC 150

RESULT 27
US-10-301-480-461153
; Sequence 461153, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; 
```



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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 461153
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-461153

Query Match      82.2%; Score 14.8; DB 12; Length 470;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATACTC 18
      ||| ||| ||| ||| ||| ||| ||| |||
Db      143 CCACACCTATTTCACAGTC 160

RESULT 28
US-10-301-480-1074562
; Sequence 1074562, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1074562
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1074562

Query Match      82.2%; Score 14.8; DB 12; Length 470;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATACTC 18
      ||| ||| ||| ||| ||| ||| ||| |||
Db      143 CCACACCTATTTCACAGTC 160

RESULT 29
US-09-925-065A-393035
; Sequence 393035, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
```

```
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 393035
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-393035

Query Match      82.2%; Score 14.8; DB 7; Length 477;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATACTC 18
      ||| ||| ||| ||| ||| ||| ||| |||
Db      143 CCACACCTATTTCACAGTC 160

RESULT 30
US-10-301-480-326616/c
; Sequence 326616, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 326616
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-326616

Query Match      82.2%; Score 14.8; DB 12; Length 484;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATACTC 18
      ||| ||| ||| ||| ||| ||| ||| |||
Db      79 CCACACCTATTTCACACAC 62

RESULT 31
US-10-301-480-940025/c
; Sequence 940025, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
```



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; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1580
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-049-1580

Query Match      82.2%; Score 14.8; DB 17; Length 503;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCTACTC 18
      ||||| ||||| ||||| |
Db      73 CCACACCTAGTCATACAC 90

RESULT 36
US-11-128-049-5222
; Sequence 5222, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5222
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-049-5222

Query Match      82.2%; Score 14.8; DB 17; Length 503;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCTACTC 18
      ||||| ||||| ||||| |
Db      73 CCACACCTAGTCATACAC 90

RESULT 37
US-10-301-480-370251
; Sequence 370251, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 370251
```

```
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-370251

Query Match      82.2%; Score 14.8; DB 12; Length 533;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCTACTC 18
      ||||| ||||| ||||| |
Db      409 CCACACCTATTCTACAC 426

RESULT 38
US-10-301-480-370252
; Sequence 370252, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 370252
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-370252

Query Match      82.2%; Score 14.8; DB 12; Length 533;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCTACTC 18
      ||||| ||||| ||||| |
Db      409 CCACACCTATTCTACAC 426

RESULT 39
US-10-301-480-983660
; Sequence 983660, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 983660
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-983660

Query Match      82.2%; Score 14.8; DB 12; Length 533;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 CCACACCTATTCTACTC 18
Db 409 CCACACCTATTCTACACAC 426

RESULT 40
US-10-301-480-983661
; Sequence 983661, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 983661
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-983661

Query Match 82.2%; Score 14.8; DB 12; Length 533;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 409 CCACACCTATTCTACACAC 426

RESULT 41
US-09-925-065A-293390
; Sequence 293390, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293390
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-293390

Query Match 82.2%; Score 14.8; DB 7; Length 535;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 411 CCACACCTATTCTACACAC 428

RESULT 42
US-09-925-065A-293391
; Sequence 293391, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293391
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-293391

Query Match 82.2%; Score 14.8; DB 7; Length 535;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 411 CCACACCTATTCTACACAC 428

RESULT 43
US-09-925-065A-523202/c
; Sequence 523202, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523202
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-523202

Query Match 82.2%; Score 14.8; DB 7; Length 538;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 492 CCACACCTGTTTCACACTC 475

RESULT 44
US-09-925-065A-523203/c
; Sequence 523203, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523203
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-523203

Query Match 82.2%; Score 14.8; DB 7; Length 538;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 492 CCACACCTGTTTCACACTC 475

RESULT 45
US-09-925-065A-143110/c
; Sequence 143110, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143110
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-143110

Query Match 82.2%; Score 14.8; DB 7; Length 565;

Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 125 CCACACCTATTTCGTACAC 108

RESULT 46
US-09-925-065A-143111/c
; Sequence 143111, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143111
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-143111

Query Match 82.2%; Score 14.8; DB 7; Length 565;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 125 CCACACCTATTTCGTACAC 108

RESULT 47
US-10-301-480-59147/c
; Sequence 59147, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59147
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-59147

Query Match 82.2%; Score 14.8; DB 11; Length 566;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | |
Db 211 CCACACCTATTCTACAC 194

RESULT 48
US-10-301-480-672556/c
; Sequence 672556, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 672556
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-672556

Query Match 82.2%; Score 14.8; DB 12; Length 566;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | |
Db 211 CCACACCTATTCTACAC 194

RESULT 49
US-09-925-065A-523201/c
; Sequence 523201, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523201
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-523201

Query Match 82.2%; Score 14.8; DB 7; Length 568;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | |
Db 493 CCACACCTGTTCTACACTC 476

RESULT 50
US-09-925-065A-523204/c
; Sequence 523204, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523204
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-523204

Query Match 82.2%; Score 14.8; DB 7; Length 568;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | |
Db 493 CCACACCTGTTCTACACTC 476

RESULT 51
US-10-301-480-237818/c
; Sequence 237818, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237818
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-237818

Query Match 82.2%; Score 14.8; DB 12; Length 570;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
| | | | | | | | | | | | | | |
Db 125 CCACACCTATTCTGTACAC 108

RESULT 52

```
US-10-301-480-237819/c
; Sequence 237819, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 237819
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-237819

Query Match      82.2%; Score 14.8; DB 12; Length 570;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      125 CCACACCTATTCGTACAC 108

RESULT 53
US-10-301-480-851227/c
; Sequence 851227, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 851227
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-851227

Query Match      82.2%; Score 14.8; DB 12; Length 570;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      125 CCACACCTATTCGTACAC 108

RESULT 54
US-10-301-480-851228/c
; Sequence 851228, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
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; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 851228
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-851228

Query Match      82.2%; Score 14.8; DB 12; Length 570;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      125 CCACACCTATTCGTACAC 108

RESULT 55
US-09-925-065A-630983/c
; Sequence 630983, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 630983
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-630983

Query Match      82.2%; Score 14.8; DB 7; Length 584;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      309 CCACTTCTATTCATCTC 292

RESULT 56
US-09-925-065A-305234/c
; Sequence 305234, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
```

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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 305234
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-305234

Query Match      82.2%; Score 14.8; DB 7; Length 589;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||||||||||
Db      292 CCACACCTATTTCACAC 275

RESULT 57
US-10-301-480-381253/c
; Sequence 381253, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 381253
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-381253

Query Match      82.2%; Score 14.8; DB 12; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||||||||||
Db      292 CCACACCTATTTCACAC 275

RESULT 58
US-10-301-480-994662/c
; Sequence 994662, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
;
,

```

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 994662
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-994662

Query Match      82.2%; Score 14.8; DB 12; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||||||||||
Db      292 CCACACCTATTTCACAC 275

RESULT 59
US-09-925-065A-614773
; Sequence 614773, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 614773
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-614773

Query Match      82.2%; Score 14.8; DB 7; Length 606;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||||||||||
Db      367 CCACACCTATTTCACAC 384

RESULT 60
US-09-925-065A-614777
; Sequence 614777, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
;
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; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 614777
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614777

Query Match      82.2%  Score 14.8;  DB 7;  Length 606;
Best Local Similarity 88.9%  Pred. No. 3.5e+02;
Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
        |||||
Db      367 CCACACCTATTTCACAC 384

Search completed: May 10, 2006, 20:40:19
Job time : 685 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: May 12, 2006, 06:55:35 ; Search time 16293 Seconds
(without alignments)
17447.622 Million cell updates/sec

Title: SEQ1-4500-9500-7328G
Perfect score: 4997.8
Sequence: 1 ctggtcatctcagttctttt.....tttgagaccagcctggacaa 5001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4997.8	100.0	8368	8 AY438977	AY438977 Homo sapi
c 2	4997.8	100.0	122302	8 AC003982	AC003982 Homo sapi
3	4986	99.8	13612	6 AX377239	AX377239 Sequence
c 4	4961.8	99.3	220384	14 AC078926	AC078926 Homo sapi
5	2690.8	53.8	3375	8 HUMPLA2A1	M22970 Human pancr
6	2226.2	44.5	189729	14 AC073930	AC073930 Homo sapi
c 7	558.6	11.2	99370	8 AC005057	AC005057 Homo sapi
8	547.8	11.0	162240	14 AC145756	AC145756 Pan trogl
9	534.4	10.7	161716	8 AC087434	AC087434 Pan trogl
c 10	524.2	10.5	121272	14 AC004956	AC004956 Homo sapi
c 11	513.6	10.3	183798	14 AC145523	AC145523 Papio ham
12	499.8	10.0	158595	8 AC010614	AC010614 Homo sapi
13	499.8	10.0	189534	14 AL354656	AL354656 Homo sapi
c 14	496.6	9.9	57320	8 AY886519	AY886519 Homo sapi
c 15	496.6	9.9	133391	8 HSDJ315G1	AL121601 Human DNA
16	481.8	9.6	147330	8 AC008753	AC008753 Homo sapi
c 17	481.6	9.6	189056	14 AC017052	AC017052 Homo sapi
c 18	473.8	9.5	43242	8 AC145647	AC145647 Homo sapi

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/rpt_family="L2"
repeat_region /rpt_type=dispersed
2086. .2165
/rpt_family="L2"
repeat_region /rpt_type=dispersed
2194. .2319
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3977. .4280
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4281. .4346
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repeat_region /rpt_type=dispersed
4347. .4634
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4635. .4723
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5103. .5404
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5556
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variation /rpt_type=dispersed
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Query Match 100.0%; Score 4997.8; DB 8; Length 8368;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4993; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTTGTGCTAGCTGT	60
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QY	121	AGATCTCACTCCTCTGGAATGGGGCCACAGGCCACAGCAACAGGGATGGCCAGCCCCG	180
Db	994	AGATCTCACTCCTCTGGAATGGGGCCACAGGCCACAGCAACAGGGATGGCCAGCCCCG	1053
QY	181	CAGTCTCAAWTCGAGGTTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG	240
Db	1054	CAGTCTCAAWTCGAGGTTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG	1113
QY	241	GCTGGCACTTTTTCACCTGCAAGTCTGAACTCAGATTGCCTGAGCTAAGAAAGCTTGCC	300
Db	1114	GCTGGCACTTTTTCACCTGCAAGTCTGAACTCAGATTGCCTGAGCTAAGAAAGCTTGCC	1173
QY	301	TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA	360

Db	1174	 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA	1233
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QY	421	 ACTAAGTAGTTAGGCAATCTCCCATTTATTTTATTTTATTTTAAATTTTATTTTATTT	480
Db	1294	 ACTAAGTAGTTAGGCAATCTCCCATTTATTTTATTTTATTTTAAATTTTATTTTATTT	1353
QY	481	 TACTTTTATTTTATTTTGGAGCGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCG	540
Db	1354	 TACTTTTATTTTATTTTGGAGCGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCG	1413
QY	541	 TGATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAAATAATTCTCTTGCTCAGCCT	600
Db	1414	 TGATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAAATAATTCTCTTGCTCAGCCT	1473
QY	601	 CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACCATGCCCAGCTAA	660
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QY	661	 TTTTTTGTGTGTTTTTTTTGGTAGAGACAGGTTTTTACCATGTTGGCCAGGTGGGTGAC	720
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Db	1714	 CGCCAAGGCTGGAGTACAGTGGTGGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGTT	1773
QY	901	 CACGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAAGCGCCTGCCACCCACG	960
Db	1774	 CACGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAAGCGCCTGCCACCCACG	1833
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QY	1021	 TCTCGATCTCATGACCTTGTGATCCGCCCTCGCTCCCAAGTGCTGGGATTACAG	1080
Db	1894	 TCTCGATCTCATGACCTTGTGATCCGCCCTCGCTCCCAAGTGCTGGGATTACAG	1953
QY	1081	 GCATGAGCCACCGTGCCCGGCTTATCACATTTTATTTATTTGTTTTTCTCTCCCACTA	1140
Db	1954	 GCATGAGCCACCGTGCCCGGCTTATCACATTTTATTTATTTGTTTTTCTCTCCCACTA	2013
QY	1141	 GGTTGTAAGCTCCATGAGTTAGAGATTATTTATTTATTTATTTATTTATTTATTTAT	1200
Db	2014	 GGTTGTAAGCTCCATGAGTTAGAGATTATTTATTTATTTATTTATTTATTTATTTAT	2073
QY	1201	 TATTATTATTATCTGTTCACTGCTGTATCTCTAGCTCTAGGACAGAGCCTGGCACAT	1260
Db	2074	 TATTATTATTATCTGTTCACTGCTGTATCTCTAGCTCTAGGACAGAGCCTGGCACAT	2133
QY	1261	 AGTAAGTGCTCAATAAATAATTCACTGGATAAACAGTGCAGATAGTTTAAAACTATCTGAC	1320
Db	2134	 AGTAAGTGCTCAATAAATAATTCACTGGATAAACAGTGCAGATAGTTTAAAACTATCTGAC	2193
QY	1321	 CTAGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGAGCTG	1380
Db	2194	 CTAGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGAGCTG	2253
QY	1381	 AAATCGTGTCACTGCACCTCCAACCTGGGCAACAGAGCAAGACTCCATCTCTCAAAAAAAAA	1440

Db	2254	AAATCGTGTCACTGCACTCCAAAGCTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAAAA	2311
Qy	1441	AAAAAACTATCAGGCCTAGCTGGGTGGCACATGCCCTGTAATCCTAGCTGAGCGGTAGGG	1500
Db	2314	AAAAAACTATCAGGCCTAGCTGGGTGGCACATGCCCTGTAATCCTAGCTGAGCGGTAGGG	2373
Qy	1501	TCCCAGAAAGAAGAAGAAAAAGAAAGATATATATATATATATATACACACACACAAA	1560
Db	2374	TCCCAGAAAGAAGAAGAAAAAGAAAGATATATATATATATATACACACACACAAA	2433
Qy	1561	GATATAAACTTTATATATATAAAGTTTTCATTAAAAAATAAAACCTCTACCCACTT	1620
Db	2434	GATATAAACTTTATATATAAAGTTTTCATTAAAAAATAAAACCTCTACCCACTT	2493
Qy	1621	TCACTTTACAGGTTCTCGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGGTCAGG	1680
Db	2494	TCACTTTACAGGTTCTCGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGGTCAGG	2553
Qy	1681	GAGGCAGCGTGGGACCCGAGGAGCAGGAAGGCAGTGTGTCCCGGGGTGCTGGCAGACC	1740
Db	2554	GAGGCAGCGTGGGACCCGAGGAGCAGGAAGGCAGTGTGTGTCCCGGGGTGCTGGCAGACC	2613
Qy	1741	GATTTGAACTCTGGCTATGTCTTCTTGCACTGGCCGCCGCMCAGCGGCATCAGCCCTC	1800
Db	2614	GATTTGAACTCTGGCTATGTCTTCTTGCACTGGCCGCCGCMCAGCGGCATCAGCCCTC	2673
Qy	1801	GGGCGGTGTGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCAGGAGTGACCCCTTAT	1860
Db	2674	GGGCGGTGTGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCAGGAGTGACCCCTTAT	2733
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Db	2734	TGGAATACAACTACCGCTGCTACTGTGGCTTGGGGGGCTCAGCACCCCCGTGGATG	2793
Qy	1921	AACTGGACAAAGTAAGTGATCCGCTGCAAGGAAATTTGGAGTGCCTGCCGGGGCGGGGTG	1980
Db	2794	AACTGGACAAAGTAAGTGATCCGCTGCAAGGAAATTTGGAGTGCCTGCCGGGGCGGGGTG	2853
Qy	1981	GGGCACACGCCAAGGATCTCAGAGGCATACAAAGGGGACTTGCAATCTGCTAAGGATA	2040
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Qy	2041	ACATATTTTCACTCTTGTCAAATAAAACAAATATGTTCCAAGAGGACCTGTAGCGAACG	2100
Db	2914	ACATATTTTCACTCTTGTCAAATAAAACAAATATGTTCCAAGAGGACCTGTAGCGAACG	2973
Qy	2101	CACCCCGTTAGAGATGGAACAATGACCGACGTGCAAAACAGTGGGCGATGCTGCCCTCC	2160
Db	2974	CACCCCGTTAGAGATGGAACAATGACCGACGTGCAAAACAGTGGGCGATGCTGCCCTCC	3033
Qy	2161	AGTGGCAGAATGTAGCAACAGTAACATCACAGCAACTATCCACGTGTCTATTTCTAGCA	2220
Db	3034	AGTGGCAGAATGTAGCAACAGTAACATCACAGCAACTATCCACGTGTCTATTTCTAGCA	3093
Qy	2221	GTGGTGTCACTGCACCTTCTGAATACAGGATTTTACTGTATTTCTGCAACCATGTTAAA	2280
Db	3094	GTGGTGTCACTGCACCTTCTGAATACAGGATTTTACTGTATTTCTGCAACCATGTTAAA	3153
Qy	2281	AATCGCTTTTCAGGCCAGGCGGCTGCTCATGCTGTAAATCCAGCACTTTGGGAGGCCG	2340
Db	3154	AATCGCTTTTCAGGCCAGGCGGCTGCTCATGCTGTAAATCCAGCACTTTGGGAGGCCG	3213
Qy	2341	AGGCGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGTGAAACC	2400
Db	3214	AGGCGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGTGAAACC	3273
Qy	2401	CTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTAAACCCCA	2460
Db	3274	CTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTAAACCCCA	3333
Qy	2461	GCTACTTGGGAGACTGAGTTGGAGGTTTCAGTGAGCCAAAGGTGCTGTCACTGCTGTCCAG	2520
Db	3334	GCTACTTGGGAGACTGAGTTGGAGGTTTCAGTGAGCCAAAGGTGCTGTCACTGCTGTCCAG	3393

Qy	2521	CCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAATGCTTTCAATAATATATGATA	2580	3601	CAAGCGTGCAACCACCATGCTTGGCTAAATTTTTTGTTATTTTTTAGCAGAGATGGGGTTTAC	3660
Db	3394	CCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAATGCTTTCAATAATATATGATA	3453	4474	CAAGCGTGCAACCACCATGCTTGGCTAAATTTTTTGTTATTTTTTAGCAGAGATGGGGTTTAC	4533
Qy	2581	AAAGGACTTATATTTTTTCAAGCCATAGGATCATTTTCTCCTGAAGCATCTTGGCGAAGTC	2640	3661	CATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTCAGTCTCC	3720
Db	3454	AAAGGACTTATATTTTTTCAAGCCATAGGATCATTTTCTCCTGAAGCATCTTGGCGAAGTC	3513	4534	CATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTCAGTCTCC	4593
Qy	2641	ATCCCACTGTTCCCTGAGAGTGGGAGGTGAGGGCTGACCTATTGCTCTGCATTTACTC	2700	3721	CAAAAGTGTGGAATTATAGGCGTGAGTCACTGTGCTGGCCGATTACTGTCTATTTTCTT	3780
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Qy	2701	CTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACATGACAACTGCTAYGAC	2760	3781	TATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAATAA	3840
Db	3574	CTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACATGACAACTGCTATGAC	3633	4654	TATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAATAA	4713
Qy	2761	CAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCACACCTAT	2820	3841	TTGATGAATGCACAGCCTAGATATAAACTTTTCTTTTAAAAACAATCTTGACA	3900
Db	3634	CAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAAACCCGTACACCCACACCTAT	3693	4714	TTGATGAATGCACAGCCTAGATATAAACTTTTCTTTTAAAAACAATCTTGACA	4773
Qy	2821	TCATACTCGTCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCCTTGACC	2880	3901	ACTTTGCAGAAATAATACAATCTTTGCATTTCTGCTTTTTCATTTAGTACT	3960
Db	3694	TCATACTCGTCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCCTTGACC	3753	4774	ACTTTGCAGAAATAATACAATCTTTGCATTTCTGCTTTTTCATTTAGTACT	4833
Qy	2881	TATGAATTTAGTTGGTTCTCAGTAGGCCGGGGGAAATATAGTAAACAACAGCCATGAT	2940	3961	TTTTCATATTGCCCTCAAAACCTTTATTGTTACTGTTTTTTTCATTTAGTACT	4020
Db	3754	TATGAATTTAGTTGGTTCTCAGTAGGCCGGGGGAAATATAGTAAACAACAGCCATGAT	3813	4834	TTTTCATATTGCCCTCAAAACCTTTATTGTTACTGTTTTTTTCATTTAGTACT	4893
Qy	2941	TTAGTGTAAATTTTCTTGGTCTGGGCAGTGTCTCCTTTAATCCTCAGAAACAACATATG	3000	4021	TGAATAATATGGCTTAATTTGCTTTATACATCCTCCTGCTCCACTTTAGAAAGGCCAAATTT	4080
Db	3814	TTAGTGTAAATTTTCTTGGTCTGGGCAGTGTCTCCTTTAATCCTCAGAAACAACATATG	3873	4894	TGAATAATATGGCTTAATTTGCTTTATACATCCTCCTGCTCCACTTTAGAAAGGCCAAATTT	4953
Qy	3001	GGATAGTACAATATCCTCATTAAACAGATAAAGAAAACTCAGAGCTCAGAAGGCTGAGCT	3060	4081	ACAAATCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAAATACACACACACACACT	4140
Db	3874	GGATAGTACAATATCCTCATTAAACAGATAAAGAAAACTCAGAGCTCAGAAGGCTGAGCT	3933	4954	ACAAATCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAAATACACACACACACACT	5013
Qy	3061	ATTGGCCAAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTGTGTTGT	3120	4141	CACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTTGCAATTAGAGGATGTT	4200
Db	3934	ATTGGCCAAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTGTGTTGT	3993	5014	CACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTTGCAATTAGAGGATGTT	5073
Qy	3121	TTAGACACAGGGTCTTGCTCTGTCACCCAGGCATGAGCAGAGTGGTGCAACCATAGGTCA	3180	4201	TGTTCATATTAAATTAATAATAACTCAGTTGGGCAGAGTGACTCAAGCCTGTAAACCACAGT	4260
Db	3994	TTAGACACAGGGTCTTGCTCTGTCACCCAGGCATGAGCAGAGTGGTGCAACCATAGGTCA	4053	5074	TGTTCATATTAAATTAATAATAACTCAGTTGGGCAGAGTGACTCAAGCCTGTAAACCACAGT	5133
Qy	3181	CTGACGCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGG	3240	4261	ACTTTGGAAGTCCAAAGTGGTGGATCACTTTGAGTGAGAAAGTTGAGACCAGCCTGGTC	4320
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Qy	3241	GACTACGAGCGTGCACCAACCGCTGGCTAAATTAATAATAATTTTGTAGAGACTGGG	3300	4321	AATATGGTGAAACCCCTATCTCTACTAAAAAATACAAAAATTAGCTGGGTGTAGTATGCAT	4380
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Db	4174	TCCTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTG	4233	5254	GCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCA	5313
Qy	3361	GCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTA	3420	4441	GAGGTTGCAGTGAGCCGAGATCCCACACTGCACTCCAGCCTGGCGACACAGCGAGACT	4500
Db	4234	GCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTA	4293	5314	GAGGTTGCAGTGAGCCGAGATCCCACACTGCACTCCAGCCTGGCGACACAGCGAGACT	5373
Qy	3421	CATTCCATCTTTCCAATAGAAATGAAGATCCACAGAACAGGGATTACTGCCTATTTTCTT	3480	4501	CTATCTCAAAAAATAATAATAATAATAAAGGATCGGAGAGAAAAACAACCTAATAAGAT	4560
Db	4294	CATTCCATCTTTCCAATAGAAATGAAGATCCACAGAACAGGGATTACTGCCTATTTTCTT	4353	5374	CTATCTCAAAAAATAATAATAATAATAAAGGATCGGAGAGAAAAACAACCTAATAAGAT	5433
Qy	3481	CCTTTCTTTTGGACAGAGTCTCACTTCATCACCTCAACCTCCGTTTCCAGTCTACTGCA	3540	4561	TCCTGAAGGTAAGCAGAGATACGTAAATTTATATGTAAATAAGTTTAAATGCAATTTAACT	4620
Db	4354	CCTTTCTTTTGGACAGAGTCTCACTTCATCACCTCAACCTCCGTTTCCAGTCTACTGCA	4413	5434	TCCTGAAGGTAAGCAGAGATACGTAAATTTATATGTAAATAAGTTTAAATGCAATTTAACT	5493
Qy	3541	ACCTCTGCTCCCGGTTCAAGYGATTTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTA	3600	4621	GTAATCTTATTTGTTTATTTGTTTATAAAAGTAAACAAGCCAAAAGTAATGCAACTTCAA	4680
Db	4414	ACCTCTGCTCCCGGTTCAAGCGATTTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTA	4473	5494	GTAATCTTATTTGTTTATTTGTTTATAAAAGTAAACAAGCCAAAAGTAATGCAACTTCAA	5553
				4681	ACKCTACATAAATATCTATTATTATGGAAAGTGGAAGGCATCTATAATCCTACTACCCAAAGA	4740

Db	5554	ACTCTACATAAAATATCTATTATGGAAGTGGGAAGGCATCTATAATCCTACTACCCAAAGA	5613
QY	4741	TAACCAGTTACATATTCCTCCAGATTTTGGGGCATACACTAGCTTTTATTGCGAA	4800
Db	5614	TAACCAGTTACATATTCCTCCAGATTTTGGGGCATACACTAGCTTTTATTGCGAA	5673
QY	4801	AATTTCATGTGCAGGCATACCTAATTTTCTAAATGCTCTATGATGATTCATTTAAGS	4860
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QY	4861	ATGTTCCATAATTTTTTAAATAACATGCTTTAAAGTAGAGAAACTAGTTGGGCATGGTG	4920
Db	5734	ATGTTCCATAATTTTTTAAATAACATGCTTTAAAGTAGAGAAACTAGTTGGGCATGGTG	5793
QY	4921	CTCAGCCTGTATCCCGACACTTTTGGGAGCCCGAGGCAAATGGATCACTTGAGGTC	4980
Db	5794	CTCAGCCTGTATCCCGACACTTTTGGGAGCCCGAGGCAAATGGATCACTTGAGGTC	5853
QY	4981	GTTTGAGACCAAGCCTGGACAA	5001
Db	5854	GTTTGAGACCAAGCCTGGACAA	5874

RESULT 2
AC003982/c
LOCUS AC003982 122302 bp DNA linear PRI 18-MAR-1999
DEFINITION Homo sapiens PAC clone 166H1 from 12q, complete sequence.
ACCESSION AC003982
VERSION AC003982.1 GI:2769695
KEYWORDS HTG.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 122302)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
PUBMED 9847074
REFERENCE 2 (bases 1 to 122302)
AUTHORS Bradshaw,H., Wu,X. and Ozersky,P.
TITLE The sequence of Homo sapiens PAC clone 166H1
JOURNAL Unpublished (1999)
REFERENCE 3 (bases 1 to 122302)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 4 (bases 1 to 122302)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT SUBMITTED BY: WUGSC
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
This clone was originally isolated in the laboratory of Professor Graeme Bell, Howard Hughes Medical Institute and Departments of Biochemistry and Molecular Biology, and Medicine, The University of Chicago, Chicago, IL, USA. The clone was provided by the laboratory of Dr. Roger Cox at The Wellcome Trust Centre For Human Genetics, Oxford, UK. Some contig information was also obtained from Yamagata et al., Nature 384:455-8 (1996).

SOURCE INFORMATION:
This clone was derived from human PAC library RPCI-1, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.
The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is 278C19; the clone sequenced to the right is 15E1. Actual start of this clone is at base position 1 of 166H1; actual end is at 122302 of 166H1.

FEATURES	Location/Qualifiers
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RESULT 3
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LOCUS AX377239 Sequence 1 from Patent WO0212562. DNA linear PAT 18-MAR-2002

DEFINITION AX377239

ACCESSION AX377239

VERSION AX377239.1 GI:19573528

KEYWORDS Homo sapiens (human)

SOURCE ORGANISM Homo sapiens

REFERENCE 1 Kazemi, A., Kliem, S.E. and Koshy, B.

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

TITLE Haplotypes of the pla2g1b gene

JOURNAL Patent: WO 0212562-A 1 14-FEB-2002;

GenCore version 5.1.8
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SUMMARIES

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AC ADJ09983
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DT 17-JUN-2004 (first entry)
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DE Human phospholipase A2 (PLA2G1B) DNA SeqID 1.
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human; gene; ds; fat reduction; fat deposition; phospholipase A2;
PLA2G1B; chromosome 12q24; single nucleotide polymorphism; SNP;
appetite suppressant; lipase inhibitor; exercise regimen; obesity;
non-insulin dependent diabetes mellitus; NIDDM; cardiovascular disorder;
hypertension; antidiabetic.
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WO2004002296-A2.

08-JAN-2004.

27-JUN-2003; 2003WO-US020831.

27-JUN-2002; 2002US-0392362P.

(SEQU-) SEQUENOM INC.

Adam GIR, Langdown ML, Denissenko MF, Dennis E, Cantor C;
Rubin B;

WPI; 2004-071944/07.
P-PSDB; ADJ09984.

Identifying a candidate therapeutic for fat reduction, useful for
treating diabetes, by introducing a test molecule to a system comprising
PLA2G1B protein or nucleic acid, and determining the presence of
interaction between the compounds.

XX

PS Claim #: SEQ ID NO 1; 116pp; English.

XX This invention relates to a novel candidate therapeutic agent useful for

CC fat reduction and disorders related to fat depositions. Specifically, it

CC refers to polymorphic variations in the phospholipase A2 (PLA2G1B) DNA,

CC which is located on chromosome 12q24 and has been associated with central

CC fat deposition. The present invention describes methods to detect the

CC presence or absence of these single nucleotide polymorphisms of PLA2G1B,

CC in particular G7328A and T9182G, and subsequently provide treatment that

CC reduces fat deposition. This treatment may consist of an appetite

CC suppressant, a lipase inhibitor, a phospholipase inhibitor, an exercise

CC regimen, a dietary regimen, psychological counseling, psychotherapy or a

CC psychotherapeutic. Accordingly, PLA2G1B is a target for reducing fat

CC deposition and it can be used to treat both obesity and non-insulin

CC dependent diabetes mellitus (NIDDM), as well as cardiovascular disorders

CC such as hypertension. As such, it exhibits antidiabetic activity. This

CC polynucleotide sequence is the human PLA2G1B DNA of the invention.

XX

SQ Sequence 12174 BP; 3220 A; 2996 C; 2739 G; 3219 T; 0 U; 0 Other;

Query Match 100.0%; Score 4997.8; DB 12; Length 12174;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 4993; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGCTAGCTGT 60

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 4500 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGCTAGCTGT 4559

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGCCCTTCTCTCCCAAGTGAGCTA 120

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 4560 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGCCCTTCTCTCCCAAGTGAGCTA 4619

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QY 121 AGATCTCACTCCTCTGGAATGGGGCCACAGGCCACAGCAACAGGGATGGCCAGCCCCG 180

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 4620 AGATCTCACTCCTCTGGAATGGGGCCACAGGCCACAGCAACAGGGATGGCCAGCCCCG 4679

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QY 181 CAGTCTCAAWTCGAGGTTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGTTCCCTCAAG 240

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QY 4680 CAGTCTCAAWTCGAGGTTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGTTCCCTCAAG 4739

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QY 241 GCTGGCACTTTTCAACCTGCAAGTCTGAACTCAGATTGCCTGAGCTAAGAAAGCTTGCC 300

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QY 4740 GCTGGCACTTTTCAACCTGCAAGTCTGAACTCAGATTGCCTGAGCTAAGAAAGCTTGCC 4799

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QY 301 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA 360

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 4800 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA 4859

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 361 TGATCATAGCTCACCA CAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCACCTTACTCA 420

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QY 421 ACTAAGTAGTTAGGCCAATCTCCCATTTATTTTATTTTAAATTTTATTTTATTTTATTT 480

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QY 4920 ACTAAGTAGTTAGGCCAATCTCCCATTTATTTTATTTTAAATTTTATTTTATTTTATTT 4979

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QY 481 TACTTTATTTTATTTTGGACGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCG 540

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QY 4980 TACTTTATTTTATTTTGGACGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCG 5039

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QY 541 TGATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAATAATTCTCTTGCCCTCAGCCT 600

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QY 601 CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACACCACCATGCCAGCTAA 660

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 5100 CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACACCACCATGCCAGCTAA 5159

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QY 661 TTTTGT 720

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QY 5160 TTTTGT 5219

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 721 CTCCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCTTTTCTTAATGCAGTATCCAGT 780

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 5220 CTCCCTTTTAGATTCTCCTCATCTCTGCTCTATTCTCCCTTTTCTAATGCAGTATCCAGT 5279

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 781 TTCTTACTTATCACATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 840

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 5280 TTCTTACTTATCACATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 5339

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QY 841 CGCCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGTT 900

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QY 901 CACGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAAGGGCGCTGCCACCACG 960

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QY 5400 CACGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAAGGGCGCTGCCACCACG 5459

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 961 CCCCGCTAAATTTTGTATTTTAAATAAAGACGGGTTTTCATCGTGTAGCCAGATGG 1020

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QY 5460 CCCCGCTAAATTTTGTATTTTAAATAAAGACGGGTTTTCATCGTGTAGCCAGATGG 5519

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QY 1021 TCTCGATCTCATGACCTTGTGATCCGCCCTGCCCTCCCAAAGTGTGGGATTACAG 1080

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QY 1141 GGTGTGAAGCTCCATGAGGTTAGAGATTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1200

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 5640 GGTGTGAAGCTCCATGAGGTTAGAGATTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 5699

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QY 1201 TATTATTATTATATCTGTTCACTGCTGTATCTCTAGCTCCTAGGACAGAGCCTGGCACAT 1260

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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QY 1261 AGTAAGTGTCTCAATAAATTAATTCACCTGGATAAAACAGTGCAGATAGTTTAAAACTATCTGAC 1320

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QY 5760 AGTAAGTGTCTCAATAAATTAATTCACCTGGATAAAACAGTGCAGATAGTTTAAAACTATCTGAC 5819

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QY 5820 CTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGAGCTG 5879

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QY 1381 AAATCGTGTCACTGCACTCCAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAA 1440

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QY 1441 AAAAAACTATCAGGCCCTAGCTGGTGGCACATGCTGTAAATCCTAGCTGAGCGGTAGGG 1500

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Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 6060 GATATAAACTTTATATATATAAAAGTTTTCATTAAAAA 6119

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 1621 TCACCTTTACCAGGTTCCCTGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGSGTCAGG 1680

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 6120 TCACCTTTACCAGGTTCCCTGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGSGTCAGG 6179

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 1681 GAGGCAGCGTGGGACCCGAGGGAGCAGGAAGGCAAGTGTGTCCCGGGGTGCTGGCAGACC 1740

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 6180 GAGGCAGCGTGGGACCCGAGGGAGCAGGAAGGCAAGTGTGTCCCGGGGTGCTGGCAGACC 6239

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 1741 GATTTGAACCTCTGGCTATGTCTTCTTGCAGTGGCCGCCCGCMCAGCGGCATCAGCCCTC 1800

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Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 1801 GGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGGTGTATCCCGGGAGTGACCCCTT 1860

Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Qy 1861 TGGAAATACAACAAC TACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGTGGATG 1920

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Db 6420 AACTGGACAAGTAA GTGATCCGCCCTGCAGGAAAAATTGGAGTGCCTGCCGGGGCGGGGTG 6479

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Db 6540 ACATATTTTCACTCT TGTGTCAAATAAACAATAATATGTTCCAAAGAGGACCTGTAGCGAACG 6599

Qy 2101 CACCCCGTTAGAGATG GAAACAATGACCGACGTGCAAAACAGTGGCGGATGCTGCCCTCC 2160

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Db 6720 GTGGTTGTCACTGCA CCTTCTGAATACAGGATTTTACTGTATTTCTTGCAACCATGTTAAA 6779

Qy 2281 AATCGTTTTAGGCCAG GCGCGGTGCATGCCTGTAAATCCAGCACTTTGGGAGGCCG 2340

Db 6780 AATCGTTTTAGGCCAG GCGCGGTGCATGCCTGTAAATCCAGCACTTTGGGAGGCCG 6839

Qy 2341 AGCGGGCGGATCACTT GAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGTGAAACC 2400

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Qy 2401 CTGTCTCTACTAAAAA ATACAAAAATTAGCGGACATGGTGGCGAGCGCCTGTAAACCCCA 2460

Db 6900 CTGTCTCTACTAAAAA ATACAAAAATTAGCGGACATGGTGGCGAGCGCCTGTAAACCCCA 6959

Qy 2461 GCTACTTTGGGAGACTG AGTTGGAGTTTTCAGTGAGCCAAAGTTCGTGTCTCACCTGCTCCAG 2520

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Qy 2701 CTATCTCAGCTGTCCCT CCCACTTTCCAGGTGCTGCCAGACACATGACAACTGCTATGAC 2760

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Qy 2941 TTAGTGTTAATTTTCTT GGTCTGGGCAGTGTCTCTCTTAATCCTCAGAACAAACACTATG 3000

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Qy 3181 CTGCAGCCTCAACCTC CTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGG 3240

Db 7680 CTGCAGCCTCAACCTC CTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGG 7739

Qy 3241 GACTACGAGCGTGCACC ACACGCTGGCTAATTAATAAAAAATTTTTTGTAGAGACTGGG 3300

Db 7740 GACTACGAGCGTGCACC ACACGCTGGCTAATTAATAAAAAATTTTTTGTAGAGACTGGG 7799

Qy 3301 TCTTACTACGTTGGCC AGGCTTGTCTTAAACTCTGGCTTCAAGCAATCCTCCTACCTTG 3360

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Qy 3481 CCTTCTTTTTTGTAG ACAGAGTCTCACTTCATCACCTCAACCTCCGTTCAGCTCACTGCA 3540

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Qy 3601 CAAGCGTGCACCACCA CTATGCTGGCTAAATTTTTTGTATTTTAGCAGAGATGGGGTTTAC 3660

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Db 8160 CATGTTGCCCAGGCTG GTCTCAAAACTCCTGACCTCAAGTGATCGCCTGCCTCAGTCTCC 8219

Qy 3721 CAAAGTGCTGGAATTAT AGCGGTGAGTCACGTGCGCTGGCCGATTACTGTCTATTTTCTT 3780

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Qy	4021	TGAATAATATGGCTTAATTTGCTTATACATCCTCTCTGTCCACTTTAGAAAGGCCAAATTT	4080
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Db	8580		8639
Qy	4141	CACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTT	4200
Db	8640		8699
Qy	4201	TGTTCATATTAATAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCCACAGT	4260
Db	8700		8759
Qy	4261	ACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAACTCGAGACCAGCCTGGTC	4320
Db	8760		8819
Qy	4321	AATATGTTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCAT	4380
Db	8820		8879
Qy	4381	GCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATGCTTGAACCTGGGAGGCA	4440
Db	8880		8939
Qy	4441	GAGTTGCAGTGAGCCGAGATCCGACCACCTGCACCTCCAGCCTGGGCGACACAGCGAGACT	4500
Db	8940		8999
Qy	4501	CTATCTCAAAAAATAAAATAAATAAAGGATCGGAGAGAAACAAAACTAATAAGAT	4560
Db	9000		9059
Qy	4561	TCCTGAAGTAAAGCAGAGATACGTAAATATATGTAATAAAGTTTAAATGCAATTTAACT	4620
Db	9060		9119
Qy	4621	GTAATCTTATGTTTATTTTGGTTATAAAAGTAAACAAGCCAAAAGTAATGCAACTTCAA	4680
Db	9120		9179
Qy	4681	ACKCTACATAAAATATCTATTATGGAAGTGGAAGGCATCTATAATCCTACTACCCAAAGA	4740
Db	9180		9239
Qy	4741	TAACCACTTACATATTCTCTCCAGATTTTGGGGCATACACTAGCTTTTTTATTTTGGGAA	4800
Db	9240		9299
Qy	4801	AATTTCCATGTGCAGGCATACCTAAATTTTCTAAATGTCTATGTAGTATTCATTTAAGG	4860
Db	9300		9359
Qy	4861	ATGTTCCATAATTTTAAAAATACATGCTTTAAAGTAGAGAAACTAGGTTGGGCATGGTG	4920
Db	9360		9419
Qy	4921	CTCACGCCTGTATCCAGCACTTTGGGAGGCCGAGGCAAAATGGATCACTTGAGGTCGGGA	4980
Db	9420		9479
Qy	4981	GTTTGAGACCAGCCTGGACAA	5001
Db	9480		
		GTTTGAGACCAGCCTGGACAA	9500

RESULT 2
ADI35082
ID ADI35082 standard; DNA; 12174 BP.
XX

AC	ADI35082;	
XX		
DT	22-APR-2004 (first entry)	
XX		
DE	Human PLA2G1B nucleotide sequence.	
XX		
KW	PLA2G1B ; fat deposition; leanness; polymorphism;	
KW	non-insulin dependent diabetes mellitus; NIDDM; hyperinsulinemia;	
KW	hypertension; glucose intolerance; dyslipidemia; hypercoagulability;	
KW	microalbuminuria; human; gene; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004002295-A2.	
XX		
PD	08-JAN-2004.	
XX		
PF	27-JUN-2003; 2003WO-US020830.	
XX		
PR	27-JUN-2002; 2002US-03923361P.	
XX		
PA	(SEQU-) SEQUENOM INC.	
XX		
PI	Adam GIR, Langdown ML;	
XX		
DR	WPI; 2004-082843/08.	
XX	P-PSDB; ADI35083.	
PT	Diagnosing a predisposition to fat deposition or leanness, useful for	
PT	diagnosing a predisposition to e.g. diabetes or hypertension, comprises	
PT	detecting the presence of a polymorphism in the PLA2G1B nucleic acid from	
PT	the subject.	
XX		
PS	Claim 1; SEQ ID NO 1; 91pp; English.	
XX		
CC	The invention relates to diagnosing a predisposition to fat deposition or	
CC	leanness in a subject comprising detecting the presence or absence of a	
CC	polymorphic variation associated with fat deposition at a polymorphic	
CC	site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a	
CC	subject, where the presence of the polymorphic variation indicates a	
CC	predisposition to fat deposition in the subject. The polymorphic	
CC	variation is a guanine at position 7328 or thymine at position 9182 of	
CC	the present sequence. The method is useful for diagnosing a	
CC	predisposition to fat deposition or leanness in a subject, and	
CC	consequently for diagnosing a predisposition to non-insulin dependent	
CC	diabetes mellitus (NIDDM) in a subject and conditions such as	
CC	hyperinsulinemia, hypertension, glucose intolerance, dyslipidemia,	
CC	hypercoagulability, or microalbuminuria, which can lead to early	
CC	prescription of preventive measures. The present sequence represents a	
CC	human PLA2G1B nucleotide sequence.	
XX		
SQ	Sequence 12174 BP; 3217 A; 2992 C; 2738 G; 3215 T; 0 U; 12 Other;	
	Query Match 100.0%; Score 4997.8; DB 12; Length 12174;	
	Best Local Similarity 99.9%; Pred. No. 0;	
	Matches 5000; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGTGCTAGCTGT	60
Db		4500
Qy	61 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGCCCTTCTCTCCCAAGTGAGCTA	120
Db		4560
Qy	121 AGATCTCACTCCTCTGGAATGGGGCCACAGGCCACAGGATGGCCAGCCCCG	180
Db		4620
Qy	181 CAGTCTCAAATCGAGGTTCCAGTGGGGCTTAAGGGCTCTCTATTGGGGTTCCCTCAAG	240
Db		4680

Qy	241	GCTGGCACTTTTCAACCTGCAAGCTGAAGTCTGAAGTCTGAGTCTGAGCTAAGAAAGCTTGCC	300
Db	4740	GCTGGCACTTTTCAACCTGCAAGCTGGAAGTCTGAACTCAGATTGCTGAGCTAAGAAAGCTTGCC	4799
Qy	301	TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA	360
Db	4800	TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA	4859
Qy	361	TGATCATAGCTCACACAGCTTCCAACCTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA	420
Db	4860	TGATCATAGCTCACACAGCTTCCAACCTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA	4919
Qy	421	ACTAAGTAGTTAGGCCAATCTCCCATTTATTTTATTTTATTTTAAATTTTATTTTATTT	480
Db	4920	ACTAAGTAGTTAGGCCAATCTCCCATTTATTTTATTTTATTTTAAATTTTATTTTATTT	4979
Qy	481	TACTTTATTTTATTTTGGACGGGCTCACTCTGTGCCCCAGGCTGGAGTGCAGTGGCG	540
Db	4980	TACTTTATTTTATTTTGGACGGGCTCACTCTGTGCCCCAGGCTGGAGTGCAGTGGCG	5039
Qy	541	TGATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAATAATTTCTTTCCTTCAGCCT	600
Db	5040	TGATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAATAATTTCTTTCCTTCAGCCT	5099
Qy	601	CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGGCACACACCACCATGCCAGCTAA	660
Db	5100	CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGGCACACACCACCATGCCAGCTAA	5159
Qy	661	TTTTTTGTGTTTTTTTTTGGTAGAGACAGGTTTTTCACCATGTGGCCAGGCTGGGTGAC	720
Db	5160	TTTTTTGTGTTTTTTTTTGGTAGAGACAGGTTTTTCACCATGTGGCCAGGCTGGGTGAC	5219
Qy	721	CTCCCTTTTAGAATCTCCTCAACCTGCTCTATTCTTCCCTTTTCTAATGCAGTATCCAGT	780
Db	5220	CTCCCTTTTAGAATCTCCTCAACCTGCTCTATTCTTCCCTTTTCTAATGCAGTATCCAGT	5279
Qy	781	TTCTCTTACTTATCACATTTATTTATTTCTTATTTATTTAGACAGAGTCTTGCTTTGT	840
Db	5280	TTCTCTTACTTATCACATTTATTTATTTCTTATTTATTTAGACAGAGTCTTGCTTTGT	5339
Qy	841	CGCCAAGGCTGAGTACAGTGGTCCGATCTCGGCTCACTGCAAGTCCACCTGCTGGGTT	900
Db	5340	CGCCAAGGCTGAGTACAGTGGTCCGATCTCGGCTCACTGCAAGTCCACCTGCTGGGTT	5399
Qy	901	CACGCCATTTCTCCGGCCTCAGCCTCCCAGTAGCTGGGACTAAAGGGCCTGCCACCACG	960
Db	5400	CACGCCATTTCTCCGGCCTCAGCCTCCCAGTAGCTGGGACTAAAGGGCCTGCCACCACG	5459
Qy	961	CCCCGCTAATTTTGTATTTTAAATAAGACGGGGTTTCATCGTTAGCCAGGATGG	1020
Db	5460	CCCCGCTAATTTTGTATTTTAAATAAGACGGGGTTTTCATCGTTAGCCAGGATGG	5519
Qy	1021	TCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAGTCTGGGATTACAG	1080
Db	5520	TCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAGTCTGGGATTACAG	5579
Qy	1081	GCATGAGCCACCGTCCCGCCTTATCACATTTATTTATTTATTTTCTCTCCCACTA	1140
Db	5580	GCATGAGCCACCGTCCCGCCTTATCACATTTATTTATTTATTTTCTCTCCCACTA	5639
Qy	1141	GGTTGTAAGCTCCATGAGGTTAGAGATTATTTATTTATTTATTTATTTATTTAT	1200
Db	5640	GGTTGTAAGCTCCATGAGGTTAGAGATTATTTATTTATTTATTTATTTATTTAT	5699
Qy	1201	TATTATTATTATCTGTTTCACCTGCTGTATCTCTAGCTCCTAGACAGAGCCTGGCACAT	1260
Db	5700	TATTATTATTATCTGTTTCACCTGCTGTATCTCTAGCTCCTAGACAGAGCCTGGCACAT	5759
Qy	1261	AGTAAGTGCTCAATAAATATTCACTGGATAAACAGTGCAGATAGTTTAAAACTATCTGAC	1320
Db	5760	AGTAAGTGCTCAATAAATATTCACTGGATAAACAGTGCAGATAGTTTAAAACTATCTGAC	5819
Qy	1321	CTAGGGAGGCTGAGGCAGGAGAATGGCGTGAAACCCGGGAAGCAGAGTTTGCAGTGAGCTG	1380

Db	5820	CTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAAACCCGGGAAGCAGAGTTTGCAGTGAGCTG	5879
Qy	1381	AAATCGTGTCACTGCACTCCAAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAAA	1440
Db	5880	AAATCGTGTCACTGCACTCCAAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAAA	5939
Qy	1441	AAAAAACTATCAGGCCTAGCTGGGTGGCACATGCCTGTAATCCTAGCTGAGCGGTAGGG	1500
Db	5940	AAAAAACTATCAGGCCTAGCTGGGTGGCACATGCCTGTAATCCTAGCTGAGCGGTAGGG	5999
Qy	1501	TCCCAGAAGAAGAAAGAAAAAAGAAAGATATATATATATATACACACACAAAA	1560
Db	6000	TCCCAGAAGAAGAAAGAAAAAAGAAAGATATATATATATATACACACACAAAA	6059
Qy	1561	GATATAAACCTTTATATATAAAGTTTTTCATTAAAAAAAACCTCTACCCACTT	1620
Db	6060	GATATAAACCTTTATATATAAAGTTTTTCATTAAAAAAAACCTCTACCCACTT	6119
Qy	1621	TCACCTTTACCAGGTTCTGCGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGTCAAG	1680
Db	6120	TCACCTTTACCAGGTTCTGCGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGTCAAG	6179
Qy	1681	GAGGCAGCGTGGACCCGAGGGAGCAGGAAGCAAGTGTGTCCCGGGTGTGGCAGACC	1740
Db	6180	GAGGCAGCGTGGACCCGAGGGAGCAGGAAGCAAGTGTGTCCCGGGTGTGGCAGACC	6239
Qy	1741	GATTTGAACCTCTGGCTATGTCTTCTTGCAGTGGCGCGCCGCMCAGCGGCATCAGCCCTC	1800
Db	6240	GATTTGAACCTCTGGCTATGTCTTCTTGCAGTGGCGCGCCGCMCAGCGGCATCAGCCCTC	6299
Qy	1801	GGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCGGGAGTGACCCCTTYT	1860
Db	6300	GGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCGGGAGTGACCCCTTYT	6359
Qy	1861	TGGAATACAACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGTGGATG	1920
Db	6360	TGGAATACAACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGTGGATG	6419
Qy	1921	AACTGGACAAGTAAGTATCGCCTGCAGGAAATTTGGAGTGCCTGCCGGGGCGGGGTG	1980
Db	6420	AACTGGACAAGTAAGTATCGCCTGCAGGAAATTTGGAGTGCCTGCCGGGGCGGGGTG	6479
Qy	1981	GGGCACACGCCAAGGATCTCACGAGGCATACAAAGGGGACTTGCAATCTGCTAAGGATA	2040
Db	6480	GGGCACACGCCAAGGATCTCACGAGGCATACAAAGGGGACTTGCAATCTGCTAAGGATA	6539
Qy	2041	ACATATTTTCACTCTTGTCAAATAAAACAAATATGTTCCAAGAGGACCTGTAGCGAACG	2100
Db	6540	ACATATTTTCACTCTTGTCAAATAAAACAAATATGTTCCAAGAGGACCTGTAGCGAACG	6599
Qy	2101	CACCCCGTTAGAGATGGAACAATGACCCGACGTGCAAAAACAGTGGCGGATGCTGCCTCC	2160
Db	6600	CACCCCGTTAGAGATGGAACAATGACCCGACGTGCAAAAACAGTGGCGGATGCTGCCTCC	6659
Qy	2161	AGTGGCAGAAATGTAGCAACAGTAAACATCACAGCAACTATCCACGTGTCAATTTCTAGCA	2220
Db	6660	AGTGGCAGAAATGTAGCAACAGTAAACATCACAGCAACTATCCACGTGTCAATTTCTAGCA	6719
Qy	2221	GTGGTTGTCACTGCACCTTCTGAAATACAGGATTTTACTGTATTTCTTGCAACCATGTTAAA	2280
Db	6720	GTGGTTGTCACTGCACCTTCTGAAATACAGGATTTTACTGTATTTCTTGCAACCATGTTAAA	6779
Qy	2281	AATCGCTTTCAGGCCAGCGCGGTGGCTCATGCCCTGTAATCCAGCACTTTTGGGAGCGG	2340
Db	6780	AATCGCTTTCAGGCCAGCGCGGTGGCTCATGCCCTGTAATCCAGCACTTTTGGGAGCGG	6839
Qy	2341	AGCGGGCGGATCACTTGAGGTGAGGATTCGAGACAGCCCTGGCCAAACATGGTGAACCC	2400
Db	6840	AGCGGGCGGATCACTTGAGGTGAGGATTCGAGACAGCCCTGGCCAAACATGGTGAACCC	6899
Qy	2401	CTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTAAACCCA	2460

Db 6900 CTGCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCAGCGCCTGTAAACCCCA 6959
Qy 2461 GCTACTTGGGAGACTGAGTTGGAGGTTTCAGTGAGCCAAAGTFCGTGTCACTGCTGTCCAG 2520
Db 6960 GCTACTTGGGAGACTGAGTTGGAGGTTTCAGTGAGCCAAAGTFCGTGTCACTGCTGTCCAG 7019
Qy 2521 CCTGGTAAACAGAGCAACTCTGTCTCAAAAAAAAAAAAAATGCTTTCAATAAATATATGATA 2580
Db 7020 CCTGGTAAACAGAGCAACTCTGTCTCAAAAAAAAAAAAAATGCTTTCAATAAATATATGATA 7079
Qy 2581 AAAGGACTTATATTTTTCAGCCATAGGATCATTTTCTCCTGAAGCATCTTGGCGAAGTC 2640
Db 7080 AAAGGACTTATATTTTTCAGCCATAGGATCATTTTCTCCTGAAGCATCTTGGCGAAGTC 7139
Qy 2641 ATCCCACTGTTCTCTGAGAGTGGCAGGTGAGGGCTGACCTATTGCTCTGCACTTACTC 2700
Db 7140 ATCCCACTGTTCTCTGAGAGTGGCAGGTGAGGGCTGACCTATTGCTCTGCACTTACTC 7199
Qy 2701 CTATCTCAGCTGTCCCTCCCACTTTCAGGCTGCTGCCAGACACATGACAACTGCTAYGAC 2760
Db 7200 CTATCTCAGCTGTCCCTCCCACTTTCAGGCTGCTGCCAGACACATGACAACTGCTAYGAC 7259
Qy 2761 CAGGCAAGAAGCTGGACAGCTGTAAATTTCTGTGGACAMMCCGTACACCCACACCTAT 2820
Db 7260 CAGGCAAGAAGCTGGACAGCTGTAAATTTCTGTGGACAMMCCGTACACCCACACCTAT 7319
Qy 2821 TCATACTCGTGTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCCTGACC 2880
Db 7320 TCATACTCRTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCCTGACC 7379
Qy 2881 TATGAATTTCTAGTTGGTTCTCAGTAGGCCGGGGGAAATATAGTAAACACAGCCATGAT 2940
Db 7380 TATGAATTTCTAGTTGGTTCTCAGTAGGCCGGGGGAAATATAGTAAACACAGCCATGAT 7439
Qy 2941 TTAGTGTTAATTTTCTTGGTCTGGGCAGTGTCTCCTTTAATCCTCAGAAACAACATATG 3000
Db 7440 TTAGTGTTAATTTTCTTGGTCTGGGCAGTGTCTCCTTTAATCCTCAGAAACAACATATG 7499
Qy 3001 GGATAGGTACAATTATCCTCACTTAACAGATAAAGAAAACCTGAGGCTCAGAAGGCTGAGCT 3060
Db 7500 GGATAGGTACAATTATCCTCACTTAACAGATAAAGAAAACCTGAGGCTCAGAAGGCTGAGCT 7559
Qy 3061 ATTTGCCAAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTGTGTGTGT 3120
Db 7560 ATTTGCCAAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTGTGTGTGT 7619
Qy 3121 TTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCAAGTGGTGCAACCATAGGTCA 3180
Db 7620 TTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCAAGTGGTGCAACCATAGGTCA 7679
Qy 3181 CTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGTGACCTCAGCCTCCCAAGTAGCTGG 3240
Db 7680 CTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGTGACCTCAGCCTCCCAAGTAGCTGG 7739
Qy 3241 GACTACGAGCGTGCAACCAACGCTGGCTAATTAAAAAATTTTGTAGAGACTGGG 3300
Db 7740 GACTACGAGCGTGCAACCAACGCTGGCTAATTAAAAAATTTTGTAGAGACTGGG 7799
Qy 3301 TCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTG 3360
Db 7800 TCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTG 7859
Qy 3361 GCATCCAAAGTGTGGGATTAACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTA 3420
Db 7860 GCATCCAAAGTGTGGGATTAACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTA 7919
Qy 3421 CATTCCTATTTTCCAAATAGAATGTAAAGTCCACAGAAACAGGGATTACTGCCTATTTTCTT 3480
Db 7920 CATTCCTATTTTCCAAATAGAATGTAAAGTCCACAGAAACAGGGATTACTGCCTATTTTCTT 7979
Qy 3481 CCTTTCTTTTGGAGACAGAGTCTCACTTTCATCACCTCAACCTCCGTTTCTGCTACTGCA 3540
Db 7980 CCTTTCTTTTGGAGACAGAGTCTCACTTTCATCACCTCAACCTCCGTTTCTGCTACTGCA 8039

Qy 3541 ACCTCTGCCCTCCCGGTTCAAGYGATTTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTA 3600
Db 8040 ACCTCTGCCCTCCCGGTTCAAGYGATTTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTA 8099
Qy 3601 CAAGCGTGACCAACCATGCTTGGCTAATTTTTTGTATTTTTTAGCAGAGATGGGTTTTTAC 3660
Db 8100 CAAGCGTGACCAACCATGCTTGGCTAATTTTTTGTATTTTTTAGCAGAGATGGGTTTTTAC 8159
Qy 3661 CATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTCAGTCTCC 3720
Db 8160 CATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTCAGTCTCC 8219
Qy 3721 CAAAAGTGTGGAATTTATAGGCGTGAGTCACCTGCTGGCCTGGCCGATTACTGCTATTTTCTT 3780
Db 8220 CAAAAGTGTGGAATTTATAGGCGTGAGTCACCTGCTGGCCTGGCCGATTACTGCTATTTTCTT 8279
Qy 3781 TATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAA 3840
Db 8280 TATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAA 8339
Qy 3841 TTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTTTAAAAACAATCTTGACA 3900
Db 8340 TTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTTTAAAAACAATCTTGACA 8399
Qy 3901 ACTTTGCAGAAATAATACAATCTTGCAATTCCTGCTTTTTCACCTTATCACCTTGTATGACT 3960
Db 8400 ACTTTGCAGAAATAATACAATCTTGCAATTCCTGCTTTTTCACCTTATCACCTTGTATGACT 8459
Qy 3961 TTTTTCATATTGCCCTCAAAACCTTTATTGTTACTGTTTTCATTGTTACTATTTTAGTCAC 4020
Db 8460 TTTTTCATATTGCCCTCAAAACCTTTATTGTTACTGTTTTCATTGTTACTATTTTAGTCAC 8519
Qy 4021 TGAATAATATGGCTTAATTTGCTTTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAATTT 4080
Db 8520 TGAATAATATGGCTTAATTTGCTTTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAATTT 8579
Qy 4081 ACAAACTCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAAATAACACACACACACACT 4140
Db 8580 ACAAACTCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAAATAACACACACACACACT 8639
Qy 4141 CACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTT 4200
Db 8640 CACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTT 8699
Qy 4201 TGTTTCATATTAAATTAATAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACACAGT 4260
Db 8700 TGTTTCATATTAAATTAATAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACACAGT 8759
Qy 4261 ACTTTGGAAGTCCAAAGTGGGTGGATCACTTGAGGTGAGAAAGTTTCGAGACCAGCCTGGTC 4320
Db 8760 ACTTTGGAAGTCCAAAGTGGGTGGATCACTTGAGGTGAGAAAGTTTCGAGACCAGCCTGGTC 8819
Qy 4321 AATATGGTGAAACCCCTATCTCTACTAAAAAATACAAAAATTAGCTGGGTGTAGTGATGCAT 4380
Db 8820 AATATGGTGAAACCCCTATCTCTACTAAAAAATACAAAAATTAGCTGGGTGTAGTGATGCAT 8879
Qy 4381 GCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCA 4440
Db 8880 GCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCA 8939
Qy 4441 GAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGCGACACAGCGAGACT 4500
Db 8940 GAGGTTGCAGTGAGCCGAGATCCCACCACTGCACTCCAGCCTGGCGACACAGCGAGACT 8999
Qy 4501 CTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAAAACAACCTAATAAGAT 4560
Db 9000 CTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAAAACAACCTAATAAGAT 9059
Qy 4561 TCCTGAAGGTAAGCAGAGATACGTAAATTTATATGTAAATAAAGTTTAAATGCAATTTTAACT 4620
Db 9060 TCCTGAAGGTAAGCAGAGATACGTAAATTTATATGTAAATAAAGTTTAAATGCAATTTTAACT 9119

Matches 4993; Conservative 8; Mismatches 0; Indels 1; Gaps 1;			
Qy	1	CTGGTCATCTCAG-TTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGTGCTAGCTG	59
Db	4015	CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGTGCTAGCTG	4074
Qy	60	TGCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCGCTTCTCTCCCAAGTGAGCT	119
Db	4075	TGCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCGCTTCTCTCCCAAGTGAGCT	4134
Qy	120	AAGATCTCACTCTCTGGAATGGGGSCACAGGCCACAGCAACAGGGATGGCCAGCCCC	179
Db	4135	AAGATCTCACTCTCTGGAATGGGGSCACAGGCCACAGCAACAGGGATGGCCAGCCCC	4194
Qy	180	GCAGTCTCAAWTCGAGGTTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAA	239
Db	4195	GCAGTCTCAAWTCGAGGTTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAA	4254
Qy	240	GGCTGGCACTTTTTC AACCTGCAAGTCTGAACTCAGATTGCCCTGAGCTAAGAAAGCTTGC	299
Db	4255	GGCTGGCACTTTTTC AACCTGCAAGTCTGAACTCAGATTGCCCTGAGCTAAGAAAGCTTGC	4314
Qy	300	CTTTATTTCTTTTTC CAGACAGGGTCTGCTCTATCACCCAGGCTGGAGTTCAGTGGC	359
Db	4315	CTTTATTTCTTTTTC CAGACAGGGTCTGCTCTATCACCCAGGCTGGAGTTCAGTGGC	4374
Qy	360	ATGATCATAGCTCACCCACAGCTTCCAACTCGTGGCTCAAGTGATCCTCCACCTTACTC	419
Db	4375	ATGATCATAGCTCACCCACAGCTTCCAACTCGTGGCTCAAGTGATCCTCCACCTTACTC	4434
Qy	420	AAC TAAGTAGTTAGGCCAATCTCCCAATTTATTTTATTTTAAATTTTATTTTATTT	479
Db	4435	AAC TAAGTAGTTAGGCCAATCTCCCAATTTATTTTATTTTAAATTTTATTTTATTT	4494
Qy	480	TTACTTTATTTTATTTT TGAGACGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGC	539
Db	4495	TTACTTTATTTTATTTT TGAGACGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGC	4554
Qy	540	GTGATCTCAGATCACTACAACTCCATCTCTGGGTTC AAATTAATTTCTTTGCCCTCAGCC	599
Db	4555	GTGATCTCAGATCACTACAACTCCATCTCTGGGTTC AAATTAATTTCTTTGCCCTCAGCC	4614
Qy	600	TCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACCATGCCAGCTA	659
Db	4615	TCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACCATGCCAGCTA	4674
Qy	660	ATTTTTTTGTGTGTTTTTTT TGGTAGACAGGTTTTTCACCATGTTGGCCAGGCTGGGTGA	719
Db	4675	ATTTTTTTGTGTGTTTTTTT TGGTAGACAGGTTTTTCACCATGTTGGCCAGGCTGGGTGA	4734
Qy	720	CCTCCCTTTTAGATTCTCCTCATCTGCTCTATTCTTCCCTTTCTAATGCAGTATCCAG	779
Db	4735	CCTCCCTTTTAGATTCTCCTCATCTGCTCTATTCTTCCCTTTCTAATGCAGTATCCAG	4794
Qy	780	TTTCCCTTACTTATCACATTTATTTATTTATTTATTTATTTAGACAGAGTCTTGCTTTG	839
Db	4795	TTTCCCTTACTTATCACATTTATTTATTTATTTATTTATTTAGACAGAGTCTTGCTTTG	4854
Qy	840	TCGCCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT	899
Db	4855	TCGCCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT	4914
Qy	900	TCACGCCATTCTCCCGCCTCAGCCTCCCACTAGCTGGGACTAAAGCGCCTGCCACCCAC	959
Db	4915	TCACGCCATTCTCCCGCCTCAGCCTCCCACTAGCTGGGACTAAAGCGCCTGCCACCCAC	4974
Qy	960	GCCCCGCTAAATTTTGTATTTTAAAGACGGGGTTTTTCATCGTGTAGCCAGGATG	1019
Db	4975	GCCCCGCTAAATTTTGTATTTTAAAGACGGGGTTTTTCATCGTGTAGCCAGGATG	5034
Qy	1020	GTCTCGATCTCATGACCTTGTGATCCGCCTCGGCTCCCAAAGTGTGGGATTACA	1079
Db	5035	GTCTCGATCTCATGACCTTGTGATCCGCCTCGGCTCCCAAAGTGTGGGATTACA	5094

Qy	1080	GGCATGAGCCACCGTGCCCGGCTTATCACATTTTATTTATTTGTTTTCTCTCCCACT	1139
Db	5095	GGCATGAGCCACCGTGCCCGGCTTATCACATTTTATTTATTTGTTTTCTCTCCCACT	5154
Qy	1140	AGTTTGTAAAGCTCCATGAGGTTAGAGATTATTATTATTATTATTATTATTATTATTA	1199
Db	5155	AGTTTGTAAAGCTCCATGAGGTTAGAGATTATTATTATTATTATTATTATTATTATTA	5214
Qy	1200	TTATTATTATTATATCTGTTCACTGCTGTATCTCTAGTCTCTAGGACAGAGCCTGGCACA	1259
Db	5215	TTATTATTATTATATCTGTTCACTGCTGTATCTCTAGTCTCTAGGACAGAGCCTGGCACA	5274
Qy	1260	TAGTAAGTGTCTCAATAAATATTCACTGGATAAACAGTGCAGATAGTTTAAAACTATCTGA	1319
Db	5275	TAGTAAGTGTCTCAATAAATATTCACTGGATAAACAGTGCAGATAGTTTAAAACTATCTGA	5334
Qy	1320	CCTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGAGCT	1379
Db	5335	CCTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGAGCT	5394
Qy	1380	GAAATCGTGTCACTGCACCTCCAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAA	1439
Db	5395	GAAATCGTGTCACTGCACCTCCAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAA	5454
Qy	1440	AAAAAAACTATCAGGCTTAGCTGGGTGGCACATGCCGTGAATCCTAGCTGAGGCGGTAGG	1499
Db	5455	AAAAAAACTATCAGGCTTAGCTGGGTGGCACATGCCGTGAATCCTAGCTGAGGCGGTAGG	5514
Qy	1500	GTCCCAGAAAGAAAGAAAAAGAAAGATAFATATATATATATATATACACACACAA	1559
Db	5515	GTCCCAGAAAGAAAGAAAAAGAAAGATAFATATATATATATATATACACACACAA	5574
Qy	1560	AGATATAAACTTTATATATAATAAAGTTTTCATTTAAAAAANAACCTCTACCCACT	1619
Db	5575	AGATATAAACTTTATATATAATAAAGTTTTCATTTAAAAAANAACCTCTACCCACT	5634
Qy	1620	TTCACTTTACCAGGTTCCCTGGGTCCAA CGGTCTTTCAGAGGAGGCAGCTGGCAGGGGTGAG	1679
Db	5635	TTCACTTTACCAGGTTCCCTGGGTCCAA CGGTCTTTCAGAGGAGGCAGCTGGCAGGGGTGAG	5694
Qy	1680	GGAGGCAGCGTGGGACCCGAGGGAGCAGGAAGGCAGTGTCCCCGGGGTGTGGCAGAC	1739
Db	5695	GGAGGCAGCGTGGGACCCGAGGGAGCAGGAAGGCAGTGTCCCCGGGGTGTGGCAGAC	5754
Qy	1740	CGATTTGAACTCTGGCTATGTCTTCTTGCACTGGCCGCCCGCMCAGCGGCATCAGCCCT	1799
Db	5755	CGATTTGAACTCTGGCTATGTCTTCTTGCACTGGCCGCCCGCGCACAGCGGCATCAGCCCT	5814
Qy	1800	CGGGCGTGTGGCAGTTCGCAAAAATGATCAAAGTGCCTGATCCCGGGAGTGACCCCTTY	1859
Db	5815	CGGGCGTGTGGCAGTTCGCAAAAATGATCAAAGTGCCTGATCCCGGGAGTGACCCCTTC	5874
Qy	1860	TTGGAATACAACAACACTACGCTGTCTGTGGCTTGGGGGCTCAGGCACCCCGTGGAT	1919
Db	5875	TTGGAATACAACAACACTACGCTGTCTGTGGCTTGGGGGCTCAGGCACCCCGTGGAT	5934
Qy	1920	GAACTGGACAAGTAAGTATCCGCTGCAGGAAAATTGGAGTGCCTGCCGGGGGCGGGGT	1979
Db	5935	GAACTGGACAAGTAAGTATCCGCTGCAGGAAAATTGGAGTGCCTGCCGGGGGCGGGGT	5994
Qy	1980	GGGCGACACGCCAAGGATCTCAGAGGCATACAAAGGGGACTTGCTATCTGCTAAGGAT	2039
Db	5995	GGGCGACACGCCAAGGATCTCAGAGGCATACAAAGGGGACTTGCTATCTGCTAAGGAT	6054
Qy	2040	AACATATTTTCACTCTTGTCAAAATAAA CAAATATGTTCCAAGAGGACCTGTAGCGAAC	2099
Db	6055	AACATATTTTCACTCTTGTCAAAATAAA CAAATATGTTCCAAGAGGACCTGTAGCGAAC	6114
Qy	2100	GCACCCCGTTAGAGATGGAACAAATGACCCGACGTGCAAAAACAGTGGCGGATGCTGCCCTC	2159
Db	6115	GCACCCCGTTAGAGATGGAACAAATGACCCGACGTGCAAAAACAGTGGCGGATGCTGCCCTC	6174

QY	2160	CAGTGGCAGAA	TGTAGCAACAGTA	AAACATCACAGCA	ACTATCCACG	TGTCA	TTTCTAGC	2219
Db	6175	CAGTGGCAGAA	TGTAGCAACAGTA	AAACATCACAGCA	ACTATCCACG	TGTCA	TTTCTAGC	6234
QY	2220	AGTGGTTG	CTCACTGCACCT	TCTGAATACAGG	ATTTTACTG	TATCTT	GCAACCATG	2279
Db	6235	AGTGGTTG	CTCACTGCACCT	TCTGAATACAGG	ATTTTACTG	TATCTT	GCAACCATG	6294
QY	2280	AAATCGCTT	TCAGGCCAGG	CGGTGGCTCAT	GCCTGTA	ATCCAG	CACCTTTGGGAGGC	2339
Db	6295	AAATCGCTT	TCAGGCCAGG	CGGTGGCTCAT	GCCTGTA	ATCCAG	CACCTTTGGGAGGC	6354
QY	2340	GAGGCGGCGG	ATCACTTGAGGT	CAGGATTCGAG	ACCAGCCTG	GCCAA	CATGGTGAAC	2399
Db	6355	GAGGCGGCGG	ATCACTTGAGGT	CAGGATTCGAG	ACCAGCCTG	GCCAA	CATGGTGAAC	6414
QY	2400	CCTGTCTCT	ACTAAAAAATA	CAAAAAATTAG	CGGACATG	TGGGAG	CGCCTGTAACCC	2459
Db	6415	CCTGTCTCT	ACTAAAAAATA	CAAAAAATTAG	CGGACATG	TGGGAG	CGCCTGTAACCC	6474
QY	2460	AGCTACTTT	GGGAGACTGAG	TTGGAGTTT	CAGTGAGC	CAAGGTC	GTCAGTGTCCA	2519
Db	6475	AGCTACTTT	GGGAGACTGAG	TTGGAGTTT	CAGTGAGC	CAAGGTC	GTCAGTGTCCA	6534
QY	2520	GCCTGGGT	AAACAGAGCA	ACTCTGTCT	CAAAAAA	AAATGCTT	CAATAAATATATGAT	2579
Db	6535	GCCTGGGT	AAACAGAGCA	ACTCTGTCT	CAAAAAA	AAATGCTT	CAATAAATATATGAT	6594
QY	2580	AAAAGGACT	TATATTTTT	TTCAAGCCATAG	GATCATTT	CTCTGA	AGCATCTTGGCGAAGT	2639
Db	6595	AAAAGGACT	TATATTTTT	TTCAAGCCATAG	GATCATTT	CTCTGA	AGCATCTTGGCGAAGT	6654
QY	2640	CATCCCCAC	CTGTCTGAG	AGTGGGAGG	TGAGGCTG	ACCTPAT	TGCTCTGCACCTTACT	2699
Db	6655	CATCCCCAC	CTGTCTGAG	AGTGGGAGG	TGAGGCTG	ACCTPAT	TGCTCTGCACCTTACT	6714
QY	2700	CCTATCTCA	GTGTCCCTCC	CACTTTCCAG	GTGTGCC	AGACATG	ACAACCTGCTAYGA	2759
Db	6715	CCTATCTCA	GTGTCCCTCC	CACTTTCCAG	GTGTGCC	AGACATG	ACAACCTGCTAYGA	6774
QY	2760	CCAGGCCAA	GAGCTGGAC	AGCTGTA	AAATTTCT	GTGGAC	AMMCGGTACACCCACACCTA	2819
Db	6775	CCAGGCCAA	GAGCTGGAC	AGCTGTA	AAATTTCT	GTGGAC	AMMCGGTACACCCACACCTA	6834
QY	2820	TTTCATACT	CGTCTGGCT	CGGCAATC	ACCTGTAG	CAGTAGG	TTTATCCCTTCCCTTGAC	2879
Db	6835	TTTCATACT	CGTCTGGCT	CGGCAATC	ACCTGTAG	CAGTAGG	TTTATCCCTTCCCTTGAC	6894
QY	2880	CTATGAAT	TCTAGTTGG	TTCTCAG	TAGGCGGG	GGAATAA	TAGTAACAACAGCCATGA	2939
Db	6895	CTATGAAT	TCTAGTTGG	TTCTCAG	TAGGCGGG	GGAATAA	TAGTAACAACAGCCATGA	6954
QY	2940	TTTAGTGTT	AAATTTCTT	GGGTCTGG	GAGTGTCT	CCTTAA	TCTCAGAAACAACACTAT	2999
Db	6955	TTTAGTGTT	AAATTTCTT	GGGTCTGG	GAGTGTCT	CCTTAA	TCTCAGAAACAACACTAT	7014
QY	3000	GGGATAGG	TACAATATC	CTCACTTA	ACAGATAA	GAAAACT	GAGGCTCAGAAGGCTGAGC	3059
Db	7015	GGGATAGG	TACAATATC	CTCACTTA	ACAGATAA	GAAAACT	GAGGCTCAGAAGGCTGAGC	7074
QY	3060	TATTTGCC	CAAGATCAC	ACAGCTT	GTAAGT	GTGACAG	TTTGGGTTTTTTTGTGTTG	3119
Db	7075	TATTTGCC	CAAGATCAC	ACAGCTT	GTAAGT	GTGACAG	TTTGGGTTTTTTTGTGTTG	7134
QY	3120	TTTAGAGAC	AGGGTCTTG	CTCTGTCA	CCCCAGG	CATGAG	CCAGTGGTGAACCATAGGTC	3179
Db	7135	TTTAGAGAC	AGGGTCTTG	CTCTGTCA	CCCCAGG	CATGAG	CCAGTGGTGAACCATAGGTC	7194
QY	3180	ACTGCAGC	CTCAACCT	CTGAGCT	CAAGGAT	CTGCTG	ACCTCAGCCTCCCAAGTAGCTG	3239
Db	7195	ACTGCAGC	CTCAACCT	CTGAGCT	CAAGGAT	CTGCTG	ACCTCAGCCTCCCAAGTAGCTG	7254
QY	3240	GGACTACG	AGCGTGCA	CCACCAC	CGCCTGG	CTAATTA	AAAAAAATTTTTTTGTAGAGACTGG	3299

Db	7255	GGACTACG	AGCGTGCA	CCACCAC	CGCCTGG	CTAATTA	AAAAAAATTTTTTTGTAGAGACTGG	7314
QY	3300	GTCTTACT	ACGTGGCC	AGGCTTGT	CTTAAAC	TCTTGG	CTTCAAGCAATCCTCCTACCTT	3359
Db	7315	GTCTTACT	ACGTGGCC	AGGCTTGT	CTTAAAC	TCTTGG	CTTCAAGCAATCCTCCTACCTT	7374
QY	3360	GGCATCC	CAAAAGT	GCTGGG	ATTACAG	GGGTGAG	CCACCATGTGCGGCTACTTATTTCT	3419
Db	7375	GGCATCC	CAAAAGT	GCTGGG	ATTACAG	GGGTGAG	CCACCATGTGCGGCTACTTATTTCT	7434
QY	3420	ACATTTCC	ATCTTTCC	AAATAG	ATGTAAG	ATCCAC	AGAACAGGGATTACTGCCTATTTCT	3479
Db	7435	ACATTTCC	ATCTTTCC	AAATAG	ATGTAAG	ATCCAC	AGAACAGGGATTACTGCCTATTTCT	7494
QY	3480	TCCTTTCT	TTTTTG	AGACAG	AGTCTC	ACTTCAT	CACCTCAACCTCCGTTCAGCTCACTGC	3539
Db	7495	TCCTTTCT	TTTTTG	AGACAG	AGTCTC	ACTTCAT	CACCTCAACCTCCGTTCAGCTCACTGC	7554
QY	3540	AACCTCT	GCCTCC	CGGTTCA	AGYGATT	CTCCT	CGCTAAGCCCTCCTGAGTAGCTGGAAT	3599
Db	7555	AACCTCT	GCCTCC	CGGTTCA	AGYGATT	CTCCT	CGCTAAGCCCTCCTGAGTAGCTGGAAT	7614
QY	3600	ACAAGCG	TGCAC	CCACCAT	GTGGCTTA	ATTTTT	TGTATTTTAGCAGAGATGGGGTTTA	3659
Db	7615	ACAAGCG	TGCAC	CCACCAT	GTGGCTTA	ATTTTT	TGTATTTTAGCAGAGATGGGGTTTA	7674
QY	3660	CCATGTT	GGCCAG	GCTGGTCT	CAAACTC	CTGAC	CTCAAGCTTGCCTGCCTCAGTCTC	3719
Db	7675	CCATGTT	GGCCAG	GCTGGTCT	CAAACTC	CTGAC	CTCAAGCTTGCCTGCCTCAGTCTC	7734
QY	3720	CCAAAGT	GCTGGA	ATTATAG	GGCGTG	AGTCA	CTGTGCTGGCCGATTACTGTCTATTTCT	3779
Db	7735	CCAAAGT	GCTGGA	ATTATAG	GGCGTG	AGTCA	CTGTGCTGGCCGATTACTGTCTATTTCT	7794
QY	3780	TTATTGCT	TATATC	CCCCAG	ATCTAG	AGCAGT	GTCTGACATATAGTAGGTTCAATAAATA	3839
Db	7795	TTATTGCT	TATATC	CCCCAG	ATCTAG	AGCAGT	GTCTGACATATAGTAGGTTCAATAAATA	7854
QY	3840	ATTGATGA	ATGCAC	AGCCTAG	ATATAAA	CTTTCT	TTTTTTTAAAACAATCTTGAC	3899
Db	7855	ATTGATGA	ATGCAC	AGCCTAG	ATATAAA	CTTTCT	TTTTTTTAAAACAATCTTGAC	7914
QY	3900	AACCTTGC	AGAAATAA	ATACAA	TCTTGC	ATTCTG	CTTTTCACTTATCACCTTGTATGAC	3959
Db	7915	AACCTTGC	AGAAATAA	ATACAA	TCTTGC	ATTCTG	CTTTTCACTTATCACCTTGTATGAC	7974
QY	3960	TTTTTCAT	ATTGCTCA	AACTTTAT	TGTTACT	GTGTTT	TTTTCATTTTACTATTTTAGTCA	4019
Db	7975	TTTTTCAT	ATTGCTCA	AACTTTAT	TGTTACT	GTGTTT	TTTTCATTTTACTATTTTAGTCA	8034
QY	4020	CTGAATAA	TATGGCTT	AAATTTG	CTTATAC	ATCCTC	CTGCTCCACTTTTAGAAGGCCAAAT	4079
Db	8035	CTGAATAA	TATGGCTT	AAATTTG	CTTATAC	ATCCTC	CTGCTCCACTTTTAGAAGGCCAAAT	8094
QY	4080	TACAAAT	CTGATGAA	AGCTATGA	ACCCTCT	CCTCC	CAGAGAAATACACACACACACAC	4139
Db	8095	TACAAAT	CTGATGAA	AGCTATGA	ACCCTCT	CCTCC	CAGAGAAATACACACACACACAC	8154
QY	4140	TCACACAC	AGTTTTTT	TTTAAATG	TTTGTCAA	CTAAG	ACAAGAAAACTGCAATTAGAGGATGT	4199
Db	8155	TCACACAC	AGTTTTTT	TTTAAATG	TTTGTCAA	CTAAG	ACAAGAAAACTGCAATTAGAGGATGT	8214
QY	4200	TTGTTCA	TATTAATTA	AAAAATAA	CTCAG	TTGGG	CACAGTGACTCAAGCCTGTAA	4259
Db	8215	TTGTTCA	TATTAATTA	AAAAATAA	CTCAG	TTGGG	CACAGTGACTCAAGCCTGTAA	8274
QY	4260	TACTTTG	GAAGTCCA	AGGTGG	TGGATCAC	TTGAG	GTGAGAAGTTTCGAGACCAGCCTGGT	4319
Db	8275	TACTTTG	GAAGTCCA	AGGTGG	TGGATCAC	TTGAG	GTGAGAAGTTTCGAGACCAGCCTGGT	8334
QY	4320	CAATATGG	TGAAAC	CCCTAT	CTCTACT	TAAAAA	TACAAAAATTAGCTGGGTGTAGTGATGCA	4379

Db 8335 CAATATGGTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCA 8394
Qy 4380 TGCCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGC 4439
Db 8395 TGCCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGC 8454
Qy 4440 AGAGTTGCAGTGAGCCGAGATCCACCACTGCACTCCAGCTGGCGACACAGCGAGAC 4499
Db 8455 AGAGTTGCAGTGAGCCGAGATCCACCACTGCACTCCAGCTGGCGACACAGCGAGAC 8514
Qy 4500 TCTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAACTAATAAGA 4559
Db 8515 TCTATCTCAAAAAATAAATAAATAAAGGATCGGAGAGAAACAAACTAATAAGA 8574
Qy 4560 TTCTGTAAGGTAAAGCAGAGATACGTAAATTATATGTAATAAAGTTTAAATGCAATTTAAC 4619
Db 8575 TTCTGTAAGGTAAAGCAGAGATACGTAAATTATATGTAATAAAGTTTAAATGCAATTTAAC 8634
Qy 4620 TGTAACTTTATTGTTTATTGTTTATAAAGTAACAAAGCAAGTAATGCAACTTCA 4679
Db 8635 TGTAACTTTATTGTTTATTGTTTATAAAGTAACAAAGCAAGTAATGCAACTTCA 8694
Qy 4680 AAKCTACATAAATATCTATTATGGAAGTGAAGGCATCTATAATCCTACTACCCAAAG 4739
Db 8695 AACTCTACATAAATATCTATTATGGAAGTGAAGGCATCTATAATCCTACTACCCAAAG 8754
Qy 4740 ATAAACAGTTACATATTCTCTCCAGATTTTTGGGGCATACACTAGCTTTTATTATTGGGA 4799
Db 8755 ATAAACAGTTACATATTCTCTCCAGATTTTTGGGGCATACACTAGCTTTTATTATTGGGA 8814
Qy 4800 AAATTTCCATGTGCAGGCATACCTAAATTTTCTAAATGTCATGTAGTATTCCATTTAAG 4859
Db 8815 AAATTTCCATGTGCAGGCATACCTAAATTTTCTAAATGTCATGTAGTATTCCATTTAAG 8874
Qy 4860 GATGTTCCATAAATTTTAAATACATGCTTTAAAGTAGAGAAACTAGTTGGGCATGGTG 4919
Db 8875 GATGTTCCATAAATTTTAAATACATGCTTTAAAGTAGAGAAACTAGTTGGGCATGGTG 8934
Qy 4920 GCTCAGCCTGTATCCCAGCACTTTTGGGAGGCCGAGGCAATGGATCACTTGAGGTCGGG 4979
Db 8935 GCTCAGCCTGTATCCCAGCACTTTTGGGAGGCCGAGGCAATGGATCACTTGAGGTCGGG 8994
Qy 4980 AGTTTGAGACCAGCCTGGACAA 5001
Db 8995 AGTTTGAGACCAGCCTGGACAA 9016

RESULT 4
AAA35101
ID AAA35101 standard; DNA; 3375 BP.
XX
AC AAA35101;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2790.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.

XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 1056-1057; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;

Query Match 53.8%; Score 2690.8; DB 3; Length 3375;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;

Qy 1 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGTGCTAGCTGT 60
Db 500 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGTGCTAGCTGT 559
Qy 61 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGCCTTTCTCTCCCAAGTGAGCTA 120
Db 560 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGCCTTTCTCTCCCAAGTGAGCTA 619
Qy 121 AGATCTCACTCCTCTGGAATGGGGCCACAGGCCACAGCAAACAGGGATGGCCAGCCCCG 180
Db 620 AGATCTCACTCCTCTGGAATGGGGCCACA---CACAGCAAACAGGGATGGCCAGCCCCG 676
Qy 181 CAGTCTCAAWTCGAGGTTCCCAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 240
Db 677 CAGTCTCAATTGAGGTTCCCAAGT-GGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 735
Qy 241 GCTGGCACTTTTTCAACTGCAAGTCTGAACTCAGATTGCCTGAGCTAAGAAAGCTTGC 300
Db 736 GCTGGCACTTTTTCAACTGCAAGTCTGAACTCAGATTGCCTGAGCTAAGAAAGCTTGC 795
Qy 301 TTTATTTTCTTTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCACTGGCA 360
Db 796 TTTATTTTCTTTTTTCCAGACAGGGTCTTGCTCTATTAACCCAGGCTGGAGTTCACTGGCA 855
Qy 361 TGATCATAGCTCACCACAGCTTCCAACTCGTGGGCTCAAGTGATCTCTCCCACCTTACTCA 420

Db	856	TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCACCTTACTCA	915
QY	421	ACTAAGTAGTTAGGCCAATCTCCCAATTTATTTTATTTTAAATTTTATTTTATTT	480
Db	916	ACTAAGTAGTTAGGCCAATCTCCCAATTTATTTTATTTTAAATTTTATTTTATTT	975
QY	481	TACTTTATTTATTTTGTAGACGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCG	540
Db	976	TACTTTATTTATTTTGTAGACGGGCTCACTCTGTGCG-CCAGGCTGGAGTGGGTGGGC	1034
QY	541	TGATCTCAGATCACTACAACCTCCATCTCTGGGTTCAAATAATTCTTTGCCTCAGCCT	600
Db	1035	TGATCTCAGATCACTACAACCTCCATCTCCT-GGTTCAAATAATTCTTTGCCTCAGCCT	1093
QY	601	CTCAAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGGCACACACCACCTAAC	660
Db	1094	CTCAAAGTAGCT-GGACTTGTAGCTCTCAAGTAGCTGGGCACACACCACCTAAC	1152
QY	661	TTTTTTGTGTTTTTTTTGGTAGAGACAGGTTTTTCACCATGTGGCCAGGCTGGGTGAC	720
Db	1153	TTTTTTGTGTTTTTTTTGGTAGAGACAGGTTTTTCACCATGTGGCCAGGCTGGGTGAC	1212
QY	721	CTCCCTTTAGATCTCCTCATCCGCTCTATTCTTCCCTTTCT-AATGCAGTATCCAG	779
Db	1213	CTCCCTTTAGATCTCCTCATCCGCTCTATTCTTCCCTTTCTAAATGCAGTATCCAG	1272
QY	780	TTTCCCTTACTTATCACATTTATTTATTTATTTTATTTATTTATTTAGACAGAGTCTT	839
Db	1273	TTTCCCTTACTTATACACTTTATTTATTTATTTATTTATTTATTTATTTAGACAGAGTCTT	1332
QY	840	TCGCCAAGGCTGGAGTACAGTGTGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT	899
Db	1333	TGCCCCAAGGCTGGAGTACAGTGGTGCATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT	1392
QY	900	TCACGCCATTTCTCCCGCCTCAGCCTCCCCAGTAGCTGGGACTAAAGGCGCCTGCCACCAC	959
Db	1393	TCACGCCATTTCTCCCGCCTCAGCCTCCCCAGTAGCTGGGACTAAA-GCGCCTGCCACCAC	1451
QY	960	GCCCGGCTAAATTTTGTATTTTAAATAAAGACGGGTTTTTCATCGTGTAGCCAGGATG	1019
Db	1452	GCCCGGCTAAATTTTGTATTTTAAATAAAGACGGGTTTTTCATCGTGTAGCCAGGATG	1511
QY	1020	GTCTCGATCTCATGACCTTGTGATCCGCTGCCCTCGGCTCCCAAAGTGTCTGGGATTACA	1079
Db	1512	GTCTCGATCTCATGACCTTGTGATCCGCTGCCCTCGGCTCCCAA--TGCTGGATTACA	1569
QY	1080	GGCATGAGCCACCGTGCCCGGCTTATFCACATTTATTTATTTATTTTCTCTCCCACT	1139
Db	1570	GGCATGAGCCACCGTGCCCGGCTTATCACAATTTATTTATTTATTTTCTCTCCCACT	1629
QY	1140	AGGTTGTAAAGCTCCATGAGGTTAGAG--ATTATTTATTTATTTATTTATTTATTTA	1196
Db	1630	AGGTTGTAAAGCTCCATGAGGTTAGAGATTATTTATTTATTTATTTATTTATTTA	1689
QY	1197	TTATTTATTTATTTATATCTGTTCACCTGCTGTATCTCTAGCTCCTAGGACAGAGCCTGGC	1256
Db	1690	TTATTTATTTATTTATATCTGTTCACCTGCTGTATCTCTAGCTCCTAGGACAGAGCCTGGC	1749
QY	1257	ACATAGTAAGTCTCAATAAATTTCACTGGATAAACAGTGCAGATAGTTTAAACCTATC	1316
Db	1750	ACATAGTAAGTCTCAATAAATTTCACTGGATAAACAGTGCAGATAGTTTAAACCTATC	1809
QY	1317	TGACCTAGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA	1376
Db	1810	TGACCTAGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA	1869
QY	1377	GCTGAAATCGTGTCACTGCACCTCCAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAA	1436
Db	1870	GCTGAAATCGTGTCACTGCACCTCCAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAA	1929
QY	1437	AAAAAAAAACTATCAGGCCTAGCTGGGTGGCACATGCCCTGTAATCCTAGCTGAGGCGGT	1496

Db	1930	AAAAAAAAAACTATCAGGCCTAGCTGGGTGGCACATGCCTGTAATCCTAGCTAGGCGGT	1989
QY	1497	AGGTTCCAGAGAAAGAAAGAAAGAAAAAGAAAGATATATATATATATACACACA	1556
Db	1990	AGGTTCCAGAGAAAGAAAGAAAGAAAAAGAAAGATATATATATATATACACACA	2049
QY	1557	CAAAGATATAAACTTTATATATATAAAGTTTTTCATTAATAAAAAAAAAAAACCTCTACCC	1616
Db	2050	CAAAGATATAAACTTTATATATATAAAGTTTTTCATTT-AAAAAAAAAAACCTCTACCC	2108
QY	1617	ACTTTCACTTTTACCAGGTTCTCTGGGTCCAAACGGTCTTTCAGAGGAGGCAGCTGGCAGGGGT	1676
Db	2109	ACTTTCACTTTTACCAGGTTCTCTGGGTCCAAACGGTCTTTCAGAGGAGGCAGCTGGCAGGGGT	2168
QY	1677	CAGGAGGCAGCGTGGACCCGAGGGAGCAGGAAGGAGTGTGTCCCGGGGTGCTGGCA	1736
Db	2169	CAGGAGGCAGCGTGGACCCGAGGGAGCAGGAAGGAGTGTGTCCCGGGGTGCTGGCA	2228
QY	1737	GACCGATTTGAACCTCTGGCTATGTCTTCTTGCAGTGGCCGCCCGCMCAGCGGATCAGC	1796
Db	2229	GACCGATTTGAACCTCTGGCTATGTCTTCTTGCAGTGGCCGCCCGCACAGCGGATCAGC	2288
QY	1797	CCTCGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCGGGAGTGACCCC	1856
Db	2289	CCTCGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCGGGAGTGACCCC	2348
QY	1857	TTYTTGGAATACAACAACTACGGCTGCTACTGTGGCTTTGGGGGCTCAGGCACCCCGTG	1916
Db	2349	TTYTTGGAATACAACAACTACGGCTGCTACTGTGGCTTTGGGGGCTCAGGCACCCCGTG	2408
QY	1917	GATGAACCTGGACAAGTAAAGTATCCGCCCTGCAGGAAAATTTGGAGTGCCTGCCGGGGCGG	1976
Db	2409	GATGAACCTGGACAAGTAAAGTATCCGCCCTGCAGGAAAATTTGGAGTGCCTGCCGGGGCGG	2468
QY	1977	GGTGGGGCA-CACGCCAAGGATCTCACGAGGCATACAAAGGGGACTTGCATATCTGCTAA	2035
Db	2469	GGTGGGGCA-CACGCCAAGGATCTCACGAGGCATACAAAGGGGACTTGCATATCTGCTAA	2528
QY	2036	GGATAACATATTTTACCTTTGTCAAAATAAAACAATATGTTTCCAAGAGGACCTGTAGC	2095
Db	2529	GGATAACATATTTTACCTTTGTCAAAATAAAACAATATGTTTCCAAGAGGACCTGTAGC	2588
QY	2096	GAACGCACCCCGTTAGAGATGGAACAATGACCGACGTGCAAAAACAGTGGCGATGCTGC	2155
Db	2589	GAACGCACCCCGTTAGAGATGGAACAATGACCGACGTGCAAAAACAGTGGCGATGCTGC	2648
QY	2156	CCTCCAGTGGCAGAAATGTAGCAACAGTAAACATCACAGCAAACTATCCACGTGTCATTTTC	2215
Db	2649	CCTCCAGTGGCAGAAATGTAGCAACATTTAAACATCACAGCACCTATCCACGTGTCATTTTC	2708
QY	2216	TAGCAGTGGTTGTCACTGCACCTTCT-GAATACAGGATTTTACTGTATTCTTGCACCAT	2274
Db	2709	TAGCAGTGGTTGTCACTGCACCTTCTTGGAAATACAGGATTTTACTGTATTCTTGCACCAT	2768
QY	2275	GTTAAAAATCGCTTTTAGCCAGGCGCGGTGGCTCATGCTGTAAATCCCAGCACCTTTGGG	2334
Db	2769	GTTAAAAATCGCTTTTAGCCAGGCGCGGTGGCTCATGCTGTAAATCCCAGCACCTTTGGG	2828
QY	2335	AGGCCGAGGCGGGCGGATCACTTGAGGTGAGGTCAGAGTTTCAGAGACAGCCTGGCCAACTGGT	2394
Db	2829	AGGCCGAGGCGGGCGGATCACTTGAGGTGAGGTCAGAGTTTCAGAGACAGCCTGGCCAACTGGT	2888
QY	2395	GAAACCCCTGTCTCTACTAAAAAATACAAAAATTTAGCCGACATGGTGGCGAGCGCTGTA	2454
Db	2889	GAAACCCCTGTCTCTACTAAAAAATACAAAAATTTAGCCGACATGGTGGCGAGCGCTGTA	2948
QY	2455	ACCCAGCTACTTTGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCAAAGGTGTCGTCAGTGT	2514
Db	2949	ACCCAGCTACTTTGGGAGACTGAGTTGGAGGTTTTC-TAGCCAAAGGTGTCGTCAGTGT	3007
QY	2515	GTCCAGCCTGGGTAAACAGACCAACTCTGTCTCAAAAAAAAAAATGCTTTCATAATAATAT	2574
Db	3008	GTCCAGCCTGGGTAAACAGACCAACTCTGTCTCAAAAAAAAAAATGCTTTCATAATAATAT	3067

QY 2575 ATGATAAAGGACTTATATTTTTCAGGCCATAGGATCATTTCTCCTGAAGCATCTTGGC 2634
|||||
Db 3068 ATGATAAAGGACTTATATTTTTCAGGCCATAGGATCATTTCTCCTGAAGCATCTTGGC 3127
|||||
QY 2635 GAAGTCATCCCCACCTGTTCCCTGAGAGTGGGCAGGTGAGGGCTGACCTATTGCTCTGCAC 2694
|||||
Db 3128 GAAGTCATCCCCACCTGTTCCCTGAGAGTGGGCAGGTGAGGGCTGACCTATTGCTCTGCAC 3187
|||||
QY 2695 TTACTCTATCTCAGCTGTCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGC 2754
|||||
Db 3188 TTACTCTATCTCAGCTGTCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGC 3247
|||||
QY 2755 TAYGACCAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCAC 2814
||:|||||
Db 3248 TAGACACAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAACCCGTACACCCAC 3307
|||||
QY 2815 ACCTATTCACTCGTCTGCTCGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 2874
|||||
Db 3308 ACCTATTCACTCGTCTGCTCGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 3367
|||||
QY 2875 TTGACCTA 2882
|||||
Db 3368 TTGACCTA 3375
|||||

RESULT 5
AAAF21223
ID AAF21223 standard; DNA; 3375 BP.
XX
AC AAF21223;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2790.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Disclosure; Page 1135-1136; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.

CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention

XX
SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;

Query Match 53.8%; Score 2690.8; DB 3; Length 3375;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;

QY 1 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGTGCTAGCTGT 60
Db 500 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGTGCTAGCTGT 559
QY 61 GCTGCTCACAGGTAGGCAAGTCTCCCGGGTCCACCGCCTTTCTCTCCCAAGTGAGCTA 120
Db 560 GCTGCTCACAGGTAGGCAAGTCTCCCGGGTCCACCGCCTTTCTCTCCCAAGTGAGCTA 619
QY 121 AGATCTCACTCCTCTGGAATGGGGGCCACAGGCCACAGGATGGCCAGCCCG 180
Db 620 AGATCTCACTCCTCTGGAATGGGGGCCACA---CACAGCAACAGGGATGGCCAGCCCG 676
QY 181 CAGTCTCAAATCGAGGTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 240
Db 677 CAGTCTCAAATCGAGGTTCCTCAGT---GGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 735
QY 241 GCTGGCACTTTTTCACCTGCAAGTCTGAACTCAGATTGCTGAGCTAAGAAAGCTTGCC 300
Db 736 GCTGGCACTTTTTCACCTGCAAGTCTGAACTCAGATTGCTGAGCTAAGAAAGCTTGCC 795
QY 301 TTTATTTTCTTTTCCAGACAGGGTCTTGETCTATCACCCAGGCTGGAGTTCAGTGGCA 360
Db 796 TTTATTTTCTTTTCCAGACAGGGTCTTGTCTCTATAACCCAGGCTGGAGTTCAGTGGCA 855
QY 361 TGATCATAGCTCACCACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA 420
Db 856 TGATCATAGCTCACCACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA 915
QY 421 ACTAAGTAGTTAGGCCAATCTCCCATTATTTTATTTTATTTTATTTTATTTT 480
Db 916 ACTAAGTAGTTAGGCCAATCTCCCATTATTTTATTTTATTTTATTTTATTTT 975
QY 481 TACTTTATTTTATTTTTCAGACGGGGCTCACTCTGTCCGCCAGGCTGGAGTGGGTGGCG 540
Db 976 TACTTTATTTTATTTTTCAGACGGGGCTCACTCTGTGCG-CCAGGCTGGAGTGGGTGGCG 1034
QY 541 TGATCTCAGATCACTACAACTCCATCTCCTGGGTCAAATAATTTCTTGCCTCAGCCT 600
Db 1035 TGATCTCAGATCACTACAACTCCATCTCCT---GGTTCAAATAATTTCTTGCCTCAGCCT 1093

Db 3248 TACGACCAGCCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAACCCGTACACCCAC 3307

Qy 2815 ACCTATTCACTACTCGTGTCTGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 2874
|||||

Db 3308 ACCTATTCACTACTCGTGTCTGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 3367

Qy 2875 TTGACCTA 2882
|||||

Db 3368 TTGACCTA 3375

RESULT 6

ABZ96917

ID ABZ96917 standard; DNA; 3375 BP.

XX AC ABZ96917;

XX DT 17-OCT-2003 (first entry)

XX XX Human nucleic acid sequence.

DE XX

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
Kw antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
Kw antisense gene therapy; respiratory; lung; adenosine sensitivity;
Kw adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
Kw lung inflammation; respiratory disease; ds.
XX

OS Homo sapiens.

XX XX

PN WO200285308-A2.

XX XX

PD 31-OCT-2002.

XX XX

PF 23-APR-2002; 2002WO-US013135.

XX XX

PR 24-APR-2001; 2001US-0286137P.

XX XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.

DR XX

PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX

PS Disclosure; SEQ ID NO 12159; 872pp; English.

XX XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;

Query Match 53.8%; Score 2690.8; DB 10; Length 3375;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2846; Conservative 6; Mismatches 18; Indels 13; Gaps 13;

Qy 1 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGCTAGCTGT 60
|||||

Db 500 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGCTAGCTGT 559
|||||

Qy 61 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGCTTCTCTCCCAAGTGAGCTA 120
|||||

Db 560 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGCTTCTCTCCCAAGTGAGCTA 619
|||||

Qy 121 AGATCTCACTCCTCTGGAATGGGGGCCACAGGCCACAGCAACAGGGATGGCCAGCCCCG 180
|||||

Db 620 AGATCTCACTCCTCTGGAATGGGGGCCACA--CACAGCAACAGGGATGGCCAGCCCCG 676
|||||

Qy 181 CAGTCTCAAATCGAGGTTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 240
|||||

Db 677 CAGTCTCAAATCGAGGTTCCAGT-GGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 735
|||||

Qy 241 GCTGGCACTTTTTCACACTGCAAGTCTGAACCTCAGATTGCCTGAGCTAAGAAAGTTGCC 300
|||||

Db 736 GCTGGCACTTTTTCACACTGCAAGTCTGAACCTCAGATTGCCTGAGCTAAGAAAGTTGCC 795
|||||

Qy 301 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA 360
|||||

Db 796 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATAACCCAGGCTGGAGTTCAGTGGCA 855
|||||

Qy 361 TGATCATAGCTCACCCACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA 420
|||||

Db 856 TGATCATAGCTCACCCACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA 915
|||||

Qy 421 ACTAAGTAGTTAGGCCAATCTCCCATTTATTTTATTTTATTTTATTTTATTTTATTT 480
|||||

Db 916 ACTAAGTAGTTAGGCCAATCTCCCATTTATTTTATTTTATTTTATTTTATTTTATTT 975
|||||

Qy 481 TACTTTATTTTATTTTGAGACGGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCG 540
|||||

Db 976 TACTTTATTTTATTTTGAGACGGGGCTCACTCTGTGCG-CCAGGCTGGAGTGGGTGGCG 1034
|||||

Qy 541 TGATCTCAGATCACTACAACCTCCATCTCCTGGGTCAAATAAATTCTCTTGCTCAGCCT 600
|||||

Db 1035 TGATCTCAGATCACTACAACCTCCATCTCCT-GGTTCAAATAAATTCTCTTGCTCAGCCT 1093
|||||

Qy 601 CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGCGACACACACCACCATGCCCGCTAA 660
|||||

Db 1094 CTCAAGTAGCT-GGACTTGTAGCTCTCAAGTAGCTGGGACACACACCACCATGCCCGCTAA 1152
|||||

Qy 661 TTTTGT 720
|||||

Db 1153 TTTTGT 1212
|||||

Qy 721 CTCCCTTTTAGATTCTCTCATCTCTGCTCTATTCTTCCCTTTTCT-AATGCAGTATCCAG 779
|||||

Db 1213 CTCCCTTTTAGATTCTCTCATCTCTGCTCTATTCTTCCCTTTTCTAAATGCAGTATCCAG 1272
|||||

Qy 780 TTTCTTACTTATCACATTTATTTATTTATTTATTTATTTATTTAGACAGAGTCTTGCTTTG 839
|||||

Db 1273 TTTCTTACTTATACATTTATTTATTTATTTATTTATTTATTTAGACAGAGTCTTGCTTTG 1332
|||||

Qy 840 TCGCCAAGGCTGGAGTACAGTGGTGGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 899
|||||

Db 1333 TGCCCAAGGCTGGAGTACAGTGGTGGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 1392
|||||

Qy 900 TCAGGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAAGGCGCCTGCCACCAC 959
|||||

Db 1393 TCAGGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAA-GGCGCTGCCACCAC 1451
|||||

Qy 960 GCCCCGCTAATTTTTTTGTATTTTTTAATAAAGACGGGGTTTCATCGTTAGCCAGGATG 1019
|||||

Db 1452 GCCCCGCTAATTTTTTTGTATTTTTTAATAAAGACGGGGTTTCATCGTTAGCCAGGATG 1511
|||||

Qy	1020	GTCTCGATCTCATGACCTTGTGATCCGCTGCCTCGGCCTCCCAAAGTGCTGGGATTACA	1079
Db	1512	GTCTCGATCTCATGACCTTGTGATCCGCTGCCTCGGCCTCCCAA- -TGCTGGATTACA	1569
Qy	1080	GGCATGAGCACCGTGCCCGCCTTATCACATTTATTATTATTTGTTTTCTCTCCCACT	1139
Db	1570	GGCATGAGCACCGTGCCCGCCTTATCACATTTATTATTATTTGTTTTCTCTCCCACT	1629
Qy	1140	AGTTTGAAGTCCTCATGAGGTTAGAG- -ATTATTATTATTATTATTATTATTATTATT	1196
Db	1630	AGTTTGAAGTCCTCATGAGGTTAGAGATTATTATTATTATTATTATTATTATTATTATT	1689
Qy	1197	TTATTATTATTATTATTATCTGTTCACTGCTGTATCTCTAGCTCCTAGGACAGAGCCTGSC	1256
Db	1690	TTATTATTATTATTATTATCTGTTCACTGCTGTATCTCTAGCTCCTAGGACAGAGCCTGSC	1749
Qy	1257	ACATAGTAAGTGCTCAATAAAATATTCTACTGGATAAACAGTGCAGATAGTTTAAAACTATC	1316
Db	1750	ACATAGTAAGTGCTCAATAAAATATTCTACTGGATAAACAGTGCAGATAGTTTAAAACTATC	1809
Qy	1317	TGACCTAGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA	1376
Db	1810	TGACCTAGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA	1869
Qy	1377	GCTGAAATCGTGTCACCTGCACCTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAA	1436
Db	1870	GCTGAAATCGTGTCACCTGCACCTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAA	1929
Qy	1437	AAAAAAAACCTATCAGGCCTAGCTGGTGGCACATGCCCTGTAATCCTAGCTGAGGCGGT	1496
Db	1930	AAAAAAAACCTATCAGGCCTAGCTGGTGGCACATGCCCTGTAATCCTAGCTGAGGCGGT	1989
Qy	1497	AGGTCCTCCAGAGAAGAAGAAGAAAAAGAAGATATATATATATATATATACACACACA	1556
Db	1990	AGGTCCTCCAGAGAAGAAGAAGAAAAAGAAGATATATATATATATATACACACACA	2049
Qy	1557	CAAAGATATAAACTTTATATATATAAAGTTTTCATTAAAAAAAACCTCTACCC	1616
Db	2050	CAAAGATATAAACTTTATATATATAAAGTTTTCATT-AAAAAAAACCTCTACCC	2108
Qy	1617	ACTTTCACTTTACAGGTTCCCTGGGTCCAACGGTCTTCAGAGGAGGCAGCTGGCAGGGGT	1676
Db	2109	ACTTTCACTTTACAGGTTCCCTGGGTCCAACGGTCTTCAGAGGAGGCAGCTGGCAGGGGT	2168
Qy	1677	CAGGAGGCAGCTGGGACCCGAGGGAGCAGGAAGGCAGTGTGCCCGGGTGCTGGCA	1736
Db	2169	CAGGAGGCAGCTGGGACCCGAGGGAGCAGGAAGGCAGTGTGCCCGGGTGCTGGCA	2228
Qy	1737	GACCGATTTGAACTCTGGCTATGTCTTTCTGCAGTGGCCGCCGCCGMCAGCGGCATCAGC	1796
Db	2229	GACCGATTTGAACTCTGGCTATGTCTTTCTGCAGTGGCCGCCGCCGACAGCGGCATCAGC	2288
Qy	1797	CCTCGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCGTGATCCCCGGGAGTGACCCC	1856
Db	2289	CCTCGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCGTGATCCCCGGGAGTGACCCC	2348
Qy	1857	TTYTTGGAATACAACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCCGTG	1916
Db	2349	TTYTTGGAATACAACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCCGTG	2408
Qy	1917	GATGAACCTGGACAAGTAAGTGATCCGCCTGCAGGAAAAATTGGAGTGCCTGCCGGGGCGG	1976
Db	2409	GATGAACCTGGACAAGTAAGTGATCCGCCTGCAGGAAAAATTGGAGTGCCTGCCGGGGCGG	2468
Qy	1977	GGTGGGGCA-CACGCCAAGGATCTCACGAGGCATACAAAGGGACTTGCCATATCTGCTAA	2035
Db	2459	GGTGGGGCACCACGCCAAGGATCTCACGAGGCATACAAAGGGACTTGCCATATCTGCTAA	2528
Qy	2036	GGATAACATATTTTCACCTCTTGTCAATAAACAATAATATGTTCCAGAGGACCCCTGTAGC	2095
Db	2529	GGATAACATATTTTCACCTCTTGTCAATAAACAATATATGTTCCAGAGGACCCCTGTAGC	2588

Qy	2096	GAAACGCACCCCGTTAGAGATGGAAAACAATGACCGACGTGCAAAAACAGTGGGCGATGCTGC	2155
Db	2589	GAAACGCACCCCGTTAGAGATGGAAAAACATTGACCGACGTGCAAAAACAGTGGGCGATGCTGC	2648
Qy	2156	CCTCCAGTGGCAGAAATGTAGCAACAGTAGTAAACATCACAGCAAACTATCCACGTGTCAATTTTC	2215
Db	2649	CCTCCAGTGGCAGAAATGTAGCAACATTAACACATCACAGCACCTATCCACGTGTCAATTTTC	2708
Qy	2216	TAGCAGTGGTTGTCACTGCACCTTCT- GAATACAGGATTTTACTGTATTCTTGCAACCAT	2274
Db	2709	TAGCAGTGGTTGTCACTGCCCTTCTTGGAATACAGGATTTTACTGTATTCTTGCAACCAT	2768
Qy	2275	GTTAAAAATCGCTTTCAGGCCAGGCGGGTGCCTCATGCCTGTAATCCCAGCACTTTGGG	2334
Db	2769	GTTAAAAATCGCTTTCAGGCCAGGCGGGTGCCTCATGCCTGTAATCCCAGCACTTTGGG	2828
Qy	2335	AGGCCGAGGCGGGCGGATCACTTGAGGTCAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGT	2394
Db	2829	AGGCCGAGGCGGGCGGATCACTTGAGGTCAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGT	2888
Qy	2395	GAAACCCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTA	2454
Db	2889	GAAACCCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTA	2948
Qy	2455	ACCCAGCTACTTTGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCAAAGTTCGTCACTGCT	2514
Db	2949	ACCCAGCTACTTTGGGAGACTGAGTTGGAGGTTTCA- TGAGCCAAGTTCGTCACTGCT	3007
Qy	2515	GTCCAGCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAAAATGCTTTCATAAATAT	2574
Db	3008	GTCCAGCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAAAATGCTTTCATAAATAT	3067
Qy	2575	ATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCTGAAGCATCTTGGC	2634
Db	3068	ATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCTGAAGCATCTTGGC	3127
Qy	2635	GAAAGTCATCCCCACCTGTTCTTGAGAGTGGGAGTGAGGGCTGACCTATTGCTCTGCAC	2694
Db	3128	GAAAGTCATCCCCACCTGTTCTTGAGAGTGGGAGTGAGGGCTGACCTATTGCTCTGCAC	3187
Qy	2695	TTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGTGCTGCCAGACACATGACAACTGC	2754
Db	3188	TTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGTGCTGCCAGACACATGACAACTGC	3247
Qy	2755	TAYGACCAGGCCAAGAGCTGGACAGCTGTAAATTTCTGTGGACAMMCCGTACACCCAC	2814
Db	3248	TAGCACCAGGCCAAGAGCTGGACAGCTGTAAATTTCTGTGGACAAACCCGTACACCCAC	3307
Qy	2815	ACCTATTCACTACTCGTCTGGCTCGGCAATCACTGTAGCAGTAGGTTTATCCCTTCC	2874
Db	3308	ACCTATTCACTACTCGTCTGGCTCGGCAATCACTGTAGCAGTAGGTTTATCCCTTCC	3367
Qy	2875	TTGACCTA 2882	
Db	3368	TTGACCTA 3375	
RESULT 7			
ABD20766			
ID	ABD20766	standard; DNA; 3375 BP.	
XX	AC	ABD20766;	
XX	DT	29-JUL-2004 (first entry)	
XX	DE	Human pulmonary and inflammatory target DNA #377.	
KW		Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;	
KW		respiratory tract inflammation; adenosine sensitivity; lung; cancer;	
KW		surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;	
KW		analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;	
KW		beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;	
KW		respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;	

KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmon ry transplantation rejection; ds.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
XX
PF 23-APR-2002; 2002WO-US013143.
XX
XX
PR 24-APR-2001; 2001US-0286036P.
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PA (EPIG-) EPIGENESIS PHARM INC.
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PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
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XX WPI; 2003-093058/08.
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PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
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PS Claim 15; SEQ ID NO 12159; 763pp; English.
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CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
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SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;
Query Match 53.8%; Score 2690.8; DB 11; Length 3375;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;
QY 1 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGCTAGCTGT 60
Db |||||||
500 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGCTAGCTGT 559
QY 61 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGCCCTTCTCTCCCAAGTGAGCTA 120
Db |||||||
560 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGCCCTTCTCTCCCAAGTGAGCTA 619
QY 121 AGATCTCACTCCTCTGGAATGGGGGCCACAGGCCACAGCAAACAGGGATGGCCAGCCCCG 180

Db ||||||| 620 AGATCTCACTCCTCTGGAATGGGGGCCACA--CACAGCAAACAGGGATGGCCAGCCCCG 676
QY ||||||| 181 CAGTCTCAAATCGAGGTTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 240
Db ||||||| 677 CAGTCTCAAATCGAGGTTCCAGT- GGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 735
QY ||||||| 241 GCTGGCACATTTTCAACCTGCAAGTCTGAACTCAGATTGCCTGAGCTAAGAAAGCTTGCC 300
Db ||||||| 736 GCTGGCACATTTTCAACCTGCAAGTCTGAACTCAGATTGCCTGAGCTAAGAAAGCTTGCC 795
QY ||||||| 301 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA 360
Db ||||||| 796 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATAAACCAGGCTGGAGTTCAGTGGCA 855
QY ||||||| 361 TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAAGTGATCCTCCCACCTTACTCA 420
Db ||||||| 856 TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAAGTGATCCTCCCACCTTACTCA 915
QY ||||||| 421 ACTAAGTAGTTAGGCCAATCTCCCATTTTATTTTATTTTAAATTTTATTTTATTT 480
Db ||||||| 916 ACTAAGTAGTTAGGCCAATCTCCATTTTATTTTATTTTAAATTTTATTTTATTT 975
QY ||||||| 481 TACTTTATTTTATTTTGAGACGGGGCTCACTCTGTCGCCCCAGGCTGGAGTGGGTGGCG 540
Db ||||||| 976 TACTTTATTTTATTTTGAGACGGGGCTCACTCTGTGCG- CCAGGCTGGAGTGGGTGGCG 1034
QY ||||||| 541 TGATCTCAGATCACTACAACCTCCATCTCCTGGGTCAAATAATTTCTTTGCCTCAGCCT 600
Db ||||||| 1035 TGATCTCAGATCACTACAACCTCCATCTCCT- GGTTCAAATAAATTTCTTTGCCTCAGCCT 1093
QY ||||||| 601 CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGCGCACACACCACCATGCCAGCTAA 660
Db ||||||| 1094 CTCAAGTAGCT-GGACTGTAGCTCTCAAGTAGCTGCGCACACACCACCATGCCAGCTAA 1152
QY ||||||| 661 TTTTGT 720
Db ||||||| 1153 TTTTGT 1212
QY ||||||| 721 CTCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCCTTTCT-AATGCAGTATCCAG 779
Db ||||||| 1213 CTCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCCTTTCTAAATGCAGTATCCAG 1272
QY ||||||| 780 TTTCTTACTTATCACATTTATTTATTTATTTCTTATTTATTTGAGACAGAGTCTTGCTTTG 839
Db ||||||| 1273 TTTCTTACTTATACACTTTATTTATTTATTTCTTATTTATTTGAGACAGAGTCTTGCTTTG 1332
QY ||||||| 840 TCGCCAAAGGCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 899
Db ||||||| 1333 TGCCCAAGGCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 1392
QY ||||||| 900 TCACGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAAGCGCGCTGCCACAC 959
Db ||||||| 1393 TCACGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAA-GCGCCTGCCACCAC 1451
QY ||||||| 960 GCCCCGCTAATTTTTTGTATTTTAAATAAAGACGGGGTTTCATCGTGTAGCCAGGATG 1019
Db ||||||| 1452 GCCCCGCTAATTTTTTGTATTTTAAATAAAGACGGGGTTTCATCGTGTAGCCAGGATG 1511
QY ||||||| 1020 GTCTCGATCTCATGACCTTGTGATCCGCTCGCTCGGCCCTCCCAAAGTCTGGGATTACA 1079
Db ||||||| 1512 GTCTCGATCTCATGACCTTGTGATCCGCTCGCTCGGCCCTCCCAA--TGCTGGATTACA 1569
QY ||||||| 1080 GGCATGAGCCACCGTGCCCGGCTTATCACATTTATTTATTTATTTTCTCTCCCACT 1139
Db ||||||| 1570 GGCATGAGCCACCGTGCCCGGCTTATCACATTTATTTATTTATTTTCTCTCCCACT 1629
QY ||||||| 1140 AGGTGTAAAGCTCCATGAGGTAGAG--ATTATTTATTTATTTATTTATTTATTTATTTA 1196
Db ||||||| 1630 AGGTGTAAAGCTCCATGAGGTAGAGATTATTTATTTATTTATTTATTTATTTATTTA 1689
QY ||||||| 1197 TTATTATTATTTATTTATTTTCACTGCTGTATCTCTAGCTCCTAGGACAGAGCCTGGC 1256

Db 1690 TTATTATTATTATATATCTGTTCACTGCTGTATCTCTAGCTCCTAGGACAGAGCCTGGC 1749

Qy 1257 ACATAGTAAGTCTCAATAAATATTCTACTGGATAAAACAGTGCAGATAGTTTAAAACTATC 1316

Db 1750 ACATAGTAAGTCTCAATAAATATTCTACTGGATAAAACAGTGCAGATAGTTTAAAACTATC 1809

Qy 1317 TGACCTAGGAGGCTGAGGCAGGAGAAATGGCGTGAAACCCGGGAAGCAGAGTTTGCAGTGA 1376

Db 1810 TGACCTAGGAGGCTGAGGCAGGAGAAATGGCGTGAAACCCGGGAAGCAGAGTTTGCAGTGA 1869

Qy 1377 GCTGAAATCGTGTCACCTGCACTCCAACTCCAGTGGGCAACAGAGCAAGACTCCATCTCAAAAA 1436

Db 1870 GCTGAAATCGTGTCACCTGCACTCCAACTCCAGTGGGCAACAGAGCAAGACTCCATCTCAAAAA 1929

Qy 1437 AAAAAAAACTATCAGGCCTAGCTGGGTGGCACATGCCCTGTAATCCTAGCTGAGGCGGT 1496

Db 1930 AAAAAAAACTATCAGGCCTAGCTGGGTGGCACATGCCCTGTAATCCTAGCTGAGGCGGT 1989

Qy 1497 AGGGTCCCAGAAAGAAAGAAAGAAAGAAAGATATATATATATATATACACACACA 1556

Db 1990 AGGGTCCCAGAAAGAAAGAAAGAAAGAAAGATATATATATATATATACACACACA 2049

Qy 1557 CAAAGATATAAAGTTTATATATATAAAGTTTTCATTAAAAAAGTTTCTACCC 1616

Db 2050 CAAAGATATAAAGTTTATATATATAAAGTTTTCATT-AAAAAAGAAAGTTTCTACCC 2108

Qy 1617 ACTTTCACTTTACAGGTTCTTGGGTCCAACGGTCTTCAGAGGAGCAGCTGGCAGGGGT 1676

Db 2109 ACTTTCACTTTACAGGTTCTTGGGTCCAACGGTCTTCAGAGGAGCAGCTGGCAGGGGT 2168

Qy 1677 CAGGAGGCAGCTGGGACCCGAGGGAGCAGGAAGGCAGTGTGCCCGGGGTGCTGGCA 1736

Db 2169 CAGGAGGCAGCTGGGACCCGAGGGAGCAGGAAGGCAGTGTGCCCGGGGTGCTGGCA 2228

Qy 1737 GACCGATTTGAACTCTGGCTATGTCTTCTTGCACTGGCGCGCGCGMCAAGCGGCATCAGC 1796

Db 2229 GACCGATTTGAACTCTGGCTATGTCTTCTTGCACTGGCGCGCGCGCACAGCGGCATCAGC 2288

Qy 1797 CCTCGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCGGGGAGTGACCCC 1856

Db 2289 CCTCGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCGGGGAGTGACCCC 2348

Qy 1857 TTYTTTGGAATACAACAACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCCGTG 1916

Db 2349 TTCTTGGAATACAACAACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCCGTG 2408

Qy 1917 GATGAACCTGGACAAGTAAGTGATCCGCCCTGCAGGAAAAATTGGAGTGCCTGCCGGGGCGG 1976

Db 2409 GATGAACCTGGACAAGTAAGTGATCCGCCCTGCAGGAAAAATTGGAGTGCCTGCCGGGGCGG 2468

Qy 1977 GGTGGGGCA-CAGGCCAAGGATCTCACGAGGCATACAAAGGGGACTTGCATATCTGCTAA 2035

Db 2469 GGTGGGGCACCAGCCAAAGGATCTCACGAGGCATACAAAGGGGACTTGCATATCTGCTAA 2528

Qy 2036 GGATAACATATTTTCACCTCTTGTCAAAATAAACAATATGTTCCAGAGGACCCCTGTAGC 2095

Db 2529 GGATAACATATTTTCACCTCTTGTCAAAATAAACAATATATGTTCCAGAGGACCCCTGTAGC 2588

Qy 2096 GAACGCACCCCGTTAGAGATGGAAACAATGACCGACGTGCAAAAACAGTGGCGATGCTGC 2155

Db 2589 GAACGCACCCCGTTAGAGATGGAAACAATTGACCGACGTGCAAAAACAGTGGCGATGCTGC 2648

Qy 2156 CCTCCAGTGGCAGAAATGTAGCAACAGTAACATCACAGCAACTATCCACGTGCTATTTTC 2215

Db 2649 CCTCCAGTGGCAGAAATGTAGCAACATTTAAACATCACAGCACCTATCCACGTGCTATTTTC 2708

Qy 2216 TAGCAGTGGTTGTCACTGCACCTTCT-GAATA CAGGATTTTACTGTATTTCTTGCAACCAT 2274

Db 2709 TAGCAGTGGTTGTCACTGCCTTCTGGAATACAGGATTTTACTGTATTTCTTGCAACCAT 2768

Qy 2275 GTTAAAAATCGCTTTTCAGGCCAGGCGGTGGCTCATGCTGTAAATCCAGCACTTTGGG 2334

Db 2769 GTTAAAAATCGCTTTTCAGGCCAGGCGGTGGCTCATGCTGTAAATCCAGCACTTTGGG 2828

Qy 2335 AGCCCGAGGCGGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGT 2394

Db 2829 AGCCCGAGGCGGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGT 2888

Qy 2395 GAAACCCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCCTGTA 2454

Db 2889 GAAACCCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCCTGTA 2948

Qy 2455 ACCCAGCTACTTGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCAAAGGTCGTGTCACTGCT 2514

Db 2949 ACCCAGCTACTTGGGAGACTGAGTTGGAGGTTTCA-TGAGCCAAAGGTCGTGTCACTGCT 3007

Qy 2515 GTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAATAATGCTTTCATAAATAT 2574

Db 3008 GTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAATAATGCTTTCATAAATAT 3067

Qy 2575 ATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCCTGAAGCATCTTGGC 2634

Db 3068 ATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCCTGAAGCATCTTGGC 3127

Qy 2635 GAAGTCATCCCCACCTGTTCCTGAGAGTGGGCAGGTGAGGCTGACCTATTGCTCTGCAC 2694

Db 3128 GAAGTCATCCCCACCTGTTCCTGAGAGTGGGCAGGTGAGGCTGACCTATTGCTCTGCAC 3187

Qy 2695 TTACTCCTATCTCAGCTGTCCCTCCACATTTCCAGTGCTGCCAGACACATGACAACTGC 2754

Db 3188 TTACTCCTATCTCAGCTGTCCCTCCACATTTCCAGTGCTGCCAGACACATGACAACTGC 3247

Qy 2755 TAYGACCAGGCCAAGAGCTGGACAGCTGTAAATTTCTGTGGACAMMCCGTACACCCAC 2814

Db 3248 TAGCACCAGGCCAAGAGCTGGACAGCTGTAAATTTCTGTGGACAACCCGTACACCCAC 3307

Qy 2815 ACCTATTTCATCTCGTCTGTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 2874

Db 3308 ACCTATTTCATCTCGTCTGTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 3367

Qy 2875 TTGACCTA 2882

Db 3368 TTGACCTA 3375

RESULT 8

AAA35103

ID AAA35103 standard; DNA; 6771 BP.

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AC AAA35103;

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DT 28-JUL-2000 (first entry)

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DE Human adenosine receptor related polynucleotide SEQ ID NO:2792.

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KW Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;

KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

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OS Homo sapiens.

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PN WO200009525-A2.

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PD 24-FEB-2000.

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PF 03-AUG-1999; 99WO-US017712.

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PR 03-AUG-1998; 98US-0095212P.

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PA (UYEC-) UNIV EAST CAROLINA.

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PI Nyce JW;
XX WPI; 2000-205971/18.
DR
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
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PS Disclosure; Page 1058-1059; 1343pp; English.
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CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;

Query Match 53.8%; Score 2690.8; DB 3; Length 6771;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;

QY 1 CTGGTCACTCAGTTCTTTTCTCACCTTGACTGCAAGATGAACCTCCTTGCTAGCTGT 60
Db |||||
QY 61 GCTGCTACAGGTAGGCAAGTCTCCCGGCTCCACCGCCTTCTCTCCCAAGTGAGCTA 120
Db |||||
QY 121 AGATCTCACTCCTCTGGAATGGGGCCACAGGCCACAGCAACAGGGATGGCCAGCCCG 180
Db |||||
QY 181 CAGTCTCAAWTCGAGGTTCCCAAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 240
Db |||||
QY 241 GCTGGCAGCTTTTCAACCTGCAAGCTGAACCTCAGATTGCCTGAGCTAAGAAAGCTTGCC 300
Db |||||
QY 301 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA 360
Db |||||
QY 361 TGATCATAGCTCACCCACAGCTTCCAACTCGTGGGCTCAAGTGATGCTCCACCTTACTCA 420
Db |||||
QY 421 ACTAAGTAGTGGCCCAATCTCCCATTTATTTTATTTTAAATTTTATTTTATTT 480
Db |||||

Db 1478 ACTAAGTAGTTAGGCCAATCTCCATTTTATTTTATTTTATTTTAAATTTTATTTT 1537
QY TACTTTTATTTTATTTTGGAGACGGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCG 540
Db |||||
QY 541 TGATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAATAAATTCCTTGCCTCAGCCT 600
Db |||||
QY 601 CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGGCACACACCACCATGCCAGCTAA 660
Db |||||
QY 661 TTTTGTGTGTTTTTTTGGTAGAGACAGGTTTTCACCATGTTGGCCAGGCTGGGTGAC 720
Db |||||
QY 721 CTCCCTTTTAGATTCTCCTCATCCTGCTCTATTCTCCCTTTCT-AATGCAGTATCCAG 779
Db |||||
QY 780 TTTCTTACTTATACATTTATTTATTTATTTATTTATTTAGACAGAGTCTTGCTTTG 839
Db |||||
QY 840 TCGCCAAGGCTGGAGTACAGTGGTGCATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 899
Db |||||
QY 900 TCACGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAAGGCGCCTGCCACCAC 959
Db |||||
QY 960 GCCCGGCTAATTTTGTATTTTAAATAAAGACGGGGTTTCATCGTGTAGCCAGGATG 1019
Db |||||
QY 1020 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAAGTGTGGGATTACA 1079
Db |||||
QY 1080 GGATGAGCCACCGTGCCGGCTTATCACATTTATTTATTTATTTTCTCTCCACT 1139
Db |||||
QY 1140 AGGTGTAAGCTCCATGAGGTAGAG--ATTATTTATTTATTTATTTATTTATTTA 1196
Db |||||
QY 1197 TTATTATTATTATTTATTTCTGCTGATCTCTAGCTCCTAGGACAGAGCCTGGC 1256
Db |||||
QY 1257 ACATAGTAAGTGCTCAATAAATATTCACTGGATAAACAGTGCAGATAGTTTAAACTATC 1316
Db |||||
QY 1317 TGACCTAGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGAGTGA 1376
Db |||||
QY 1377 GCTGAAATCGTGTCACTGCACCTCAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAA 1436
Db |||||
QY 1437 AAAAAAAACTATCAGGCTAGCTGGGTGGCACATGCTGTAACTCCTAGCTGAGCGGT 1496
Db |||||
QY 1497 AGGTCCCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1556
Db |||||
QY 2074 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2075 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2076 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2077 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2078 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2079 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2080 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2081 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2082 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2083 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2084 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2085 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2086 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2087 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2088 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2089 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2090 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
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QY 2092 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2093 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2094 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2095 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2096 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2097 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2098 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2099 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2100 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2101 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2102 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
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QY 2106 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2107 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2108 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2109 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2110 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2111 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2112 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2113 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2114 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2115 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2116 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2117 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2118 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2119 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2120 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2121 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2122 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2123 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2124 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2125 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2126 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2127 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2128 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2129 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2130 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2131 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2132 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2133 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2134 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2135 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
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QY 2302 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2303 GTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAA--TGCTGGATTACA 2131
QY 2304 GTCTCGATCTCATGAC

Qy	1557	CAAAGATATAAACTTTATATATATAAAGTTTTCATTAAAAA	1616
Db	2612	CAAAGATATAAACTTTATATATATAAAGTTTTCATT - AAAAA	2670
Qy	1617	ACTTTCACTTTACCAGGTTCCCTGGGTCCAACGGTCTTCAGAGGAGCAGCTGGCAGGGGT	1676
Db	2671	ACTTTTCACTTTACCAGGTTCCCTGGGTCCAACGGTCTTCAGAGGAGCAGCTGGCAGGGGT	2730
Qy	1677	CAGGAGGCAGCGTGGGACCCGAGGGAGCAGGAAGGCAGTGTGTC	1736
Db	2731	CAGGAGGCAGCGTGGGACCCGAGGGAGCAGGAAGGCAGTGTGTC	2790
Qy	1737	GACCGATTGAACTCTGGCTATGTCTTCTTGCACTGGCCGCCGCGM	1796
Db	2791	GACCGATTGAACTCTGGCTATGTCTTCTTGCACTGGCCGCCGCG	2850
Qy	1797	CCTCGGGCCGTGTGGCAGTTCGCGCAAAATGATCAAGTGCCTGAT	1856
Db	2851	CCTCGGGCCGTGTGGCAGTTCGCGCAAAATGATCAAGTGCCTGAT	2910
Qy	1857	TTYTTGGAAATACAACAACTACGGCTGCTACTGTGGCTTGGGGG	1916
Db	2911	TTCTTGGAAATACAACAACTACGGCTGCTACTGTGGCTTGGGGG	2970
Qy	1917	GATGAACCTGGACAAAGTAAGTGATCCGCCCTGCAGGAAAAATT	1976
Db	2971	GATGAACCTGGACAAAGTAAGTGATCCGCCCTGCAGGAAAAATT	3030
Qy	1977	GGTGGGGCA - CACGCCAAGGATCTCACGAGGCATACAAAGGG	2035
Db	3031	GGTGGGGCACCAAGCCAAAGGATCTCACGAGGCATACAAAGGG	3090
Qy	2036	GGATAACATATTTTACACCTCTTGTCAAAFAAAACAAATATGTT	2095
Db	3091	GGATAACATATTTTACACCTCTTGTCAAAFAAAACATATATGTT	3150
Qy	2096	GAACGCACCCCGTTAGAGATGGAAACAATGACCGACGTGCAAAA	2155
Db	3151	GAACGCACCCCGTTAGAGATGGAAACAATGACCGACGTGCAAAA	3210
Qy	2156	CCTCCAGTGGCAGAAATGTAGCAACACAGTAACATCACAGCAAC	2215
Db	3211	CCTCCAGTGGCAGAAATGTAGCAACATTAACATCACAGCACCTA	3270
Qy	2216	TAGCAGTGGTTGTCACTGCACCTTCT - GAATACAGGATTTTAC	2274
Db	3271	TAGCAGTGGTTGTCACTGCCTTCTTGGAAATACAGGATTTTACT	3330
Qy	2275	GTTAAAAATCGCTTTCAGGCCAGGCGGGTGGCTCATGCCCTGT	2334
Db	3331	GTTAAAAATCGCTTTCAGGCCAGGCGGGTGGCTCATGCCCTGT	3390
Qy	2335	AGGCCGAGGCGGGCGGATCACTTGAGGTCAGGAGTTCGAGACC	2394
Db	3391	AGGCCGAGGCGGGCGGATCACTTGAGGTCAGGAGTTCGAGACC	3450
Qy	2395	GAACCCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACAT	2454
Db	3451	GAACCCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACAT	3510
Qy	2455	ACCCAGCTACTTGGGAGACTGAGTTGGAGTTTCAGTGAGCCAA	2514
Db	3511	ACCCAGCTACTTGGGAGACTGAGTTGGAGTTTCA - TGAGCCAA	3569
Qy	2515	GTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAA	2574
Db	35*0	GTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAA	3629
Qy	2575	ATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCT	2634
Db	3630	ATGATAAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCT	3689

Qy	2635	GAAGTCATCCCCACCTGTTCTCTGAGAGTGGGAGGTGAGGGCTG	2694
Db	3690	GAAGTCATCCCCACCTGTTCTCTGAGAGTGGGAGGTGAGGGCTG	3749
Qy	2695	TTACTCCTATCTCAGCTGTCTCCCTCCACCTTTCAGGTGCTGCC	2754
Db	3750	TTACTCCTATCTCAGCTGTCTCCCTCCACCTTTCAGGTGCTGCC	3809
Qy	2755	TAYGACCAGGCCAAGAGCTGGACAGCTGTAAATTTCTGCTGGAC	2814
Db	3810	TACGACCAGGCCAAGAGCTGGACAGCTGTAAATTTCTGCTGGAC	3869
Qy	2815	ACCTATTCATCTCGTCTGTGGCTCGGCAATCACCTGTAGCAGTA	2874
Db	3870	ACCTATTCATCTCGTCTGTGGCTCGGCAATCACCTGTAGCAGTA	3929
Qy	2875	TTGACCTA 2882	
Db	3930	TTGACCTA 3937	
RESULT 9			
AAAF21225			
ID	AAF21225	standard; DNA; 6771 BP.	
XX			
AC	AAF21225;		
XX			
DT	14-MAR-2001	(first entry)	
XX			
DE	Human low adenosine antisense oligonucleotide related sequence #2792.		
XX			
KW	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;		
KW	human; airway disorder; bronchoconstriction; lung inflammation;		
KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;		
KW	immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;		
KW	respiratory obstruction; pulmonary obstruction; impeded respiration;		
KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;		
KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;		
KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;		
KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;		
KW	cancer; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200062736-A2.		
XX			
PD	26-OCT-2000.		
XX			
PF	24-MAR-2000; 2000WO-US008020.		
XX			
PR	06-APR-1999; 99US-0127958P.		
XX			
PA	(UYEC-) UNIV EAST CAROLINA.		
PA	(NYCE/) NYCE J W.		
XX			
PI	Nyce JW;		
XX			
DR	WPI; 2000-679539/66.		
XX			
PT	Low adenosine (A) content antisense oligonucleotides which do not trigger		
PT	adenosine receptors during metabolism, useful e.g. for treating cancers		
XX	and respiratory obstructions.		
PS	Disclosure; Page 1137-1139; 1592pp; English.		
XX			
CC	The present invention describes low adenosine (A) content antisense		
CC	oligonucleotides and compositions (I) comprising them. In the antisense		
CC	oligonucleotides the A is replaced by a 'Universal' or alternative base.		
CC	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,		
CC	immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.		
CC	The antisense oligonucleotides and (I) can be used to down-regulate the		
CC	expression and or activity of target polypeptides associated with		
CC	lung/respiratory disorders and malignancies, such as stimulating and		

activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;

Query Match 53.8%; Score 2690.8; DB 3; Length 6771; Best Local Similarity 98.5%; Pred. No. 0; Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;

Qy	1	CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGCTAGCTGT	60
Db	1062	CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGCTAGCTGT	1121
Qy	61	GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGGCTTCTCTCCCAAGTGAGCTA	120
Db	1122	GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCCGGCTTCTCTCCCAAGTGAGCTA	1181
Qy	121	AGATCTACTCCTCTGGAATGGGGCCACAGGCCACAGCAACAGGGATGGCCAGCCCG	180
Db	1182	AGATCTACTCCTCTGGAATGGGGCCACA--CACAGCAACAGGGATGGCCAGCCCG	1238
Qy	181	CAGTCTCAAWTCGAGGTTCCCAAGTCTGAAGTCTAAGGGCTCCTCTATTGGGTTCCCTCAAG	240
Db	1239	CAGTCTCAATTCGAGGTTCCCAAGT-GGGCTTAAGGGCTCCTCTATTGGGTTCCCTCAAG	1297
Qy	241	GCTGGCACTTTTCAACCTGCAAGTCTGAAGTCTGAGTTCCTGAGCTAAGAAAGCTTGCC	300
Db	1298	GCTGGCACTTTTCAACCTGCAAGTCTGAAGTCTGAGTTCCTGAGCTAAGAAAGCTTGCC	1357
Qy	301	TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA	360
Db	1358	TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATAACCCAGGCTGGAGTTCAGTGGCA	1417
Qy	361	TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA	420
Db	1418	TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA	1477
Qy	421	ACTAAGTAGTTAGGCCAATCTCCCATTTATTTTATTTTAAATTTTATTTTATTT	480
Db	1478	ACTAAGTAGTTAGGCCAATCTCCCATTTATTTTATTTTAAATTTTATTTTATTT	1537
Qy	481	TACTTTATTTATTTTGTAGACGGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCG	540
Db	1538	TACTTTATTTATTTTGTAGACGGGGCTCACTCTGTGCG-CCAGGCTGGAGTGGGTGGCG	1596
Qy	541	TGATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAATAATTCTCTGCGCTCAGCCT	600
Db	1597	TGATCTCAGATCACTACAACCTCCATCTCCT-GGTTCAAATAATTCTCTGCGCTCAGCCT	1655
Qy	601	CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCAACCATGCCCCAGCTAA	660
Db	1656	CTCAAGTAGCT-GGACTTGTAGCTCTCAAGTAGCTGGCACACACCAACCATGCCCCAGCTAA	1714
Qy	661	TTTTTTGTGTGTTTTTTTTTGGTAGAGACAGGTTTTTCAACCATGTGGCCAGGCTGGGTGAC	720

Db	1715	TTTTTTGTGTGTTTTTTTTTGGTAGAGACAGGTTTTTACCACATGTTGGCCAGGCTGGGTGAC	1774
Qy	721	CTCCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCTTTTCT-AATGCAGTATCCAG	779
Db	1775	CTCCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCTTTTCTAAATGCAGTATCCAG	1834
Qy	780	TTTCCTTACTTATCACATTTTATTATTATTCTTTATTATTATTGAGACAGAGTCTTGCTTG	839
Db	1835	TTTCCTTACTTATACACTTTATTATTATTCTTTATTATTATTGAGACAGAGTCTTGCTTG	1894
Qy	840	TCGCCAAGGCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT	899
Db	1895	TGCCCAAGGCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT	1954
Qy	900	TCACGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAAGGCGCCTGCCACCAC	959
Db	1955	TCACGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAA-GCGCCTGCCACCAC	2013
Qy	960	GCCCCGCTAAATTTTTTGTATTTTTAAATAAGACGGGGTTTCATCGTGTAGCCAGGATG	1019
Db	2014	GCCCCGCTAAATTTTTTGTATTTTTAAATAAGACGGGGTTTCATCGTGTAGCCAGGATG	2073
Qy	1020	GTCTCGATCTCATGACCTTGATCCGCTCGCCTCGGCTCCCAAGTGTCTGGGATTACA	1079
Db	2074	GTCTCGATCTCATGACCTTGATCCGCTCGCCTCGGCTCCCAAA--TGCTGGATTACA	2131
Qy	1080	GGCATGAGCCACCGTGCCGGCCTTATCACATTATTATTATTATTGTTTTCTCTCCCACT	1139
Db	2132	GGCATGAGCCACCGTGCCGGCCTTATCACATTATTATTATTATTGTTTTCTCTCCCACT	2191
Qy	1140	AGGTTGTAAGCTCCATGAGGTTAGAG--ATTATTATTATTATTATTATTATTATTATT	1196
Db	2192	AGGTTGTAAGCTCCATGAGGTTAGAGATTATTATTATTATTATTATTATTATTATTATT	2251
Qy	1197	TTATTATTATTATTATCTGTTCACCTGCTGTATCTCTAGCTCCTAGGACAGAGCTGGC	1256
Db	2252	TTATTATTATTATTATATCTGTTCACCTGCTGTATCTCTAGCTCCTAGGACAGAGCTGGC	2311
Qy	1257	ACATAGTAAGTGTCTCAATAAATATTTCACCTGGATAAACAGTGCAGATAGTTTAAAACTATC	1316
Db	2312	ACATAGTAAGTGTCTCAATAAATATTTCACCTGGATAAACAGTGCAGATAGTTTAAAACTATC	2371
Qy	1317	TGACCTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA	1376
Db	2372	TGACCTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA	2431
Qy	1377	GCTGAAATCGTGTCACTGCACTCCAACTGGGCAAACAGAGCAAGACTCCATCTCAAAAAA	1436
Db	2432	GCTGAAATCGTGTCACTGCACTCCAACTGGGCAAACAGAGCAAGACTCCATCTCAAAAAA	2491
Qy	1437	AAAAAAAACCTATCAGGCTAGCTGGGTGGCACATGCTGTAATCCTAGCTGAGGCGGT	1496
Db	2492	AAAAAAAACCTATCAGGCTAGCTGGGTGGCACATGCTGTAATCCTAGCTGAGGCGGT	2551
Qy	1497	AGGTTCCCAGAAGAAGAAGAAAGAAAGAAAGAAAGATATATATATATACACACACA	1556
Db	2552	AGGTTCCCAGAAGAAGAAGAAAGAAAGAAAGAAAGATATATATATATACACACACA	2611
Qy	1557	CAAGATATAAACTTTTATATATAAAGTTTTTCATTAAAAAAAACCTCTACCC	1616
Db	2612	CAAGATATAAACTTTTATATATAAAGTTTTTCATT-AAAAAAAACCTCTACCC	2670
Qy	1617	ACTTTCACCTTACCAGTTCTCTGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGT	1676
Db	2671	ACTTTCACCTTACCAGTTCTCTGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGT	2730
Qy	1677	CAGGGAGGCAGCGTGGGACCCGAGGGAGCAGGAAGCAGTGTGTCCCGGGGTGCTGGCA	1736
Db	2731	CAGGGAGGCAGCGTGGGACCCGAGGGAGCAGGAAGCAGTGTGTCCCGGGGTGCTGGCA	2790
Qy	1737	GACCGATTTGAACCTCTGGCTATGTCTTCTTGCAGTGGCGCCGCCGMCAGCGGCATCAGC	1796

2791	Db	GACCGATTGAACTCTGGCTATGTTCTTTGAGTGGCCCGCCGACAGCGCATCAGC	2855
1797	Qy	CTTCGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCGGGAGTGACCCC	1856
2851	Db	CCTCGGCCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCGGGAGTGACCCC	2910
1857	Qy	TTTCTTGGAAATACAAACAACACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGTG	1916
2911	Db	TTTCTTGGAAATACAAACAACACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGTG	2970
1917	Qy	GATGAACCTGGACAAGTAAGTGATCCGCCCTGCAGGAAATTTGGAGTGCCTGCCGGGGCGG	1976
2971	Db	GATGAACCTGGACAAGTAAGTGATCCGCCCTGCAGGAAATTTGGAGTGCCTGCCGGGGCGG	3030
1977	Qy	GGTGGGGCA-CACGCCAAGGATCTCACGAGGGCATACAAAGGGACTTGCATATCTGCTAA	2035
3031	Db	GGTGGGGCACACGCCAAGGATCTCACGAGGGCATACAAAGGGACTTGCATATCTGCTAA	3090
2036	Qy	GGATAACATATTTTACCTCTTGTCAAAATAACAAATATGTTCCAAGAGGACCTGTAGC	2095
3091	Db	GGATAACATATTTTACCTCTTGTCAAAATAACAAATATGTTCCAAGAGGACCTGTAGC	3150
2096	Qy	GAACGCACCCGTTAGAGATGGAACAATGACCGACGTGCAAAACAGTGGCGATGCTGC	2155
3151	Db	GAACGCACCCGTTAGAGATGGAACAATGACCGACGTGCAAAACAGTGGCGATGCTGC	3210
2156	Qy	CTCCAGTGGCAGAAATGACCAACAGTAAACATCACAGCAACTATCCACGTGTCATTTTC	2215
3211	Db	CTCCAGTGGCAGAAATGACCAACATTAACATCATCACAGCACCTATCCACGTGTCATTTTC	3270
2216	Qy	TAGCAGTGGTGTCACTGCACCTTCT-GAATACAGGATTTTACTGTATTTCTTGCAACCAT	2274
3271	Db	TAGCAGTGGTGTCACTGCCCTTCTTGGAAATACAGGATTTTACTGTATTTCTTGCAACCAT	3330
2275	Qy	GTTAAAAATCGCTTTTCAAGCCAGGCGGTGGTGCATGCCTGTAAATCCAGCACTTTGGG	2334
3331	Db	GTTAAAAATCGCTTTTCAAGCCAGGCGGTGGTGCATGCCTGTAAATCCAGCACTTTGGG	3390
2335	Qy	AGCCGAGGCGGCGGATCACTTGAGGTCAGGAGTTCGAGACCCAGCCTGGCCAAACATGGT	2394
3391	Db	AGCCGAGGCGGCGGATCACTTGAGGTCAGGAGTTCGAGACCCAGCCTGGCCAAACATGGT	3450
2395	Qy	GAAACCCCTGTCTACTAAAAAATACAAAAATAGCCGGACATGGTGGCGAGCGCTGTA	2454
3451	Db	GAAACCCCTGTCTACTAAAAAATACAAAAATAGCCGGACATGGTGGCGAGCGCTGTA	3510
2455	Qy	ACCCAGCTACTTTGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCCAAGGTCGTGTCTGCT	2514
3511	Db	ACCCAGCTACTTTGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCCAAGGTCGTGTCTGCT	3569
2515	Qy	GTCCAGCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAATGCTTTCAATAAATAT	2574
3570	Db	GTCCAGCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAATGCTTTCAATAAATAT	3629
2575	Qy	ATGATAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCTGAAGCATCTTTGGC	2634
3630	Db	ATGATAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCTGAAGCATCTTTGGC	3689
2635	Qy	GAAGTCATCCCACTGTTCTCTGAGAGTGGGCAAGTGGAGGCTGACCTATTGCTCTGCAC	2694
3690	Db	GAAGTCATCCCACTGTTCTCTGAGAGTGGGCAAGTGGAGGCTGACCTATTGCTCTGCAC	3749
2695	Qy	TTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGC	2754
3750	Db	TTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGC	3809
2755	Qy	TAYGACCGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCAC	2814
3810	Db	TACGACCGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAAACCCCGTACACCCAC	3869
2815	Qy	ACCTATTCTACTCGTGTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC	2874
3870	Db	ACCTATTCTACTCGTGTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC	3929

Qy	2875	TTGACCTA	2882
Db	3930	TTGACCTA	3937

RESULT 10	
ABZ96919	
ID	ABZ96919 standard; DNA; 6771 BP.

RESULT 10
ABZ96919
ID ABZ96919 standard; DNA; 6771 BP.
XX
XX
AC
AC ABZ96919;
XX
XX
DT 17-OCT-2003 (first entry)
XX
XX
DE Human nucleic acid sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
KW

OS Homo sapiens.
XX
XX
PN WO200285308-A2.
XX
XX
PD 31-OCT-2002.
XX
XX
PF 23-APR-2002; 2002WO-US013135.
XX
XX
PR 24-APR-2001; 2001US-0286137P.
XX
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI: 2003-229219/22.
DR

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

XX
PS Disclosure; SEQ ID NO 12161; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct sequences

SQ Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;
 Query Match 53.8%; Score 2690.8; DB 10; Length 6771;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 1

Qy '1 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGTGCTAGCTGT 60
Db 1062 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGTGCTAGCTGT 1121
Qy 61 GCTGCTCAGGTAGGCAAGTCTCCCGGCTCCACCCGCCCTTCTCTCCAAAGTGAGCTA 120
Db 1122 GCTGCTCAGGTAGGCAAGTCTCCCGGCTCCACCCGCCCTTCTCTCCAAAGTGAGCTA 1181
Qy 121 AGATCTCACTCCTCTGGAATGGGGGCCACAGGCCACAGCAAACAGGGATGGCCAGCCCCG 180
Db 1182 AGATCTCACTCCTCTGGAATGGGGGCCACA--CACAGCAAACAGGGATGGCCAGCCCCG 1238
Qy 181 CAGTCTCAAWTCGAGGTTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 240
Db 1239 CAGTCTCAAWTCGAGGTTCCCAGT-GGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAAG 1297
Qy 241 GCTGGCACTTTTCAACCTGCAAGTCTGAACCTCAGATTGCCCTGAGCTAAGAAAGCTTGCC 300
Db 1298 GCTGGCACTTTTCAACCTGCAAGTCTGAACCTCAGATTGCCCTGAGCTAAGAAAGCTTGCC 1357
Qy 301 TTTATTCTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA 360
Db 1358 TTTATTCTCTTTTCCAGACAGGGTCTTGCTCTATAACCCAGGCTGGAGTTCAGTGGCA 1417
Qy 361 TGATCATAGCTCACCAAGCTTCCAACTCGTGGGCTCAAGTGATCTCTCCACCTTACTCA 420
Db 1418 TGATCATAGCTCACCAAGCTTCCAACTCGTGGGCTCAAGTGATCTCTCCACCTTACTCA 1477
Qy 421 ACTAAGTAGTTAGGCCAATCTCCCAATTAATTTATTTTAATTAATTTTATTTTATTT 480
Db 1478 ACTAAGTAGTTAGGCCAATCTCCCAATTAATTTATTTTAATTTTATTTTATTT 1537
Qy 481 TACTTTATTTATTTTGGACGGGGTCACTCTGTGCGCCAGGCTGGAGTGCGGTGGCG 540
Db 1538 TACTTTATTTATTTTGGACGGGGTCACTCTGTGCG-CCAGGCTGGAGTGCGGTGGCG 1596
Qy 541 TGATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAATPAATTTCTTTGCCTCAGCCT 600
Db 1597 TGATCTCAGATCACTACAACCTCCATCTCCT-GGTTCAAATPAATTTCTTTGCCTCAGCCT 1655
Qy 601 CTCAAGTAGCTGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACTGCCCCAGCTAA 660
Db 1656 CTCAAGTAGCT-GGACTTGTAGCTCTCAAGTAGCTGGCACACACCACTGCCCCAGCTAA 1714
Qy 661 TTTTGT 720
Db 1715 TTTTGT 1774
Qy 721 CTCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCCTTTCT-AATGCAGTATCCAG 779
Db 1775 CTCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCCTTTCTAAATGCAGTATCCAG 1834
Qy 780 TTTCCCTTACTTATCACATTTATTAATTAATTTATTTATTTATTTAGACAGAGTCTTGCTTTG 839
Db 1835 TTTCCCTTACTTATACACTTTATTAATTAATTTATTTATTTATTTAGACAGAGTCTTGCTTTG 1894
Qy 840 TCGCCAAGGCTGGAGTACAGTGGTGGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 899
Db 1895 TGCCCAAGGCTGGAGTACAGTGGTGGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 1954
Qy 900 TCACGCCATTCTCCCGCCTCAGCCTCCCCAGTAGCTGGGACTAAAGGGCCTGCCACCAC 959
Db 1955 TCACGCCATTCTCCCGCCTCAGCCTCCCCAGTAGCTGGGACTAAA-GGCGCTGCCACCAC 2013
Qy 960 GCCCGCTAATTTTTTGTATTTTAAAGACGGGGTTTCATCGTGTAGCCAGGATG 1019
Db 2014 GCCCGCTAATTTTTTGTATTTTAAAGACGGGGTTTCATCGTGTAGCCAGGATG 2073
Qy 1020 GTCTCGATCTCATGACCTTGTGATCCGCCCTGCCCTCGGCCTCCCAAAGTGTGGGATFACA 1079
Db 2074 GTCTCGATCTCATGACCTTGTGATCCGCCCTGCCCTCGGCCTCCCAAA--TGCTGGATTACA 2131

Qy 1080 GGCATGAGCCACCGTGCCCGCCTTATCACATTTATTATTATTATTGTTTTTCTCTCCCACT 1139
Db 2132 GGCATGAGCCACCGTGCCCGCCTTATCACATTTATTATTATTATTGTTTTTCTCTCCCACT 2191
Qy 1140 AGTTGTAAAGCTCCATGAGGTTAGAG--ATTATTATTATTATTATTATTATTATTATTATT 1196
Db 2192 AGTTGTAAAGCTCCATGAGGTTAGAGATTATTATTATTATTATTATTATTATTATTATTATT 2251
Qy 1197 TTATTATTATTATTATCTGTTCACTGCTGTATCTCTAGTCTCTTAGGACAGAGCCTGGC 1256
Db 2252 TTATTATTATTATTATCTGTTCACTGCTGTATCTCTAGTCTCTTAGGACAGAGCCTGGC 2311
Qy 1257 ACATAGTAAGTGCTCAATAAATATTCACTGGATAAAACAGTGCAGATAGTTTAAAACTATC 1316
Db 2312 ACATAGTAAGTGCTCAATAAATATTCACTGGATAAAACAGTGCAGATAGTTTAAAACTATC 2371
Qy 1317 TGACCTAGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA 1376
Db 2372 TGACCTAGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA 2431
Qy 1377 GCTGAAATCGTGTCACTGCACTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAAA 1436
Db 2432 GCTGAAATCGTGTCACTGCACTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAAA 2491
Qy 1437 AAAAAAAACTATCAGGCCTAGTGGTGGCACAATGCTTAATCCTAGTGAAGCGGT 1496
Db 2492 AAAAAAAACTATCAGGCCTAGTGGTGGCACAATGCTTAATCCTAGTGAAGCGGT 2551
Qy 1497 AGGTCCCAGAGAAGAAGAAGAAAAAGAAAGATATATATATATATACACACA 1556
Db 2552 AGGTCCCAGAGAAGAAGAAGAAAAAGAAAGATATATATATATATACACACA 2611
Qy 1557 CAAAGATATAAACTTTATATATATAAAGTTTTTCATTAATAAAAAAAACCTCTACCC 1616
Db 2612 CAAAGATATAAACTTTATATATATAAAGTTTTTCAATT-AAAAAANAACCTCTACCC 2670
Qy 1617 ACTTTCACTTTACCAGGTTCTGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGT 1676
Db 2671 ACTTTCACTTTACCAGGTTCTGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGT 2730
Qy 1677 CAGGAGGCAGCGTGGACCCGAGGAGCAGGAAGCAGTGTGTCCCAGGGGTGCTGGCA 1736
Db 2731 CAGGAGGCAGCGTGGACCCGAGGAGCAGGAAGCAGTGTGTCCCAGGGGTGCTGGCA 2790
Qy 1737 GACCGATTTGAACTCTGGCTATGTCTTCTTGAGTGGCCGCCCGCMCAGCGGCATCAGC 1796
Db 2791 GACCGATTTGAACTCTGGCTATGTCTTCTTGAGTGGCCGCCCGCMCAGCGGCATCAGC 2850
Qy 1797 CCTCGGCCGTGTGSCAGTTCGCAAAATGATCAAGTGCATGCCGGGGAGTGACCCC 1856
Db 2851 CCTCGGCCGTGTGSCAGTTCGCAAAATGATCAAGTGCATGCCGGGGAGTGACCCC 2910
Qy 1857 TTYTTGGAATACAACAATACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCCGTG 1916
Db 2911 TTCTTGGAAATACAACAATACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCCGTG 2970
Qy 1917 GATGAACCTGGACAAAGTGAATCGCCTGCAGGAAATTTGGAGTGCCTGCCGGGGCGG 1976
Db 2971 GATGAACCTGGACAAAGTGAATCGCCTGCAGGAAATTTGGAGTGCCTGCCGGGGCGG 3030
Qy 1977 GGTGGGCA-CACGCCAAAGGATCTCACGAGGCATACAAAGGGGACTTGCATATCTGCTAA 2035
Db 3031 GGTGGGCAACCACGCCAAAGGATCTCACGAGGCATACAAAGGGGACTTGCATATCTGCTAA 3090
Qy 2036 GGATAACATATTTTCACTCTTGTCAAATAAACAATATGTTCCAAGAGGACCTGTAGC 2095
Db 3091 GGATAACATATTTTCACTCTTGTCAAATAAACAATATATGTTCCAAGAGGACCTGTAGC 3150
Qy 2096 GAAACGACCCCGTTAGAGATGGAAACAATGACCGACGTGCAAAACAGTGGSCGATGCTGC 2155
Db 3151 GAAACGACCCCGTTAGAGATGGAAACAATGACCGACGTGCAAAACAGTGGGCGATGCTGC 3210
Qy 2156 CCTCCAGTGGCAGAAATGTAGCAACAGTAAACAATCAACAGCAACTATCCACGTGTCATTTTC 2215

Db 3211 CCTCCAGTGGCAGAATGTAGCAACATTAACATCACAGCACCTATCCACGTGTCAATTTTC 3270
Qy 2216 TAGCAGTGGTTGTCACTGCACCTTCT-GAATACAGGATTTTACTGTATTCTTGCAACCAAT 2274
Db 3271 TAGCAGTGGTTGTCACTGCCCTTCTGGAATACAGGATTTTACTGTATTCTTGCAACCAAT 3330
Qy 2275 GTTAAAAATCGCTTTCAGGCCAGGCGGTGGCTCATGCCTGTAATCCAGCACATTGGG 2334
Db 3331 GTTAAAAATCGCTTTCAGGCCAGGCGGTGGCTCATGCCTGTAATCCAGCACATTGGG 3390
Qy 2335 AGGCCGAGGCGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGCT 2394
Db 3391 AGGCCGAGGCGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGCT 3450
Qy 2395 GAAACCCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTA 2454
Db 3451 GAAACCCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTA 3510
Qy 2455 ACCCCAGCTACTTGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCAAAGGTCGTCACTGCT 2514
Db 3511 ACCCCAGCTACTTGGGAGACTGAGTTGGAGGTTTCA-TGAGCCAAAGGTCGTCACTGCT 3569
Qy 2515 GTCCAGCCTGGTAAACAGAGCAACTCTGTCTCAAAAAAATAATGCTTTCAATAAATAT 2574
Db 3570 GTCCAGCCTGGTAAACAGAGCAACTCTGTCTCAAAAAAATAATGCTTTCAATAAATAT 3629
Qy 2575 ATGATAAAAGGACTTATATTTTTCAAGCCATAGGATCATTTCTCCTGAAGCATCTTGGC 2634
Db 3630 ATGATAAAAGGACTTATATTTTTCAAGCCATAGGATCATTTCTCCTGAAGCATCTTGGC 3689
Qy 2635 GAAGTCATCCCACTGTTCTTGAGAGTGGGCAGGTGAGGGCTGACCTATTGCTCTGCAC 2694
Db 3690 GAAGTCATCCCACTGTTCTTGAGAGTGGGCAGGTGAGGGCTGACCTATTGCTCTGCAC 3749
Qy 2695 TTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACCTGC 2754
Db 3750 TTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACCTGC 3809
Qy 2755 TAYGACCAGGCCAAGAAGCTGGACAGCTGTAATTTCTGCTGGACAMMCCGTACACCCAC 2814
Db 3810 TACGACCAGGCCAAGAAGCTGGACAGCTGTAATTTCTGCTGGACAACCCGTACACCCAC 3869
Qy 2815 ACCTATTCACTCGTGTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 2874
Db 3870 ACCTATTCACTCGTGTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 3929
Qy 2875 TTGACCTA 2882
Db 3930 TTGACCTA 3937

RESULT 11
ABD20768
ID ABD20768 standard; DNA; 6771 BP.
XX
AC ABD20768;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human pulmonary and inflammatory target DNA #379.
XX

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
OS Homo sapiens.
XX

PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 12161; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;

Query Match 53.8%; Score 2690.8; DB 11; Length 6771;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;

Qy 1 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGCTAGCTGT 60
Db 1062 CTGGTCATCTCAGTTCTTTTCTCACCTTGACTGCAAGATGAAACTCCTTGCTAGCTGT 1121
Qy 61 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCGCTTCTCTCCCAAGTGAGCTA 120
Db 1122 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCGCTTCTCTCCCAAGTGAGCTA 1181
Qy 121 AGATCTCACTCCTCTCGGAATGGGGCCACAGGCCACAGCAAAACAGGGATGGCCAGCCCG 180
Db 1182 AGATCTCACTCCTCTCGGAATGGGGCCACA---CACAGCAAAACAGGGATGGCCAGCCCG 1238
Qy 181 CAGTCTCAAWTCGAGGTTCCAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCTCAAG 240
XX

Db 1239 CAGTCTCAATTCGAGGTTCCCAAGT - GGGCTTAAGGGCTCCTCTAATGGGGTTCCCTCAAG 1297
Qy 241 GCTGGCACTTTTCAACCTGCAAGTCTGAAGTCTGAACTCAGATTGCCTGAGCTAAGAAAGCTTGCC 300
Db 1298 GCTGGCACTTTTCAACCTGCAAGTCTGAACTCAGATTGCCTGAGCTAAGAAAGCTTGCC 1357
Qy 301 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTTCAGTGGCA 360
Db 1358 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATAACCCAGGCTGGAGTTTCAGTGGCA 1417
Qy 361 TGATCATAGCTCACCCACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA 420
Db 1418 TGATCATAGCTCACCCACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA 1477
Qy 421 ACTAAGTAGTTAGGCCAATCTCCCAATTTATTTTATTTTATTTTAAATTTTATTTTATTT 480
Db 1478 ACTAAGTAGTTAGGCCAATCTCCCAATTTATTTTATTTTATTTTAAATTTTATTTTATTT 1537
Qy 481 TACTTTATTTATTTTGGACGGGGCTCACTCTGTGCGCCAGGCTGGAGTGCGGTGGCG 540
Db 1538 TACTTTATTTATTTTGGACGGGGCTCACTCTGTGCG - CCAGGCTGGAGTGCGGTGGCG 1596
Qy 541 TGATCTCAGATCACTACAACCTCCAATCTCTGAGCTCAAGTAGCTGGCACACACCACCATGCCCCAGCTAA 660
Db 1656 CTCAAGTAGCT - GGACTGTAGCTCTCAAGTAGCTGGCACACACCACCATGCCCCAGCTAA 1714
Qy 661 TTTTTTTGTGTTTTTTTTTGGTAGACAGGTTTTTCACCATGTTGGCCAGGCTGGGTGAC 720
Db 1715 TTTTTTTGTGTTTTTTTTTGGTAGACAGGTTTTTCACCATGTTGGCCAGGCTGGGTGAC 1774
Qy 721 CTCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCTTTCT - AATGCAGTATCCAG 779
Db 1775 CTCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCTTTCTAAATGCAGTATCCAG 1834
Qy 780 TTTCCCTTACTTATCACATTTTATTTATTTCTTATTATTATTGAGACAGAGTCTTGCTTTG 839
Db 1835 TTTCCCTTACTTATACACTTTTATTTATTTCTTATTATTATTGAGACAGAGTCTTGCTTTG 1894
Qy 840 TCGCCAAGGCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 899
Db 1895 TGCCCAAGGCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAAGCTCCAACCTGCTGGGT 1954
Qy 900 TCACGCCATTCTCCCGCCTCAGCCTCCCAGTAGCTGGGACTAAAGGCGCCTGCCACCAC 959
Db 1955 TCACGCCATTCTCCCGCCTCAGCCTCCCCAGTAGCTGGGACTAAA - GCGCCTGCCACCAC 2013
Qy 960 GCCCCGCTAATTTTTTTGTATTTTAAATAAAGACGGGGTTTTCATCGTGTAGCCAGGATG 1019
Db 2014 GCCCCGCTAATTTTTTTGTATTTTAAATAAAGACGGGGTTTTCATCGTGTAGCCAGGATG 2073
Qy 1020 GTCTCGATCTCATGACCTTGATCCGCCCTGCCCTCGGCTCCCAAAGTGTGGGATTACA 1079
Db 2074 GTCTCGATCTCATGACCTTGATCCGCCCTGCCCTCGGCTCCCAA - - TGCTGGATTACA 2131
Qy 1080 GGATGAGCCACCGTGCCCGCCTTATCACATTTATTTATTTATTTTCTCTCCCACT 1139
Db 2132 GGCATGAGCCACCGTGCCCGCCTTATCACATTTATTTATTTATTTTCTCTCCCACT 2191
Qy 1140 AGGTTGPAAGCTCCATGAGGTTAGAG - - ATTATTTATTTATTTATTTATTTATTTATTTA 1196
Db 2192 AGGTTGPAAGCTCCATGAGGTTAGAGATTATTATTATTATTATTATTATTATTATTATTATTA 2251
Qy 1197 TTATTATTATTATTATATCTGTTCACTGCTGTATCTCTAGTCTCTAGGACAGAGCCCTGGC 1256
Db 2252 TTATTATTATTATTATATCTGTTCACTGCTGTATCTCTAGTCTCTAGGACAGAGCCCTGGC 2311
Qy 1257 ACATAGTAAGTGCTCAATAAATAATTCACTGGATAAACAGTGCAGATAGTTTAAACTATC 1316
Db 2312 ACATAGTAAGTGCTCAATAAATAATTCACTGGATAAACAGTGCAGATAGTTTAAACTATC 2371

Qy 1317 TGACCTAGGGAGGCTGAGGAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTTGCAGTGA 1376
Db 2372 TGACCTAGGGAGGCTGAGGAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTTGCAGTGA 2431
Qy 1377 GCTGAAAATCGTGTCACTGCACTCCAACTGGGCAACAGAGCAAGACTCCAATCTCAAAAAA 1436
Db 2432 GCTGAAAATCGTGTCACTGCACTCCAACTGGGCAACAGAGCAAGACTCCAATCTCAAAAAA 2491
Qy 1437 AAAAAAAAACCTATCAGGCTAGCTGGGTGGCACATGCTGTAATCCTAGCTAGGCGGT 1496
Db 2492 AAAAAAAAACCTATCAGGCTAGCTGGGTGGCACATGCTGTAATCCTAGCTAGGCGGT 2551
Qy 1497 AGGTCCCAGAAGAAAGAAAGAAAAAGAAAGATATATATATATACACACACA 1556
Db 2552 AGGTCCCAGAAGAAAGAAAGAAAAAGAAAGATATATATATATACACACACA 2611
Qy 1557 CAAAGATATAAACCTTTATATATATAAAGTTTTTCATTAATAAAAAAAACCTCTACCC 1616
Db 2612 CAAAGATATAAACCTTTATATATATAAAGTTTTTCAT - AAAAAAAAACCTCTACCC 2670
Qy 1617 ACTTTCACTTTACAGGTTCTGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGT 1676
Db 2671 ACTTTCACTTTACAGGTTCTGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGT 2730
Qy 1677 CAGGGAGGCAGCGTGGACCCGAGGGAGCAGGAAGGAGTGTCCTCCCGGGGTGCTGGCA 1736
Db 2731 CAGGGAGGCAGCGTGGACCCGAGGGAGCAGGAAGGAGTGTCCTCCCGGGGTGCTGGCA 2790
Qy 1737 GACCGATTTGAACTCTGGCTATGTCTTCTTGCACTGGCGCCCGCMCAGCGGCATCAGC 1796
Db 2791 GACCGATTTGAACTCTGGCTATGTCTTCTTGCACTGGCGCCCGCAGCAGCGGCATCAGC 2850
Qy 1797 CCTCGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCGGGAGTGACCC 1856
Db 2851 CCTCGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCGGGAGTGACCC 2910
Qy 1857 TTYTTGGAATACAACAACACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGGTG 1916
Db 2911 TTCTTGGAATACAACAACACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGGTG 2970
Qy 1917 GATGAACCTGGACAAGTAAAGTATCCGCCTGCAGGAAATTTGGAGTGCCTGCCGGGGCGG 1976
Db 2971 GATGAACCTGGACAAGTAAAGTATCCGCCTGCAGGAAATTTGGAGTGCCTGCCGGGGCGG 3030
Qy 1977 GGTGGGGCA - CACGCCAAGGATCTCACGAGGCATACAAAGGGGACTTGCTATCTGCTAA 2035
Db 3031 GGTGGGGCACCAACGCAAGGATCTCACGAGGCATACAAAGGGGACTTGCTATCTGCTAA 3090
Qy 2036 GGATAACATATTTTCACTCTTGTCAAATAAACAATAATGTTCCAAGAGGACCCCTGTAGC 2095
Db 3091 GGATAACATATTTTCACTCTTGTCAAATAAACAATATATGTTCCAAGAGGACCCCTGTAGC 3150
Qy 2096 GAACGCACCCCGTTAGAGATGGAAACAATGACCCGACGTGCAAAACAGTGGGCGGATGCTGC 2155
Db 3151 GAACGCACCCCGTTAGAGATGGAAACAATTGACCCGACGTGCAAAACAGTGGGCGGATGCTGC 3210
Qy 2156 CCTCCAGTGGCAGAAATGTAGCAACAGTAAACATCACAGCAACTATCCAAGTGTCAATTTTC 2215
Db 3211 CCTCCAGTGGCAGAAATGTAGCAACATTTAAACATCACAGCACCTATCCAAGTGTCAATTTTC 3270
Qy 2216 TAGCAGTGGTTGTCACTGCACCTTCT - GAATAAGGATTTTACTGTATTTCTGCAACCCAT 2274
Db 3271 TAGCAGTGGTTGTCACTGCCTTCTTGGAAATACAGGATTTTACTGTATTTCTTGGCAACCAT 3330
Qy 2275 GTTAAAAATCGTTTTCAGGCCAGGCGGCTGGCTCATGCTGTAATCCCAGCACTTTGGG 2334
Db 3331 GTTAAAAATCGTTTTCAGGCCAGGCGGCTGGCTCATGCTGTAAATCCCAGCACTTTGGG 3390
Qy 2335 AGCCCGAGGCGGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGT 2394
Db 3391 AGCCCGAGGCGGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGT 3450

QY 2395 GAAACCCCTGCTCTACTAAAAATACAAAAATTAGCCGGACATGGTGGCGGCTGTA 2454
|||||
Db 3451 GAAACCCCTGCTCTACTAAAAATACAAAAATTAGCCGGACATGGTGGCGGCTGTA 3510
|||||
QY 2455 ACCCCAGCTACTTGGGAGACTGAGTTGGAGGTTTCAGTGAGCCCAAGGTCGTCACTGCT 2514
|||||
Db 3511 ACCCCAGCTACTTGGGAGACTGAGTTGGAGGTTTCA -TGAGCCCAAGGTCGTCACTGCT 3569
|||||
QY 2515 GTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAAATGCTTTCAATAAATAT 2574
|||||
Db 3570 GTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAAATGCTTTCAATAAATAT 3629
|||||
QY 2575 ATGATAAAAGGACTTATATTTTTCAGGCATAGGATCATTTCTCCTGAAGCATCTTGGC 2634
|||||
Db 3630 ATGATAAAAGGACTTATATTTTTCAGGCATAGGATCATTTCTCCTGAAGCATCTTGGC 3689
|||||
QY 2635 GAAGTCATCCCACTGTTCTCTGAGAGTGGGCAGGTGAGGGCTGACCTATTGCTCTGCAC 2694
|||||
Db 3690 GAAGTCATCCCACTGTTCTCTGAGAGTGGGCAGGTGAGGGCTGACCTATTGCTCTGCAC 3749
|||||
QY 2695 TTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGC 2754
|||||
Db 3750 TTACTCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGC 3809
|||||
QY 2755 TAYGACCAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCAC 2814
||:|||||
Db 3810 TACGACCAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAAACCCGTACACCCAC 3869
|||||
QY 2815 ACCTATTCTACTCGTCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 2874
|||||
Db 3870 ACCTATTCTACTCGTCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 3929
|||||
QY 2875 TTGACCTA 2882
|||||
Db 3930 TTGACCTA 3937

RESULT 12
ABD33466/c
ID ABD33466 standard; DNA; 42360 BP.
XX
AC ABD33466;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated (CA) gene HD07-089.
XX
KW Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW ds; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004058146-A2.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040081.
XX
PR 17-DEC-2002; 2002US-00322281.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
XX WPI; 2004-499109/47.
DR Novel human cancer associated protein encoded within open reading frame
XX of cancer associated gene, useful as targets for diagnosing cancer.
PT
XX
XX Claim 16; SEQ ID NO 618; 182pp; English.
PS
XX The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates

CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene.
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a human CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 42360 BP; 11698 A; 9658 C; 10445 G; 10559 T; 0 U; 0 Other;
Query Match 9.1%; Score 456.6; DB 13; Length 42360;
Best Local Similarity 99.8%; Pred. No. 3.5e-74;
Matches 456; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4545 ACAAAACTAATAAGATTCTCTGAAGGTAAGCAGAGATACGTAATATATGTAATAAGTT 4604
|||||
Db 42360 ACAAAACTAATAAGATTCTCTGAAGGTAAGCAGAGATACGTAATATATGTAATAAGTT 42301
|||||
QY 4605 TAAATGCATTTTAACTGTAATCTTATTGTTTATTGTTTATAAAAGTAAACAAGCCAAA 4664
|||||
Db 42300 TAAATGCATTTTAACTGTAATCTTATTGTTTATTGTTTATAAAAGTAAACAAGCCAAA 42241
|||||
QY 4665 AGTAATGCAACTTCAAACTCTACATAAATATCTATTATGGAAGTGGAAGGCATCTATAA 42181
|||||
Db 42240 AGTAATGCAACTTCAAACTCTACATAAATATCTATTATGGAAGTGGAAGGCATCTATAA 42181
|||||
QY 4725 TCCTACTACCCAAAGATAAACCAGTTACATATTTCCTCCAGATTTTTGGGGCATACACTAGC 4784
|||||
Db 42180 TCCTACTACCCAAAGATAAACCAGTTACATATTTCCTCCAGATTTTTGGGGCATACACTAGC 42121
|||||
QY 4785 TTTTTTTATTTGGGAAAATTTCCATGTGCAGGCATACCTAAATTTTCTAAATGTCATGT 4844
|||||
Db 42120 TTTTTTTATTTGGGAAAATTTCCATGTGCAGGCATACCTAAATTTTCTAAATGTCATGT 42061
|||||
QY 4845 AGTATTCCATTTAAGGATGTTCCATAATTTTAAATACATGCTTTAAAGTAGAGAACT 4904
|||||
Db 42060 AGTATTCCATTTAAGGATGTTCCATAATTTTAAATACATGCTTTAAAGTAGAGAACT 42001
|||||
QY 4905 AGGTTGGGCATGGTGGCTCACGCCTGTATCCCAGCACTTTGGGAGGCCGAGGCAAATGGA 4964
|||||
Db 42000 AGGTTGGGCATGGTGGCTCACGCCTGTATCCCAGCACTTTGGGAGGCCGAGGCAAATGGA 41941
|||||
QY 4965 TCACTTGAGGTCCGGAGTTTGAGACCAGCCTGGACAA 5001
|||||
Db 41940 TCACTTGAGGTCCGGAGTTTGAGACCAGCCTGGACAA 41904
|||||

RESULT 13
ADP13332/c
ID ADP13332 standard; DNA; 126990 BP.
XX
AC ADP13332;
XX
DT 26-AUG-2004 (first entry)
XX
DE Renal cell carcinoma differentially expressed gene #68.
XX
KW ds; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression.
XX
OS Homo sapiens.
XX
PN WO2004048933-A2.
XX
PD 10-JUN-2004.

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XX 21-NOV-2003; 2003WO-US037481.
PF
XX
XX 21-NOV-2002; 2002US-0427982P.
PR
XX 03-APR-2003; 2003US-0459782P.
PR
XX
XX (AMHP ) WYETH.
PA
XX (TWIN/) TWINE N C.
PA
XX (BURC/) BURCZYNSKI M E.
PA
XX (TREP/) TREPICCHIO W L.
PA
XX (DORN/) DORNER A.
PA
XX (STOV/) STOVER J A.
PA
XX (SLON/) SLONI D K.
XX
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA,
PI Sloni DK;
PI
XX
XX WPI; 2004-460799/43.
DR
XX
XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 68; 350pp; English.
PS
XX
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a gene that
CC is differentially expressed and detected by the method of the invention.
CC (Note: this sequence is not given as part of the printed specification
CC but was obtained from WIPO in electronic format at
CC ftp.wipo./pub/published_pct_sequences).
XX
XX Sequence 126990 BP; 36683 A; 27389 C; 27065 G; 35853 T; 0 U; 0 Other;
SQ
Query Match 8.9%; Score 444.4; DB 12; Length 126990;
Best Local Similarity 54.1%; Pred. No. 7.2e-72;
Matches 1225; Conservative 3; Mismatches 987; Indels 51; Gaps 14;
QY 2291 AGCCAGCGCGGTGGCTCATGCCCTGTGATCCAGCACTTTGGAGGCCAAGGTGGGTGG 2350
Db
28169 AGCCAGCGGTGATGGCTCATGCCCTGTGATCCAGCACTTTGGAGGCCAAGGTGGGTGG 28110
QY 2351 ATCACTGAGGTCAGGAGTTTCGAGACCAGCCCTGGCCAACATGGTGAAACCCTGTCTCTAC 2410
Db
28109 ATCACGTGAGGTCAGGAGTTTGAGAACAGCCCTGGCCAACATGATGAAACCTTGTGCGCCAC 28050
QY 2411 TAAAAAATACAAAAAATTAGCCGGACATGGTGGCGAGCGCC-----TGTAACCCCGAGCTAC 2465
Db
28049 T-AAAAATACAAAAATTAGCTGGCCGTGGTGCGAGACACCTATAGTCTAGTCCTAGCTAC 27991
QY 2466 TTGGGAGACTGAGTTGGAGGTTTCAGTGAGCCAAAGGTCGTGTCTACTGCTGTCCAGCCTGG 2525
Db
27990 TTGGGAGGCTGAGCGGGGGAATCGTTGAAACCCGGGAGGTAGAGGCTGAAAGTGAGCTGAG 27931
QY 2526 GTAACAGCAACTCTGTCTCAA-----AAAAAAAATGCTTTCAATAAATATATGATAA 2581
Db
27930 ATCACACCACTGCACCTCCAGCCTAGGTGACAGAGCAAGGCCCTCATCTCAAAAAACAATG 27871
QY 2582 AAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCCTGAAGCATCTTGGCGAAGTCA 2641
Db
27870 GTGGGCCAGGCACGGTGGCTCACGTCAGTAATCCAGCACTTTGGGAGGCCAAGGCGGGC 27811
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QY 2642 TCCCCACCTGTTCTCTGAGAGTGGGCAGGTGAGGGCTGACCTATTGCTCTGCACTTACTCC 2701
Db
27810 AGATCATGAGGTCAGGAGATCAAGACCATCTCTGGCTAACACGGTGAAACCCCGTCTCTAC 27751
QY 2702 TATCTCAGCTGTCCCTCCCACTTTTCCAGGTGCTGCCAGACACATGACAACTGCTAYGACC 2761
Db
27750 TAAAAATACAAAAAATTAGCCGGGCATCGTGGTGGCGCCTGTAAATCCCAGCTACTTGGG 27691
QY 2762 AGCCCAAGAAGCTGGACAGCTGTAAATTTCTGTGGACAMMCCGTACACCCACACCTATT 2821
Db
27690 AGGCTGAGCGGGGAGAAATGGCGTGAACCCGGGAGCGGAGCTTGCAGGGAGCGAGATCG 27631
QY 2822 CATACTCGTGTCTGTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTCTTGACCT 2881
Db
27630 CACTGTGCGCTCCATFTCCAGCCTGGGAGACAGAGTGAGACTCCATCTCTCAAAACAACA 27571
QY 2882 ATGAATTCTAGTTGGTTCTCAGTAGGCCGGGGGAAAAATAATAGTAAC-----AACAG 2933
Db
27570 AAACAAACAAACAAAGTGGTGGGCATGCCTCTAATCCTAGCTACTTGGAGAGGTGAG 27511
QY 2934 CCATGATTTAGTGTTAATTTTCTTGGTTCTGGGAGTGCTCTCCTTTAATCCTCAGAACAA 2993
Db
27510 GCAGGAGAAATCGCTTGAAACCCCGGAAGCAGAGGCTGCAGTGAGCCCAAGATCACACCACTG 27451
QY 2994 CACTATGGGATAGGT-ACAATTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAAG 3052
Db
27450 TACTCCAGCCTGGGTGACAGAAACGAGACTCTCCATAAGTTTCACATGAAAAATACACCAAT 27391
QY 3053 GCTGAGCTATTTGCCCAAGATCACACAGCTTTGTAAGTGGTGACAGTTTGGGTTTTTTTTT 3112
Db
27390 TCTAATCCGACACCGCAAGATTTACTCTAGCCTTCACCATGTCCATATCTTTAACTCCTT 27331
QY 3113 GTTGTGTTTAGAGACAGGGTCTTGTCTGTCAACCCAGGCATGAGCACAGTGGTGAACC 3172
Db
27330 TCTCTAATGCTGAGATGGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGGTGTGATC 27271
QY 3173 ATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGCCTCCCAA 3232
Db
27270 TCA-----CCTCCACCTCCAGGTTCAAGGATTTCTCTGCTCAGCCTCC-TG 27223
QY 3233 GTAGCTGGGACTACGAGCGTGCACACCACCGCCTGGCTAATTAATAAAAAATTTTTTTGTAG 3292
Db
27222 GTAGCTGGGAATACAGCGTGCACCACCATGCCCCGGCTAATTTTTTATA--TTTTCAGTAG 27165
QY 3293 AGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTC 3352
Db
27164 AGTCGCAGTTTCAACCATGTTTCCAGGCTGGTCTCAAAACTCCTGACCTCAAGTGATCCAC 27105
QY 3353 CTACCTTGGCATCCCAAGTGTGGGATTACAGGGTGAGCCACCATGTGCGGCTACTTA 3412
Db
27104 CCGCCGAGCCTCCCAACGTGTGGGATAATAGGGGTGAGCCACTGCACCTGGCCTTCT 27045
QY 3413 TTTCCTTTACATTCCATCTTTTCCAATAGAATGTAAAGATCCACAGAACAGGATTAAGCCT 3472
Db
27044 GTACTCTTTATTCTATTTCAGTGGTCTGTTTCTTTGGTTTCAGTATCATAGTACTTTTG 26985
QY 3473 ATTTTCTTCTTTCTTTTGGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTCAGC 3532
Db
26984 TTCTGTAGCTTAAATAAT-ATATAATTTTAAGACTGGAATGCAGTGGCATGATCTCAGC 26927
QY 3533 TCACTGCAACCTCTGCTCCCGGTTTCAAGYATTTCTCTGCTGCCCTAAGCCTCCTGAGTAGC 3592
Db
26926 TCACTGCAACCTCCACCTCCAGGCTCAAAATTATTCTTGTGACTCAGCCTCCTGAGTAGC 26867
QY 3593 TGGAAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTTTTGTATTTTTTAGCAGATGG 3652
Db
26866 TGGGATTACAGGCAGGCAGCCACCATGCCCCACTAA-TTTTTGTATTTTTCAGTAGAGTGA 26808
QY 3653 GGTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGTATCTGCTGCCT 3712
Db
26807 AGTTTCACCATGTTTCTTAGGCTGATCTTTAAACTCCTGACCTCGAGTGTATCCGCCCGCT 26748
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QY	3581	CTCCTGAGTAGCTGGAATTACAAGCGGTGCACCAACCATGCTTGGCTAAATTTTGTGATTTT	3640
Db	18577	CTCCCAAGTAGCTGGGACTACAGGCATGCGCCACCCACCTGGCTAA-TTTTTGTGATTTT	18635
QY	3641	TAGCAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTG	3700
Db	18636	TAGTAGAGACGGGTTTACCATGCTGGCCAGGCTGGTCTCGAACTCCTGACCTC--GTG	18693
QY	3701	ATCTGCCCTGCCTCAGTCTCCCAAAGTGTGGAAATTATAGGCGTGAGTCACGTGTGCCTGGC	3760
Db	18694	ATCCACCCGCTCAGCTTCCCAAAGTGTGGGATTACAGGCATGAGCCACCATACCTGGC	18753
QY	3761	CGATTACTGTCTATTTT-----CTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTG	3814
Db	18754	CAGGAACCTAGACAGTTTTTAGAGACATCTTTCTGAAATAGGGCTGGTGGCCCTCATATTTC	18813
QY	3815	ACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTT	3874
Db	18814	ATTAATGCTATTTTCTCCAAAACCCGGGAACCAAAATAGATGTGATAGCATGGCATCCCTC	18873
QY	3875	TTTCTTTTTTAAAAACAATCTTGACAACCTTTGCAGAAATAAATACAAATCTTGCATTTCTGCT	3934
Db	18874	ATGATCTGAAGTTACTGTCCGTAACCTGCGGTCCCAATTCGATTTGGATATTGGGGGATGCC	18933
QY	3935	TTTTCACTTATCA-CTTGTATTGACTTTTTCATATTGCCCTCAAAACCTTTATTGTGTACTG	3993
Db	18934	TGCACGTGTGTGTCATGTGTCATGTCTGCGGTGCCATCAGTCTGTGAGCTCCCTCT	18993
QY	3994	TTTTTTTCATTGTTACTATTTTAGTCACCTGAATAATATGSGCTTAATTTGCTTATACATCCT	4053
Db	18994	GGGCTGCGTCCGTTTTTCTCATCTCTTGTATTATCTCAGCACTTTGTACAATACCTGGC	19053
QY	4054	CCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCCTCC	4113
Db	19054	ACTCAATGAATTAAAAATAATCTGAACGGGGGTTGGGGGAGCTTGTCAATATAGCCCC	19113
QY	4114	AGAGAAATACACACACACACACACTCACACAGTTTTTTTTTAATGTTTGCACCTAA	4173
Db	19114	ACCTTGTTTGGCCCTTGGACTTGATGAAGCCGTTTGTGCTATGCATATGTCATCTCTT	19173
QY	4174	GACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATAAAAAATAACTCA-----	4226
Db	19174	TTCTAGACATGAGTTACTTGGATGAATAGGCAGATCTCTTGTTAAACCATAAAGACAG	19233
QY	4227	GTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTGGAGTCCAAGGTGGGTGAT	4286
Db	19234	GCTGGCGCGGTGGCTCACATCTGTAACTCCAGCACTTTGAGAGGCCGAGCGGGCAGAT	19293
QY	4287	CACCTGAGGTGAGAAAGTTCGAGACCGAGCTGGTCAATATGTTGAAACCTTATCTCTACTA	4346
Db	19294	CACCTGAGGTAGAAAGTTCGATACCCAGCTGGCCACACATGTTGAAACCCCAATCTCTACTA	19353
QY	4347	AAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGSGAGG	4406
Db	19354	AAAAATACAAAAATTAGCCGAGTGGGTGGCGCATGCCCTGTAATCCTAGCTACTTTGGGAGG	19413
QY	4407	CTGAGGCAAGAGAATTGCTTGAACCTTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCAC	4466
Db	19414	CTGAGGCAAGAGAATCGCTTGAACCCCGGAGGTGAAGCTTTTCAGTGAGCCGAGATTGTGC	19473
QY	4467	CACCTGCACTCCAGCCTGGGCGACACGCGAGACTCTATCTCAAAAAATAAATAATAA	4526
Db	19474	CATTACACTCCAGCCTGGGCAACAGAGCCAGACTGTGTCTCAAAATGAAAAACCCATAAAG	19533
QY	4527	ATA	4529
Db	19534	ACA	19536

AC	ACN43914;
XX	18-NOV-2004 (first entry)
XX	Human genomic sequence HCG26773.
DE	Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX	Homo sapiens.
KW	WO2003073826-A2.
XX	12-SEP-2003.
PD	28-FEB-2003; 2003WO-US006235.
XX	01-MAR-2002; 2002US-00087192.
PX	(SAGR-) SAGRES DISCOVERY.
XX	Morris DW;
PI	WPI; 2003-328604/31.
XX	Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
PT	Claim 1; SEQ ID NO 100; Opp; English.
PT	The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
XX	Sequence 160482 BP; 44060 A; 32143 C; 33530 G; 49875 T; 0 U; 874 Other;
SQ	Query Match 8.7%; Score 434.2; DB 11; Length 160482; Best Local Similarity 60.2%; Pred. No. 5.7e-70; Matches 888; Conservative 1; Mismatches 525; Indels 61; Gaps 8;
QY	3106 TTTTGTGTTGGTTTAGAGACAGGGTGCTTGCTCTGTACCCAGGCATGAGCACAGTGG 3165
Db	5181 TGTTTTTTTTTCTCTCGATACGGAGTCTTGCTCTGTTGCCAGGCTGGAGTCAGTGG 5122
QY	3166 TGCAACCATAGGTCACTGCAGCCTCAACTCTCTGAGCTCAAGGGATCTGCTGACCTCAGC 3225
Db	5121 CATGATCTGGGCTCACTGAACCTCTGCCTCTCTGGGTTACGTGATTCTCCTGCCTCAGA 5062
QY	3226 CTCCCAGTAGCTGGGACTACGAGCGTGCAACCACCCAGCCTGG--CTAATTAATAAAATT 3283
Db	5061 CTCCCAGTAGCTGGGATTACAGGCGTGAGCCACCATGCTGCCCCCTAATGTTTGTATT 5002
QY	3284 TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCAA 3343
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QY	3344 GCAATCCTCCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGC 3403
Db	4942 GTGATCCGCCTGCCTTGATGTACCAAGTGTCTGGGATTACAGATGTGAGCCACCCGCC 4883
QY	3404 GGCTACTTATTTCTTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGA 3463
Db	4882 GGCCAGTCATTCACTTCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTGTC 4823

QY	3464	TTACTGCCTATATTTTCTTCCTTTCTTTTTTTTGAGACAGAGTCTCATTTCATCACCCTCAACCT	3523
Db	4822	ATCCAGGCTGGAGTGT-----AGTGGCAC	4799
QY	3524	CCGTTCACTCACTGCAACCTCTGCCCTCCCGGGTTCAAGYGATTTCTCCTGCCTAAGCCTC	3583
Db	4798	GATCTCGGCTCACTTCAACTTTTCACCTCCCGGGTTCAAGTGATTTCTCCTGCCTCAGCCTC	4739
QY	3584	CTGAGTAGCTGGAATTACAAGCGTGCACCACTCATGCTTGGCTAAATTTTTTGTAATTTTAG	3643
Db	4738	TTGAGTAGCTGGGATTACAGGCATGCACACCGCACCCGCTAAATTTTATATTTTGG	4679
QY	3644	CAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC	3703
Db	4678	GAGAGATGGGTTTACCATGTTAGACAGGCTGGTCTCAAACTCCTGACCTCAAGCAATC	4619
QY	3704	TGCCTGCCTCAGTCTCCCAAAGTCTCGGAATTATAGGCGTGAGTCACCTGTGCCCTGGCCGA	3763
Db	4618	TGCTCGCCTTGGCCTCCTAAAGTCTGGGATTACAGGCGTGAGCCACACACCCGGCCAA	4559
QY	3764	TTACTGTCTATTTTCTTTATTGCTATATATCCCCAGATCTAGAGCAGTGCTTGACATATAGT	3823
Db	4558	--ATCATTCACCTTCTACAACAAGTTCGTCTGTATGCCAATGAATCTCAGGACTGTACT	4501
QY	3824	AGTGCTCAATAAATAAATTGATGAATGCACAGCCTAGATATAAACTTTTCTTTTCTTTT	3883
Db	4500	TCTAGCTCTAAACCTCTAAACATATATTTAAAGTGTCTTTAAAGCCAGGACTTAGATTCT	4441
QY	3884	TTAAACAATCTTGACAACTTTTGCAGAAATAAATAACAATCTTGCAFTCTGCTTTTTCACTT	3943
Db	4440	CAGAATCTCAAAATCAACAAATCCAAATTCAAATATATTTTCCCTAAATTTCTGCCCT	4381
QY	3944	ATCACCTTGTA-----TGACTTTTTCATATTGCCTCAAACTTTTATTGTTACTGTTTT	3997
Db	4380	TTCTCTGTATTTCCCTAGTTTGCTTAATAGTATCACCTTAAATTCAGGAAGAAATTTCAAA	4321
QY	3998	TTCAATTGTTACTATTTTAGTCACTGAAT--AATATGGCTTAATTTGCTTATACATCCTCC	4055
Db	4320	GTCATCTTCAATTTTCTCTCTCAACGCAATAAAGCACTAATTCCTAGAAGCTCAACC	4261
QY	4056	TGCTCCACTTTAGAAGGCCAAATTTACAATCTGATGAAAGCTATGAACCTCTCCTCCAG	4115
Db	4260	TTAAACAGTCCCTCTGGAAATGAGATGAAGGTTAACAGTTACTGAACACAGACCCAAACTAG	4201
QY	4116	AGAAATACACACACACACACACTCACACAGTTTTTTTTTTAAATGTTTGCAACTAAGA	4175
Db	4200	GCACAGCAGCAAGGTTGTTCAATTGAATTCAATTTCTCTCAGAAGCCCTAAGGAATAGCT	4141
QY	4176	CAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAATAAAT-----AACTCAGTT	4229
Db	4140	CCAATTTTATAGGAAGAAACTGAGGTTCCAAGAAGTAAGAAATTCACACAAGGAGCT	4081
QY	4230	GGGCACAGTGACTCAAGCCTGTTAACCACAGTACTTTGGAAGTCCAAGTGGGTGGATCAC	4289
Db	4080	GGGTGGTGGCTCAGCCTGTAATCCTAGCACTTTGGGAGGCCAAGCGGGCAGATCAC	4021
QY	4290	TTGAGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAA	4349
Db	4020	CTGAGGTCAAGAGCTCGAGACCAGCCTGACAAACATGGTGAAACCCCATCTCTACTAAAA	3961
QY	4350	ATACAAAAATTAGTGGGTGTAGTGATGCTGCTGTAGTCCCAGCTACTCGGGAGGCTG	4409
Db	3960	ATACAAAAATTACCAGGTGTGGTGGTGACGCTGTAATCCCAGCTATTTGGGAGGCTG	3901
QY	4410	AGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCC-----GAGATCC	4463
Db	3900	ACGAGGAGAAATTGTTTGAACCCAGGAGGCGAGGTTGCAGTGAGCCAAAGATGGAGATCG	3841
QY	4464	CACCACTGCACCTCCAGCCTGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAT	4523
Db	3840	TGCCACTGCACCTCCAGCCTGGGCAACACAGCGAGACTCTGTCTCCAAAAAATAAATAA	3781

QY	4524	AAAAATAAAGGATCGGAGAGAAAAACAACTAATAAG	4558
Db	3780	AGAAAGAAAGAAAGAAAAATAAATTCACACAAG	3746
RESULT 16			
ACN44410/C			
ID	ACN44410	standard; DNA; 91760 BP.	
XX	AC	ACN44410;	
XX	DT	18-NOV-2004 (first entry)	
DE		Human genomic sequence hCG41365.	
XX		Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.	
OS		Homo sapiens.	
XX	PN	WO2003073826-A2.	
XX	PD	12-SEP-2003.	
XX	PF	28-FEB-2003; 2003WO-US0006235.	
XX	PR	01-MAR-2002; 2002US-00087192.	
XX	PA	(SAGR-) SAGRES DISCOVERY.	
XX	PI	Morris DW;	
XX	DR	WPI; 2003-328604/31.	
XX		Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.	
PT		Claim 1; SEQ ID NO 844; Opp; English.	
PS		The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published	
SQ		Sequence 91760 BP; 21177 A; 23589 C; 24129 G; 22845 T; 0 U; 20 Other;	
		Query Match 8.7%; Score 433.2; DB 11; Length 91760;	
		Best Local Similarity 61.6%; Pred. No. 8e-70;	
		Matches 906; Conservative 1; Mismatches 474; Indels 89; Gaps 10;	
QY	3106	TTTTTTTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTACCCAGGCATGAGCACAGTGG	3165
Db	5566	TTTTTTGTTTAAATTAGAGACTGGGTTTGCTCTGTGCCCCAGGATGGAGTACAGTGG	5507
QY	3166	TGCAACCATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGTCACCTCAGC	3225
Db	5506	CATGATCATGGCTCACTACAACTCTGCCTCCTGGGCTCAGGCAATCCTCCACCTCAGC	5447
QY	3226	CTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCTGGTAAATAAAAAAT-TT	3284
Db	5446	CT-CCGAGTAGCTGGAACACTACAGGTGAGCACCCACACACCTGGCTAATTTATTTTATT	5388
QY	3285	TTTTGTAGAGACTGGGTCTTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAG	3344

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QY 3345 CAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATTGTGC 3404

Db 5333 TGATCCTCCCACTCGGCCTCTCAAAGCGTGGGATTCCAGGTGTGAGCCTCTACACCCA 5274

QY 3405 GCTACTTATTTCCTTT-----ACATTCCATCTTTCC 3434

Db 5273 GCTCATAAATACCTTTTAAATACCCAGATAATCTTGCTGCTGGCCAAAGAACAACTTTT 5214

QY 3435 AATAGAAATGAAGATCCACAGAACAGGGATTACTGCCTATTCTTCCTCTTCTTTTGA 3494

Db 5213 ACTTGCTCCCAAAATCTAAAGAAATAGTACTATAG--ACTTGATTCTCTTTTAA 5157

QY 3495 GACAGAGTCTCACTTCATCACCTCAACCTCCGTTTCAG-----CTCACTGCA 3540

Db 5156 GGTGAGTATTGTTCTGTGCGCTAGGCTTGAGTGCAGTGGTGTGATCTTGACTCACTGCA 5097

QY 3541 ACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTA 3600

Db 5096 ACCTCCTCTTCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCAGAGTAGTGGGACTG 5037

QY 3601 CAAGCGTGACCAACCATTGCTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGTTTTAC 3660

Db 5036 CAGGTGCGTCCACCACGCCAGCCAGCTAAATTTTATATTTTGTAGAGATGGGTTTCAC 4977

QY 3661 CATGTTGCCAGGCTGGTCTCAAACCTCTGACCTCAAGTGATCGCTGCCTCAGTCTCC 3720

Db 4976 CACTTTGGCCAGGCTGGTCTCGAACTCTGACCTCAAGTGATCCACCTGCCTCGACCTCC 4917

QY 3721 CAAAGTGCTGGAATTATAGCGGTGAGTCACTGTGCTGCGCCGATTACTGTCTATTTTCTT 3780

Db 4916 CAAAGCGCTGGGATTATAGGCATGAGCCAATGCATCTGGCTGAAAGGATAAATCTTCTC 4857

QY 3781 TATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATATAGTGGTCTCAATAAATAA 3840

Db 4856 TTTTTTAGCATTTTCTTCTGGTCAATACAGCCA-----TGCTGGTACATACA 4810

QY 3841 TTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTAAACAATCTTGACA 3900

Db 4809 TGTTTTCTGGCTGATTTTGACCTGTGACTTTCTTTTCTTCTCTCTTCTTCTTCTTCT 4750

QY 3901 ACTTTGCAGAATAAAATACAATCTTGCAATCTGCTTTTTCATCTATCACCTTGTTATGACT 3960

Db 4749 CTTCCTCTCTT--CCTCCTCCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTCTT 4692

QY 3961 TTTTCATATTGCTTCAAACCTTTATTGTACTGTTTTTTTCAITGTACTATTTTAGTCAC 4020

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QY 4021 TGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAATTT 4080

Db 4631 CTTTCCTCTTCT 4584

QY 4081 ACAAAATCGATGAAAGCTATGAACCTCTCTCCCGAGAGAAATACACACACACACACT 4140

Db 4583 CCTCCTCTCCCT 4524

QY 4141 CACACACAGTTTTTTTTTAATGTTGGAACTAAGACAAGAACCTGCATTAGAGGATGTT 4200

Db 4523 TCTTCTCTTCTCTTCT 4471

QY 4201 TGTTCAATTAATAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACTAGT 4260

Db 4470 CTTTTCTTTTTTAAATATAGAGACAGGCCAGGTGCGGTGGCTGACGCCTGTAATCCCAAC 4411

QY 4261 ACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTTCGAGACCAGCCTGCTC 4320

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QY 4321 AATATGGTGAACCCCTATCTCTACTAAAAATACAAAAATTTAGCTGGGTGTAGTGATCAT 4380

Db 4350 AACATGGTGAAACTCGGTCTCTACTAAAAATAAAAAATTAGCTGGGTGTGGTGGGT 4291

QY 4381 GCCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGSCA 4440

Db 4290 GCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCCCTTGAACCCAGGAGCG 4231

QY 4441 GAGGTTGCAGTGAGCCGAGATCCCACCACCTGCACCTCAGCCTGGCGGACACAGCGAGACT 4500

Db 4230 GAGGTTGCAGTGAGCCGAGATCACGCCACTGCACCTCAGCCTGGGATATATAGAGAGAA 4171

QY 4501 CTATCTCAAAAAATAATAATAATAATAA 4530

Db 4170 CCATCTCAAATAATAATAATAATAATAATAA 4141

RESULT 17

ADP45591

ID ADP45591 standard; DNA; 92500 BP.

XX

AC ADP45591;

XX

DT 26-AUG-2004 (first entry)

XX

DE Human intercellular adhesion molecule ICAM-1/ICAM-4/ICAM-5 gDNA.

XX

KW breast cancer; cytostatic; gene therapy; human;

KW intercellular adhesion molecule; ICAM-1; human rhinovirus receptor; BB2;

KW CD54; cell surface glycoprotein P3.58; ICAM-4;

KW Landsteiner-Wiener blood group; ICAM-5; telencephalin; chromosome 19p13;

KW ds; gene; SNP; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

PH Key

FT variation

FT Location/Qualifiers

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Query Match 8.6%; Score 429.8; DB 12; Length 92500;
Best Local Similarity 50.9%; Pred. No. 3.4e-69;

Db 19197 AAGTAAATAAAATACAA 19215

RESULT 18

ADX98568

ID ADX98568 standard; DNA; 92600 BP.

XX

AC ADX98568;

XX

DT 05-MAY-2005 (first entry)

XX

DE Human intercellular adhesion molecule (ICAM1, ICAM4, ICAM5) genomic DNA.

XX

KW SNP detection; breast tumor; endocrine disease;

KW gynecology and obstetrics; neoplasm; cytostatic; metastasis;

KW gene therapy; RNA interference; intercellular adhesion molecule; ICAM1;

KW ICAM4; ICAM5; chromosome 19; ds; SNP; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

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FT /*tag= an

FT /standard_name= "Single nucleotide polymorphism (SNP)"

FT 29877

FT /*tag= ao

FT /standard_name= "Single nucleotide polymorphism (SNP)"

FT 30194

FT /*tag= ap

FT variation

8

Db	16302	AATCACTTGAA	CCCAGGAGGTGGAGGTTGCAGTGAGCCGACACATC	CACGGCACATCT	16361	
QY	1562	ATATAAACTTTATATATATAA	AGTTTTTCATTA	AAAAAAAAAAAAACCTCTACCCACTTT	1621	
Db	16362	AAAAAAAAAAAAAGTTTTTCTG	TTTTTGT	TTTTTGTGCAAACTACTGAAATAAATACAGTGA	16421	
QY	1622	CAC	TTTACCAGGTTCTCTGGGTCCAA	CGGTCTTTCAGAGGAGGCAGCTGGCAGGGTCAGGG	1681	
Db	16422	GATA	TTTATTTATAAAATGAGAACGAATTA	ATAATGAGCCGTFAGGCTGGGTGTGGTGGCTC	16481	
QY	1682	AGGC	-----	AGCGTGGGACCCGAGGGAGGAGGCAAGGCAGTGTGTCCC	1723	
Db	16482	ATGCCTATAATCCAGCA	TTTTTGGGGGCCAAGGCAGGTGGAACAC	ATTGAGGTCAAGAGT	16541	
QY	1724	CGGGGTGCTGGCAGAC	CCGATTTTGA	ACTCTGGCTATGTCTTTCTTTCAGTGGCCCGCCCGM	1783	
Db	16542	TCGAGACCAGGCTGACCA	ATATAGTGGAA	CCCCCATCTCTACTAAAAATACAAAAGAA	TTA 16601	
QY	1784	CAGCGGCATCAGCCCTCGGGCCG	TGTGGCAGTTC	CGCAAAATGATCAAGTGGC	----- 1836	
Db	16602	GCCGGGCA	TGGTGC	CGGCCCTGTAATCTCAGCTATGGGAGGCTGAGGTAGGAGAA	TCG 16661	
QY	1837	-TGATCCCGGGAGTGAC	CCCTTYTTTGAATACAA	CAACTACGGCTGCTACTGTGGCTTG	1895	
Db	16662	CTTAA	CCCTGGAGGCGGAGGTTGCAGTGAGGCGGATATC	ACGCCCACTGC	CACTCCAGCCTG 16721	
QY	1896	GGGGGCTCAGGCAC	CCCCCGTGGATGA	ACTTGACAAGTAAGTATCCGCTGCAGG	AAAAAT 1955	
Db	16722	GGGACAGAGCGGAGACT	CCATCTCTAAATAAATAAATAAGGAGCTGTATTTCA	AAAAATTG	16781	
QY	1956	TGGAGTGCCTGCCGGGGGGGGTGGG	CACACGCGCAAGGATCTCAGGAGGCATAC	AAAG	2015	
Db	16782	GAGAAGGTGACACTGAGAGTACTGA	ATACACAGTTTTTTTGT	TTTTTTTGAG	16841	
QY	2016	GGGACTTGCATATCTGCTA	AGGA-----	TAACATATTTTCACCTCTTGTCAA	2062	
Db	16842	ACAGAGTCTCGCTCTGTCA	CCCAGGCTGGAGTGCA	GTGGTGCAACCTCGGCTCACTGCAA	16901	
QY	2063	ATAACA	AAATATGTTTCCAAGAGGAC	CCCTGTAGCGAACGCA	CCCCGTTAGAGATGGA	AAACA 2122
Db	16902	TCTCTGCCTCCCGGTTTCAAGCA	AAATCTCTGCCTCAGCCTCCGCGTAGCTGGGAT	TACA	16961	
QY	2123	ATGACCGACGTGCA	AAACAGTGGGCGATGCTGCCCTCCAGTGGCAGAA	TGTAGCAACAGT	2182	
Db	16962	GGCACGCATCCCA	TGCCCTGGCTAATTTTGTATTTTATAGTAGACGGGATTT	CACCAT	17021	
QY	2183	AAACATCA-----	CAGCAACTATCCACGTGTCA	TTTTTCTAGCAGTGGTTGTCACTGCA	2235	
Db	17022	ATTGGTCAGGCTGATCTCAA	ACTCTGACCTCGTGATCTGCCTGCCTCGGCCTCCCAAG	17081		
QY	2236	CCTTCTGAATACAGGATTTT	TACTGTATTTCTTGCAACCATGTTAA	AAAAAT-----	2283	
Db	17082	TGCTGGGATTACAGGCGTGAGCC	ACCGAGCCTGGCCCCCAAAAAATATTTATCA	AAAAACTAT	17141	
QY	2284	-CGCTTTCAGGCCAGGCGGTGGCT	CATGCTGTAAATCCAGCACTTTGGGAGGCCGAG	2342		
Db	17142	GTTAATGCTGGCCGGGTGCGGTGGGCT	CATGCTGTAAATCCAGCACTTTGGGAGGCCGAG	17201		
QY	2343	GCGGGCGGATCACTTGAGGT	CAGGATTCGAGACCGCTGGCAACATGGTGAA	ACCCT	2402	
Db	17202	GCAGGTGGAACAC--	GAGGTGAGGAGATTGAGACCATCCTGGCTAACACCGGTGAA	ACCCC	17259	
QY	2403	GTCTCTACTAAAAA	TAC-AAAAATTAGCCGGACATGGTGGCGAGCGCCTGT	AACCCAG	2461	
Db	17260	GTCTCTACTAAAAA	TACAAAAAATTAGCCGGCGGCTGGTGGGTGCCTGTAGTCCCAG	17319		
QY	2462	CTACTTGGGAGACT-	-----	GAGTTGGAGGTTTCA	GTGAG 2495	
Db	17320	CTACTCAGGAGGCTGA	AGCAGGAGAA	TGGCAGGAACCGGGAGGCAGAGGTTGTAGT	GAG 17379	
QY	2496	CCAAGGTCTGTCTACTGT	CTCAGCCTGGGTAA	CAGAGC--AACTCTGTCTCA	AAAAAAA 2553	
Db	17380	CTGAGATCGGCCAT	TGCAC	TCCAGCCTGGGCGACAGAGCGAGAA	TCCGTCTCG	AAAAAAA 17439

Qy	2554	AAAAATGCTTTTCAATAAAATATATGATAAAAAAGGACTTATATTTTTTCAAGCCATAGGATCA	2613		
Db	17440	AAAAAATAATACACACACACACACAAAAAACTGTGTTAATGCTTAACCTACACAAAAATGAT	17499		
Qy	2614	TTTCTCCTGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCTCTGAGAGTGGCAGGTGAG	2673		
Db	17500	AATCAGATAAAATATGCAATTTATTTAGAGAACTGCAATGTTGGTCAGTCCAGTCCCTGCAGA	17559		
Qy	2674	GGCTGACCTATTGCTCTGCACCTTACTCCTATCTCAGCTGTCCCTCCCACCTTTCAGGTGC	2733		
Db	17560	GGGAATTCCCAGCATGACCTCATTCACITGTGAAGACAGAGCAATCCTTGTGTTTATTT	17619		
Qy	2734	TGCCAGACACATGACAACTGCTAYGACCAGGCCAAGAGCTGGACAGCTGTAAATTTCTG	2793		
Db	17620	TTTTAAGATGGATCTCACTCTGTTGCCAGACTGGAGTGCAGTGGCATGATCTCAGCCCT	17679		
Qy	2794	CTGGACAMMCCGTACACCCACACCTATTTCATACTCGTGTCTGGCTCGGCAATCACCTGT	2853		
Db	17680	CTGCCACCTCCACCTCCGGGTTCAAGAGATTCTCATGCCTCAGCCTCCTGAGTAGCTGA	17739		
Qy	2854	AGCAGTAGGTTTATCCCTTCCCTTGACCTATGAATTTCTAGTTGGTTCTCAGTAGGCCGGG	2913		
Db	17740	GATTACAGGCTTGTGCTCCATGCCAGCTAATTTTTTATTTTACTAGAGATGAGGTT	17799		
Qy	2914	GGAAATAATAGTAAACAACAGCCATGATTTAGTGTAAATTTTCTTGGTTCTGGCAGTGTC	2973		
Db	17800	TCACCAGTTTGGGCAGGCCG-----GTCTCAAACTCCTGACCTCAAGTGATCCAC	17849		
Qy	2974	TCCTTTAATCCTCAGAAACAACACTATGGGATAGGTACAATTTATCCTCACTTAAACAGATAA	3033		
Db	17850	CCACCTCGGCCTCCCGAAGTGCTGGGATGACAGGTG-----CTGGTCAGCAAC	17898		
Qy	3034	GAAAACTGAGGCTCAGAAAGCTGAGCTATTTGCCCAAAGATCACACAGCTTGTAAAGTGGTG	3093		
Db	17899	TGTTGTTTAGACATAACATTTTATCTGCTCGTCCAGCATGGTCAGCCCTCCACTT----	17954		
Qy	3094	ACAGTTTGGGTTTTTTTTTGTGTTGTAGACAGGGTCTTGCTGTGTCACCCCAGGCA	3153		
Db	17955	---TTTAAATTTTATTTATTTTATTTTGTAGACAGAGTCTCACITCTGTGTCTCAGGTT	18011		
Qy	3154	TGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCT	3213		
Db	18012	GGAGTCCAGTGGCGTGATTTTCGGCTCACTGCAACCTCTACTTCCCAGGTTTCGAGCAATTC	18071		
Qy	3214	GCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCAACCACCACGCTTGGCTAAT	3273		
Db	18072	TCCTGCCTCAGCTTCCGAGTAGCTGGGATTACAGGCCCGCGTCCCCACACCTAGCTAAT	18131		
Qy	3274	TAAAAAAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTC	3333		
Db	18132	TTTTTGTA--TTTTTAGTAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTC	18189		
Qy	3334	CTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGTCTGGGATTACAGGGGTGAGC	3393		
Db	18190	CTGACCTCAGGTGATTCTCTGCCTTGGCCTCCCAAAGTGTGAGATTACAGGTGTGAGC	18249		
Qy	3394	CACCATGTGCGGTACTTATTTCTTTACATTTCCATCTTTCCAATAGAAATGTAAGATCCAC	3453		
Db	18250	CAC	TGCACACGGCCCTTAAATTTTATTTATTTATTTATTTATTTATTTATTTATAGAGA-----	18304	
Qy	3454	AGAACAGGGATTACTGCCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTCA	3513		
Db	18305	-----	CTTAGTCTCACTCTGTTGCCAGGCTGGAGTGCAGT	18340	
Qy	3514	ACCTCAACCTCCGTT	CAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYATTTCTCCTG	3573	
Db	18341	GGCATGGTCTCGGCTCACTGC	ACTCCA-----CCTCCTGGGTTACG	CCCATTTCTCCTG	18393
Qy	3574	CCTAAGCCTCCTGAGTAGCTGGAATTA	CAGCGTGCACCA	CCATGCTTGGCTAATTTTTT	3633
Db	18394	CCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCACCA	CCACTCCCGGCTAA-TTTTT	18452	

QY 3634 GTATTTTACGAGAGATGGGTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACC 3693
|||||
Db 18453 GTATTTTAGTAGAGATGGGTTTCACTGTGTTAGCCAGGATAGTCTCGATCCTCGACC 18512
|||||
QY 3694 TCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGCGGTGAGTCACTGT 3753
|||
Db 18513 TC--GTGATCGGCTGCCTCGGCTCCCAAAGTGCTGGGATTACTATTTTGTTTTTGT 18570
|||||
QY 3754 GCCTGGCCGATTACTGTCTATTTTCTTTATTG--CTATATCCCCAGATCTAGAGCAGTGT 3811
|||
Db 18571 AGAGACAGGTTCTCACTGTGTTGCCAGGCTGGTCTTGAACTCCTGATCTCAAGTGATCT 18630
|||||
QY 3812 CTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTT 3871
|||
Db 18631 TCCCACCTCAGTCTCTCAAAGGCTGGGATTACAGGGGTGAGCCACTGCACCCCACTTC 18690
|||||
QY 3872 CTTTTTCTTTTTTAAACAACATCTTGACAACTTTGCAGAAATAAATAACAATCTTGCAATTCT 3931
|||
Db 18691 CCTCTACTTTTT-----GACGGTTTCCTTCTGCTATGAATGT 18727
|||||
QY 3932 GCTTTTTCACCTTATCACCTTGTTATGACTTTTTCATATTGCTCAAAACCTTTATTGTTAC 3991
|||
Db 18728 GCATGTCCAGTTGCTGCTTCTTAGAACTGATATTACCTTCCTCATCCATCA----- 18780
|||||
QY 3992 TGTTTTTTCATTGTTACTATTTTGTACCTGAATAATATGGCTTAATTGCTTATACATC 4051
|||
Db 18781 -----GCCATTGGAGGAGGACTGGGACCGCTCAGATTATTGATCTGACCCATT 18828
|||||
QY 4052 CTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCC 4111
|||
Db 18829 CTTTCGGCAGGGTTTCTGCTGCTTCCATCACCAAACTGGAATCAGAAGAGTTT 18888
|||||
QY 4112 CCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTTTTAATGTTTGCAACT 4171
|||
Db 18889 CCATAGCCCTTTTTTTTCCCCACATCTTGTGTAAGCAGAGTTTGA-----AAAC 18941
|||||
QY 4172 AAGACAAGAAACCTGCATTAGAGGATGTTGTTCATATTAAATTAATAAATAAATCACTCAGTTGG 4231
|||
Db 18942 AAACCCACAATAAAGCTATTCCCCAGAAGAAATCTGTAATCAAAAGATAAGCTCTGCCGG 19001
|||||
QY 4232 GCACAGTGACTCAAGCCGTGTAACCACAGTACTTTTGAAGTCCCAAGGTGGGTGGATCACTT 4291
|||||
Db 19002 GCACAGTGGTCAAGC-----CTTTGGAGGCCAAGCGGGCGGATCACTT 19047
|||||
QY 4292 GAGGTGAGAGTTTCGAGACCAGCCCTGGTCAATATGTTGAACCCCTATCTCTACTAAAAAT 4351
|||||
Db 19048 GAGGTGAGAGTTCTAGACCTGCCAGGCCAACATGGTAAACCTCATCTCTACTAAAAAT 19107
|||||
QY 4352 AAAAAATTAGCTGGGTGTAGTATGCATGCCTGTAGTCCCAGGTACTCGGGAGGCTGAG 4411
|||||
Db 19108 AAAAAATTAGCTAGATGTGTGGTGGGTACCTGTAGTCTCAGTACCTGGGAGGCTGAG 19167
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QY 4412 GCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAAGCGAGATCCCACCACTG 4471
|||||
Db 19168 GCAAGAGAAATCGCTTGAACCTGGGAAGTAGAGGTTGCAGTGAAGCGAGATTGCACCACTG 19227
|||||
QY 4472 CACTCCAGCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAA 4531
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Db 19228 CACTCCAGCTGGGCGACGAGTGAGACGACCTCACAAAAATTACATAAATAAATAA 19287
|||||
QY 4532 GGATCGGAGAGAAACAAA 4550
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Db 19288 AAGTAAATAAAAAATACAA 19306
|||||

RESULT 19
ABD33357/c
ID ABD33357 standard; DNA; 38538 BP.
XX
AC ABD333357;
XX
DT 18-NOV-2004 (first entry)
XX

DE Human cancer-associated (CA) gene HD07-065.
XX
KW Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW ds; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004058146-A2.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040081.
XX
PR 17-DEC-2002; 2002US-00322281.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-499109/47.
XX
PT Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS Claim 16; SEQ ID NO 448; 182pp; English.
XX
CC The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a human CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 38538 BP; 9418 A; 9893 C; 9523 G; 9684 T; 0 U; 20 Other;

Query Match 8.5%; Score 425.4; DB 13; Length 38538;
Best Local Similarity 60.0%; Pred. No. 1.9e-68;
Matches 879; Conservative 1; Mismatches 552; Indels 33; Gaps 9;
QY 3067 CCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTAGAG 3126
|||
Db 35304 CAAAAATAAAAAATTAATATTTTTTGTCTTAGATTATAGTTAAGGGGCTTTTTTGAG 35245
|||
QY 3127 ACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACCTGCA 3185
|||
Db 35244 ATGAAGTTTGTCTCTTGTGCCAGGCTGGAGTGCAATGGTGTGATCTTGGCTCACAGCA 35185
|||
QY 3186 GCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTA 3245
|||
Db 35184 ACCTCCACCTCCAGGGTCAAGCGATTCTCCTCTCTCAGCCTCCTGAGTAGCTGGGATTA 35125
|||
QY 3246 CGAGCGTGCACCAACCGCTGGCTAATTAATAAAATTTTTTTGTAGAGACTGGGCTTTA 3305
|||
Db 35124 CAGGCATGCGCCACCACACCCAGCTAATTTTGTA---TTTTAGTAGAGATGGGGTTTCT 35068
|||
QY 3306 CTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATC 3365
|||
Db 35067 CCATGTTGGTCAGGCTGCTTGAACCTCCTGACCTCAGGTGATCCACCCCTCCTTGGCTTC 35008
|||
QY 3366 CCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTCTTTACATTC 3425
|||
Db 35007 CCGAAGTGTGGGATTACAGGCATGAGCCACTGCGCCTGGC-----CTCAGTTAAGGGA 34954
|||

infection, viral infection, parasitic infection, protozoal infection,
fungal infection and M5 is useful for treating one of the above
conditions. The present sequence represents a gene differentially
expressed in granulocytes. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

Sequence 122888 BP; 28761 A; 33410 C; 31919 G; 28798 T; 0 U; 0 Other;

Query Match	Best Local Similarity	Score	DB 6;	Length
Mismatches	Conservative	0;	Mismatches	503;
Indels	Gaps	65;		

QY	Db	3104	TTTCTTTTTGTTGGTTAGACACAGGTCTTGCTCTGTCAACCCAGGCATGAGCACAGT	3163
		70248	TTTCTTTTTTAATTTTTAAACACACAGGTCTTGCTTTGTCAACCAGGCTGGAGTGCGT	70307
		3164	GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA	3223
		70308	GGTGCAACACAGCTGACAGCAACCTCAAAC-CCTGGGCTCAAGCAATCCTTCACCTCA	70366
		3224	GCCTCCCNACTAGCTGGGACTACGAGCGTGCAACCAACCGCCTGGCTAA-----	3272
		70367	GCTTCCCAAGAAGCTGGGACTACAGGCATGTGACACCATGCCAGCTAATTTTTTTTTT	70426
		3273	-----TTAAAAAAAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTT	3327
		70427	TTTACTTTTTAAAAATTTTTTGTAGAAAATGGGAGTCTCACTATATTGCTTAGGCTGGTCTC	70486
		3328	AAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGGG	3387
		70487	AAATCTTGGGCTTAAAGCAATCCTCCTGCCTCGGCTCCCAAAGTTGTGGGATTATAGT	70546
		3388	GTGAGCCACCATGTGGGCTACTTATTTCTTTACATTCCTTCCAATAGAAATGTAAG	3447
		70547	GTG----ACCACTGCAGCCAGCCTTAAATTTCTAATATGGTAAGTATTAATAGCATTTTGG	70602
		3448	ATCCACAGAACAGGGATTACTGCCTAATTTTCTTCTTCTTTTGTAGACAGAGTCTCAC	3507
		70603	GGATGCTCAATAAT---TTTCTTCTCTTTTCTTTTCTTTTGTAGATGGGCTCTAGC	70657
		3508	TTCATCACCTCAACCTCCG-----TTCAGCTCACTGCAACCTCTGCTCCCTCC	3553
		70658	ACTGTCACCTAGACTGGAGTGCAATGGCGCGATTTTCAGTTCACTGCAACCTCTGCTCTCT	70717
		3554	GGGTTCAAGYGATTCCTCGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCA	3613
		70718	GGGTTCAAGAGATTCTCGTGCCTCAGCCTCCTGAGTAGCTGGGACTACAGGCACCCGCCA	70777
		3614	CCATGCTTGGCTAAATTTTTTGATTTTAGCAGAGATGGGGTTTACCATGTTGCCCAGG	3673
		70778	CCACATCCGGCTAAATTTTTTGATTTTAGTAGAGATAGGGTTTCGCTATGTTGGCCAGG	70837
		3674	CTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTCTGGAA	3733
		70838	CTGGTCTCAAACTCCTGACCTC--GTGATCCGACTGCCTCAGCCTCCCAAAGTCTGGGA	70895
		3734	TTATAGGCGTGAGTCACGTGCTGCCTGGCCGATTA CTGCTATTTTCTTTATTTGCTATATCC	3793
		70896	TTACAGGTGTGAGCCACCACACTCGG-----CAATAATTTTAAAGGTATAAAA	70944
		3794	CCAGATCTAGACGAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCAC	3853
		70945	ATGTCCAGAGACCAAAAAGGTCAAGAACCACTGCTTTTAAATACATAAATGAT-----ATC	70999
		3854	AGCCTAGATATAAACTTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTTGCAGAATA	3913
		71000	AAACTATTTTATATTTTCAAAATTAACITTTTAAAAAAAATTTCAACACAGAGCATAAG-CTC	71058
		3914	AATACAAATCTTGCATCTCTGCTTTTTCACCTTATCACCTTGTTATGACTTTTTCATATTGCC	3973
		71059	CATGAAGCAGAGGTTTTCTTTTGTGTTTATTTCAATTTATGGAACCTAAGTCCCTAGAACAA	71118

Human lp36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs.

Example 8; Page 93-95; 226pp; Japanese.

The present invention describes a homozygosity deletion domain co-existing in the 36-position of the first chromosome short arm (lp36) in human neuroblastoma. Also described are base sequences from the lp36 position of human neuroblastoma cell lines (NB-1 and MASS-NB-SCH-1), which are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes, base sequence data of which are applicable as tumour markers and reagents in studying mechanism of tumour body formation, and gene diagnosis of tumours as well as in developing anti-cancer drugs. AAF97874 to AAF97829 represent PCR primers used in the exemplification of the present invention, and AAF97830 to AAF97874 represent sequences given in the exemplification of the present invention

Sequence 6405 BP; 1650 A; 1449 C; 1383 G; 1923 T; 0 U; 0 Other;

Query Match 8.3%; Score 416.2; DB 5; Length 6405;
 Best Local Similarity 59.9%; Pred. No. 7.2e-67;
 Matches 856; Conservative 1; Mismatches 504; Indels 68; Gaps 7;

QY	3103	GT	TTTTTTTTTTGTTGTTT	TAGACAGGGTCTT	GTCTGTCA	CCCCAGGCATG	GACACAG	3162
DB	3636	GT	CTTTATTTTTTATTTTT	TTGAGGTGAGTTT	CACTCTTGT	TGCCAGGCTG	GAGTGCAA	3577
QY	3163	TGGT	GC AACCATAGTCACT	GCAGCCTCAAC	CTCTGAGCTCA	AGGGGATCTG	CTGACCTC	3222
DB	3576	TGGC	ACGATCTCAGCTTACA	CAACCACTCTG	CTCTGAGTTCA	AGTGATTCTC	CTCGCTC	3517
QY	3223	AG	CTCCCAAGTAGCTGGG	ACTACGAGCGTGC	ACCACCA	CGCTGGCTAAT	TAAAAAAAT	3282
DB	3516	AG	CTCCCGAGTAGCTGGG	ATTACAGGCATGC	ACCACCA	CACATCTCAGCTGAT	TTTTTTGTA	3457
QY	3283	TT	TTTTTGTAGAGACTGG	GTCTTACTACGTT	TGGCCAGGCTTG	TCTTAAACTCCT	GGCTTCA	3342
DB	3456	TT	TTTTTAGTAGAGA-TGG	GGTTCTCCATGTT	TGTCAGGCTAG	TCTCAAACCTCC	CGACCTCA	3398
QY	3343	AG	CAATCCTCCTACTTGG	CATCCCAAGTGT	CTGGGATTAC	AGGGGTGAGCC	ACCATGTG	3402
DB	3397	GG	TGATCCGCCTGCCTCG	GCCTCCGAAAGTG	CTGGGATTAC	AGGCGTGAGCC	ATAAGGCC	3338
QY	3403	CG	GCTACTTATTTCTTTA	CTATCTCCATCTTT	TCCAATAGA	ATGTAAGATCC	ACAGACAGGG	3462
DB	3337	TG	GCCTATTTTTTACT--	-----	-----	-----	-----	3322
QY	3463	AT	TACTGCCTATTTTCT	CTCTTCTTTT	TGAGACAGAGTCT	CACTTCA	TACACCTCAACC	3522
DB	3321	-TT	TAAAGATGGAGTTT	TGCTCTTGT	TGCCCAAGCTG	GAGTGCAATGG	CATGATC-----	3269
QY	3523	TCC	GTTTCAGCTCACTGCA	CAACCTCTGCCT	CCCCGGGTTCA	AGYGATTCTC	CTGCCTAAAGCCT	3582
DB	3268	----	TCGGCTCACTGCAAC	CACTCCGCCTCC	CCAGGTTCAAGT	GATTCTCTT	CGCTCAGTCT	3214
QY	3583	CCT	GAGTAGCTGGGAATTAC	AAAGCGTGCACC	ACCATGCTTGG	CTTAATTTT	TGTATTTT	3642
DB	3213	CC	CAAGTAGCTGGGATTAC	AGGCATGCACC	ACCATGCCCCG	CTAA--ATTT	TGTATTTT	3156
QY	3643	GC	AGATGGGGTTTTTACC	ATGTTGCCCCAGG	CTGGTCTCAA	ACTCTGACCTC	AGTGTAT	3702
DB	3155	GT	AGATGGGGTTTCTCC	ATGTTGGTTAGG	CTGGTCTCAA	ACTCCCCAAC	CTC-AGTGTAT	3097
QY	3703	CT	GCCTGCCTCAGTCTCC	CAAAAGTGTGGA	ATTATAGGCGT	GAGTCACTGT	GCCTGGCCG	3762
DB	3096	GC	ACCAAGCCTCGGCCT	CCCCAAAGTGTGG	GATTACAGGCAT	GAGCCACCG	CGCCCGCCG	3037
QY	3763	AT	TACTGTCTATTTTCT	TATTGCTATAT	CCCCAGATCT	TAGAGCAGTGT	CTGCATATAG	3822
DB	3036	TAC	GTATCTTTATATCAGG	ATGTTTATAACA	CAATTTTCTCT	TAGAACATCT	TTTAGAATTTA	2977

Qy	3823	TAGTGGCTCAATAAATAATTGATGAATGCACAGCCTAGATATATAAACTTTCTTTTCTTTT	3883
Db	2976	ATACTAGGAAAAAAGGTTT-----CTCTCGACAAACTATTAGGCTTTCTTTTACCAGA	2924
Qy	3883	TTTAAACAATCTTGACAACCTTTGCAGAAATAAATACAATCTTGCAATCTGCTTTTCTCACT	3942
Db	2923	GTGAAAAATTGTACAATTTATCTTTCCCTTTTTCATTTAAATTCATGTTCCAAATTAAT	2864
Qy	3943	TATCACCTTGTTATGACTTTTTTCATATTGCCTCAAACCTTTTATTGTTACTGTTTTCAT	4002
Db	2863	TACAATAACCACTTAGCCGAGGCAACCTATACATTTTAGTTTTCTTGTTACATAAATTT	2804
Qy	4003	TGTTACTATTTTAGTCACTGAATATATATGGCTTAATTGCTTTATACATCCTCCTGCTCCA	4062
Db	2803	TTACTATTATATTTTAAATAGCTTCACTGTATATATTTTGTGGTAAGCTGCTCAAAATCCT	2744
Qy	4063	CTTTAGAAGGCCAAATTTTACAAATCTGATGAAAGCTATGAACCTCTCTCCAGAGAAATA	4122
Db	2743	TTCTAGAAAGTAGTAACTGGTATAAATATATAAATAAATAAATAAATAAATAAATAAATA	2684
Qy	4123	CACACACACACACACTC-ACACACAGTTTTTTTTTAATGTTTGCAACTTAAGACAAGAA	4181
Db	2683	TCTGCTATTTAAACACTGTAAATATGTTGTGTAGTCAAAGTTCTAGTTCTTAAAAACAAT	2624
Qy	4182	ACCTGCATTAGAGGATGTTTTGTTTCATATTAAATTAATAAATAAATAAATAAATAAATA	4241
Db	2623	AAAACCAACGACACAGCAAGCTTTTAAAGTTACATAAAGATCGGCTGGGCATCGTGGC	2564
Qy	4242	TCAAGCTGTAACCAAGTACTTTTGGAACTCAAGGTGGGTGGATCACTTGAGGTGAGAA	4301
Db	2563	TCACGCGTATAATCCCAACACTTTGGAGGCCAAGGCGGTGGATCACTTGAGGTGAGGA	2504
Qy	4302	GTTTCGAGACCAGCCTGGTCAATATGTTGAAACCCCTATCTCTACTAAAAATACAAAAATTA	4361
Db	2503	GTTCAAGACCAGCCTGGCCAACATGATGAAACGCTGTCTCTACTAAAAATACAAAAATTA	2444
Qy	4362	GCTGGGTGTAGTGATGCATGCCCTGTAGTCCAGCTACTCGGAGGCTGAGGCAAGAGAAT	4421
Db	2443	GCTGGGTGTGTGGCACATGACTGTAATCCAGCTACTCGGAGGCTGAGGCAAGAGAAT	2384
Qy	4422	TGCTTGAACCTGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCCTGCTGCTCAGCC	4481
Db	2383	CACTTGAACCCGGGAGATGAAGGTTGCAGTGAGCCAAAGTCAACCACTGCTGCTAGCC	2324
Qy	4482	TGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAAATAAATAAATAA	4530
Db	2323	TGGATGACAGCGGAGACTCTGTCTCAAAAAATAAATAAATAAATAAATAAATAAATAA	2275
RESULT 22			
ADC89520			
ID	ADC89520	standard; DNA; 139257 BP.	
XX	AC	ADC89520;	
XX	AC	ADC89520;	
DT	01-JAN-2004	(first entry)	
XX	DE	Human COREST genomic DNA #SEQ ID 11.	
XX	DE	Human COREST genomic DNA #SEQ ID 11.	
KW	KW	Cytostatic; antisense therapy; co-repressor;	
KW	KW	RE1 silencing transcription factor; COREST; antisense oligonucleotide;	
KW	KW	developmental; hyperproliferative; disorder; neuronal cancer; ds.	
XX	OS	Homo sapiens.	
XX	OS	Homo sapiens.	
PN	PN	WO2003011890-A1.	
XX	XX	13-FEB-2003.	
PD	PD	31-JUL-2002; 2002WO-US024370.	
PF	PF	01-AUG-2001; 2001US-00920671.	
XX	XX		
XX	XX		

PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Bennett CF, Freier SM;	
XX		
DR	WPI; 2003-256431/25.	
XX		
PT	New antisense oligonucleotide compounds, useful for the diagnosis,	
PT	prevention and/or treatment of conditions with aberrant expression or	
PT	activity of CoREST, such as developmental and/or hyperproliferative	
PT	disorders.	
XX		
PS	Example 15; SEQ ID NO 11; 145pp; English.	
XX		
CC	The invention relates to a new antisense compound comprising 8-50	
CC	nucleobases in length targeted to a nucleic acid molecule encoding a co-	
CC	repressor for RE1 silencing transcription factor (CoREST), where the	
CC	compound specifically hybridises with and inhibits the expression of	
CC	CoREST. The CoREST antisense oligonucleotide has any of 72 specifically	
CC	claimed sequences of 20 bp, given in the specification. The methods and	
CC	compositions of the present invention are useful for the diagnosis,	
CC	prevention and/or treatment of diseases or conditions associated with	
CC	aberrant expression or activity of CoREST, such as a developmental	
CC	disorder and/or a hyperproliferative condition like neuronal cancer. The	
CC	current sequence represents the human CoREST genomic DNA sequence that	
CC	was used to design antisense oligonucleotides of the invention.	
XX		
SQ	Sequence 139257 BP; 35155 A; 29706 C; 30833 G; 43561 T; 0 U; 2 Other;	
Query Match		8.3%; Score 416; DB 10; Length 139257;
Best Local Similarity		54.0%; Pred. No. 1.2e-66;
Matches 1222; Conservative		3; Mismatches 948; Indels 89; Gaps 15;
QY	2291 AGGCCAGGCGGGTGGCTCATGCCCTGTAATCCAGCACCTTTGGGAGGCCGAGCGGGGG 2350	
DB	63398 AGGCTGAGCATAGTGGCTCATACCTGTAATCCTAGCACCTTTGGGAGGCTGAGGCGAGCGA 63457	
QY	2351 ATCACTTGAGTCAAGGATTCGAGACCGACGCTGGCCAAACATGGTGAAACCCCTGTCTCTAC 2410	
DB	63458 ATTGCCTGAGTCAGGAGTTAAAGACCGCCTGGCCAAACATGGTGAAACCCCGTCTCTAC 63517	
QY	2411 TAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTAACCCCGACTACTTGGG 2470	
DB	63518 T-AAAAATACAAAAATTAGCCGGGTGGTGCACAGGCGTCTGTAATCCAGCTACTCAGG 63576	
QY	2471 AGACTGA-GTTGGAGGTTTCAGTGAGCCAAAGGTCGTCTACTGCTGTCCAGCCTGGGTAA 2529	
DB	63577 AGGCTGAGGCAAGAGAATTCCTTGAACCTGGGAGGTGGAGGTGCGGTCAGTCGAGATCG 63636	
QY	2530 CAGAGCAACTCTGTCTCAAAAAAATAAATGCTTTCAATAAATATATATAAAGGACTT 2589	
DB	63637 CGCCACTGCACTCCAGCCTGGGCAACAGAGTGAGACTTTTTTGTACACACACACACAC 63696	
QY	2590 ATATTTTTTCAAGCCATAGGATCAATTTCTCCTGAAGCATCTTGGCGAAGTCATCCCCACC 2649	
DB	63697 ACACACACACACACACACACGTCGAATAAAACCTATGAACC--AACTAATGCAGTGGATT 63754	
QY	2650 TGTTCCTGAGATGGGCAGGTGAGGGCTGACCTATTGCTCTGCACCTACTCCTATCTCAG 2709	
DB	63755 CAAAAATTAAGATTAACTTGTGTAAGTTGTAATGTTTCTTGTATGTACCCATTATTGAG 63814	
QY	2710 CTGTCCTCCCACTTTCCAGGTGCTGCCA-GACACATGACAACTGCTAYGACCAGGCCAA 2768	
DB	63815 TGGAAACAGATTCTTTTTCATTTCTTTGAAATCACTTTTGTGAGATTTTTTTTATTTT 63874	
QY	2769 GAAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACCCACACCTATTTCATATCTC 2828	
DB	63875 TTTTTTTTTTGGAGACAGAGTCTCGCTGTGTGCGCCAGACTGGAGTGCAGTGGTGTGATC 63934	
QY	2829 GTGCTCTGGCTCGGCAATCACCTGTAGCAGT-AGGTTTATCCCTTCCTTGACCTATGAAT 2887	
DB	63935 TAGGCTCACTGCAACCTCCACCTCCCGGTTCAAGCGAATTCCTCCTGCCTCAGCCTCCTGA 63994	
QY	2888 TCTAGTTGGTTCTCAGTAGGCGGGGGGAAATAATAGTAACAACAGCCATGATTTAGTGT 2947	

DB	63995 GTAGCTAGGATTATAGGCATGTGCCACCACACTCAGCTAAATTTTGTATTTTCTAGTAGAGG 64054	
QY	2948 TAAATTTTCTTGGTCTGGGCAGTGTCTCCTTTAATCCTCAGAACAACACTATGGGATAGG 3007	
DB	64055 TAGGGTTTCACCATGTAGGCCAGGCTGGTCTCAAAACTCCTGACCTCAAGCGATCCGCGCTG 64114	
QY	3008 TACAATTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGGCTGAGCTATTGTC 3067	
DB	64115 CTCAGCCTCCCTGAGTATTGGGATTATAGGTGTGAGCCAC-----GGTGTCCCGC 64164	
QY	3068 CAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTGTTAGAGA 3127	
DB	64165 CAAGCTGAGACATTTTAAAGAAAATGTTTCTGTTTTTGTATTATTTGTTTGTGAGA 64224	
QY	3128 CAGGGTCTTGGCTCTGTCAACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGC 3187	
DB	64225 TGGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGGTGCCA-----TCACTGCAAC 64277	
QY	3188 CTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTAGC 3247	
DB	64278 CTCTGCCTCCTGGGTTCAAGCAATTCTCCTGTTCAGCCTCCTAGGTAACITGGGACTGCA 64337	
QY	3248 AGCGTGCACCAACCGCCTGGCTAATTAATAAAATTTTTTTGTAGAGACTGGTCTTACT 3307	
DB	64338 GGCTTGCCACCATAATACCTGGCTGATTTTTTGTATTTTTA-GTAGAGATGGGTTTACC 64396	
QY	3308 ACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCC 3367	
DB	64397 ATGTTGGCCAGGCTGCTTGAACCTCTGAC-TCAAGCGATCTACCCACCTCAGCCTCCC 64455	
QY	3368 AAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTCCA 3427	
DB	64456 AAAGTCTGGGATTACTCCACAGCACCTGCTCAGAAAAGGTTTCTTTTCTTTTCTTTT 64515	
QY	3428 TCTTTCCAATAGAATGTAAGATCCACAGAACAGGATTACTGCCTATTTTCTTCCTTTCT 3487	
DB	64516 TTTTTTGAGATCAGGTCTCACTCTGTGCGCCAGGGTGTAGTGCAGTCGCGCAATC----- 64570	
QY	3488 TTTTTGAGACAGTCTCACTTTCATCACTCAACCTCCGTTTCAGTCACTGCAACCTCTG 3547	
DB	64571 -----TCAGCTCACTGCAACCTCCG 64590	
QY	3548 CCTCCCGGTTTCAAGYGAATCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGT 3607	
DB	64591 CCTTCCAGGTTTCAGGTGATTTCTTGGCTCAGCCTCCCAAGCAGGTGGGATTTCAGGCAT 64650	
QY	3608 GCACCACCATGCTTGGCTAATTTTTTGTATTTTAGCAGAGATGGGTTTTACCATGTTG 3667	
DB	64651 ACACCACCATGCATGCTCA-TTTTTGTATTTTAGTAGAGA-GGGGTTTTCACCATGTTG 64708	
QY	3668 CCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTG 3727	
DB	64709 GCCAGGATGGTCGCGAATCCTGACCTCATGTGATCCACCCGCATCAGCCTCCCAAAGTG 64768	
QY	3728 CTGGAATTATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTCTTTATTGCT 3787	
DB	64769 CTGGGATTATAAGCGTGAATCACTGCACCTGGCTAGAAAACATCTTCTAAAGCCTAATCTT 64828	
QY	3788 ATATCCCCAGATCTAGACGAGTGTCTGACATATAGTAGGTGCTCAATAAATAATATGATGA 3847	
DB	64829 TTTTTTTTTTCCTTATATAAATTTAGGTTGACTATGTAAACCCCAAACACATAGGGTAGAA 64888	
QY	3848 A---TGCACAGCCTAGATATAAACTTTTCTTTTCTTTTAAAAACAATCTTGACAAC 3903	
DB	64889 ACTCGTGAAAAAATATTTTGTAGGATATCTTTGCAAGTGTGTGCTCAGCGTGTGGAT 64948	
QY	3904 TTGCAGAAATAAATACAATCTTGCAATCTCTGCTTTTTCACCTTATCACCTTGTATGACTTTT 3963	
DB	64949 ATGGATGTGTGCTTAGTGTGATGATAGATTTAGGATTTCCACCTGTATGTATGCTTT 65008	
QY	3964 TCATATTGCTCCTCAAACTTTATTGTTACTGTTTTTTCATTGTTA--CTATTTTACTCAC 4020	

Db 65009 TGGTGAGTCCTTTTAGGGGATATGTCCTCATGTTCAAGGAGTAATGGCATACTGGTTTCAT 65068
QY 4021 TGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAAGGCCAAATTT 4080
Db 65069 TTAACACCCATGTTTAAATCCTAATTTAAAGACCGATTTTACTTCTCTTGGAGCTAATTTCT 65128
QY 4081 ACAAAATCGATGAAAGCTATGAACCCTCTCCCCAGAGAAATACACACACACACACACT 4140
Db 65129 TAACTTTTCTGATGATGTTTTTTGTTGCTTAAAGTTAAGACTAATATAACACAGAACTCTTA 65188
QY 4141 CACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCAATTAGAGGATGTT 4200
Db 65189 CTCATCCTTTTGGATATTAGAGATTTTGGTTTATTAACTAGTGAATTTTAAATATCAT 65248
QY 4201 TGTTCATATTAAATAAACTCA-----GTTGGGCACAGTGACTCAAGCCCTG 4250
Db 65249 TTTACATGTTTACTCTCAAGATCTGATGATTGACTGACTGGGTGCAGTGCATCACACCTG 65308
QY 4251 TAACCACTACTTTTGGAAAGTCCAAAGTGGGTGGGATCACTTGAGGTGAGAAGTTCGAGAC 4310
Db 65309 TAATCTCAGCACTTTGGGAGGCCAAGCGGGCAGATCACTTGAGGTTCAGGAGTTCGAGAC 65368
QY 4311 CAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGT 4370
Db 65369 CAGCCTGGCTAAACATGGTGAACCCCTGTCTGTAGTAAAAATACAAAAATTAGCCGGACTT 65428
QY 4371 AGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAAC 4430
Db 65429 GGTGGTGCCTGCTGTAATCCCAGCTACTGGGGAGACAGAGGTGAGAGAATCACTTGAAC 65488
QY 4431 CTGGGAGGCAGAGGTTGCAGTGCAGCCGAGATCCCACCACCTGCACCTCCAGCCTGGGCGACA 4490
Db 65489 CCCAGAGCGGAGGTTGCAGTGCAGCCCTAGATCACTCCATTGCACTCCAGCCTGGGCGACA 65548
QY 4491 CAGCGAGACTCTATCTCAAAAAAATAAAATAAAATAAAG 4532
Db 65549 GAGTGAGACTCCGTCCTCAAAAAAATAAAAAAATAAAAAAAGAG 65590

RESULT 23
AAK77880
ID AAK77880 standard; DNA; 17170 BP.
XX
AC AAK77880;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32692.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
FN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.
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PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0224519P.
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PR 14-AUG-2000; 2000US-0225757P.
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PR 14-AUG-2000; 2000US-0225759P.
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PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
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PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
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PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.

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Qy	3153	ATGAGCAGAGTGGTGTCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATC	3212
Db	14139	TGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAAGCTCTGCCTCCAGGTTACACCAATT	14198
Qy	3213	TGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGACACCACCGCCTGGCTAA	3272
Db	14199	CTCCTGCTTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCACCAACCATGCC--CTAA	14255
Qy	3273	TTAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCAGGCTTGCTTAAACT	3332
Db	14256	TTTTCTGTACTTTTGTAGTAAAGACAGAGGTTTCACCATGTTAGCAGGATGGTCTGGATCT	14315
Qy	3333	CCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGGTGAG	3392
Db	14316	CCTGACCTCATG--ATCCACTTGCTCAGCTTCCCAAGTGCTGGGATTACAGGTGTGAG	14373
Qy	3393	CCACCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCA	3452
Db	14374	CCACTGCGCCTGGCCCTTTTTTTTTTTTTTCTTTTGAGA-----	14410
Qy	3453	CAGAACAGGGATTACTGCCTATTTTCTTCTCTTTCTTTTGTGAGACAGAGTCTCACTTCAT	3512
Db	14411	-----CTGAGTCTCGTTGTGTCGCCCCAGGCTGGAGTGCAG	14445
Qy	3513	CACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCTCCGGGTTCAAGYGATTCTCCT	3572
Db	14446	TGGTCCAATC----TTGGCTCACTGCAACCTCTGCCTCCTGGGTTCAACAGATTCTCCT	14500
Qy	3573	GCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTT	3632
Db	14501	GCCTCAGACTCCCAAGTATCTGGGATTACAGGCGCTGCCACCACACCTGGCTAA-TTTT	14559
Qy	3633	TGTATTTTTCAGCAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGAC	3692
Db	14560	TGTATTTTTCAGGAGAGATGGGGTTTCACCATCTTGGCCAGACTGGTCTCAAACTCCCGAC	14619
Qy	3693	CTCAAGTGATCTGCCTGCCTCAGTCTCCCAAGTCTGGAATTATAGGCGTGAGTCACTG	3752
Db	14620	CTCAGGTAATCCACCTGCCTTGGCCTCCCAAGTCTGGGATTACAGGCATGAGCCACCG	14679
Qy	3753	TGCCTGGCGGATTACTGTCTATTTTCTTTA-----TTGCTATATCCCCAGATCTAG	3803
Db	14680	AGCCTGGCGGGAATAAGATAATCTTAAACAATCATGGAGTGCTTAGCTAGTGCCAGACAC	14739
Qy	3804	AGCAGTGCTGACATATAGTAGGTCTCAATAATAATTAATGATGAATGCACAGCCTAGATA	3863
Db	14740	GGCACTGAGGCTCTACCTACATCGTCCATGAACTTTTCATAAAAACCCATCAGGAAG	14799
Qy	3864	TAACTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTCAGAAATAAATACAATCT	3923
Db	14800	GTGTGATTATTATCATCTCTGTTTTATAGTAGAGAACACCCAGTCTTCAAGGGTAAAAA	14859
Qy	3924	TGCATTCTGCTTTT-TTCACTTATCACCTTGTTATGACTTTTTTCATATTGCCTCAAACTT	3982
Db	14860	ATCACTCACCCCAAGGTCACACAAGCACAGGAGCCAGGACTTGAACCAAGATCAGTTTAT	14919
Qy	3983	TATTGTTACTGTTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTGC	4042
Db	14920	GCCAGGTTCAAAACCCCTTAAGTCCAGTGATTGATTTCATGACTAGAAGCAGCATAATGTTG	14979
Qy	4043	TTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGA	4102
Db	14980	TGGGAAAAGTACAAAAACACCTATCAGCTGTGACATCCAGTTTGTAGTTCTGAACAGACTG	15039
Qy	4103	ACCCTCTCCCCAGAGAAATACACACACACACACACTCA-----CACA	4146
Db	15040	CACATTAATTTGTTTAAATAGCCATGATAAAATGATGATGACTCATTTGTTGAGCATA	15099
Qy	4147	CAGTTTTTTTTTAATGTTTGCAACTTAAGACAAGAAACCTGCTATGAGGATGTTTGTC-	4205
Db	15100	CGCTTTTCTTGCAAGTATCACAAATACTGATAACAGACCTCAGAGGAAAAGTATTATTTTC	15159
Qy	4206	-----ATATTAATTAATAATACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCA	4256

Db	15160	TGACTTTTATAGATGAAAAACAATCTCAGGCGCGAGGCGGTGGCTCATGCCTGTAATCC	15219
Qy	4257	CAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAAGCCT	4316
Db	15220	CAGCACTTTGGGAGGCCAAGGCAGGAGGATCGCCTGAGGTGAGGAGTTCGAGACCAAGCCT	15279
Qy	4317	GGTCAATATGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGAT	4376
Db	15280	GGCCAACATGGCAAAACCCCATCTCTACTAAAAACACAAAAATTAGTTGGGTGTAGTGGC	15339
Qy	4377	GCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGA	4436
Db	15340	AGGTGCCTGCAGTCCCACCTACTTTGGGAGGCTAAGGCAGGAGATCGCTTGAACCCAGGA	15399
Qy	4437	GGCAGAGGTTGCAGTGAGCGGAGATCCCACCACTGCACCTCCAGCCTGGGCGACACAGCGA	4496
Db	15400	GGCGGAGATTGCAGTGAACCTGAGATCGTGCCATTGCACTCCAGCCTGGGAGACAGAGCAA	15459
Qy	4497	GACTCTATCTCAAAAAATAAAATAAAATAAAAGGATCGGAGAGAAAAAACTAATA	4556
Db	15460	GACTTCGTCTCAAAACAACAATCTTAGAGAGATTGTTGAAACTCACACAACACGTGAA	15519
Qy	4557	AGATTCCCTGAAGGTAA--GCAGAGATACGTAAATATATATATGTAATAAAGTTTAAATGCATT	4614
Db	15520	ATGTGGCTGATCCAAATTGAGATGCTCTGTCTGTAATATACACCAGATTTTCAAAGACTTA	15579
Qy	4615	TTAACTGTAATCTTATTGTTTATTTTGGTTAT	4646
Db	15580	GTATCAGAAAGAGAAATTAATATTCTTTTTT	15611
RESULT 24			
ACN44170/c			
ID	ACN44170	standard; DNA; 196686 BP.	
XX			
AC	ACN44170;		
XX			
DT	18-NOV-2004	(first entry)	
XX			
DE	Human genomic sequence	hCG39530.	
XX			
KW	Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.		
OS	Homo sapiens.		
XX			
PN	WO2003073826-A2.		
XX			
PD	12-SEP-2003.		
XX			
PF	28-FEB-2003; 2003WO-US0006235.		
XX			
PR	01-MAR-2002; 2002US-00087192.		
XX			
PA	(SAGR-) SAGRES DISCOVERY.		
XX			
PI	Morris DW;		
XX			
DR	WPI; 2003-328604/31.		
XX			
PT	Recombinant nucleic acid useful for diagnosis and treatment of carcinoma		
PT	comprises a nucleotide sequence.		
XX			
PS	Claim 1; SEQ ID NO 484; Opp; English.		
XX			
CC	The present invention relates to novel DNA and protein sequences which		
CC	are associated with carcinomas. The sequences are useful for: (i) for		
CC	screening drug candidates; (ii) for screening of bioactive agent capable		
CC	of binding to Carcinoma Associated Protein (CAP); (iii) for screening of		
CC	a bioactive agent capable of modulating the activity of CAP; (iv) for		
CC	evaluating the effect of a candidate carcinoma drug; (v) for diagnosing		
CC	carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating		
CC	carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;		

PT New isolated cancer associated nucleic acids comprising at least 10
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT cancers such as leukemia and lymphoma.

XX
PS Claim 1; SEQ ID NO 500; 199pp; English.

XX
CC The present invention relates to cancer associated sequences (ADQ97025-
CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic formate directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

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SQ Sequence 215974 BP; 56601 A; 42897 C; 46516 G; 65586 T; 0 U; 4374 Other;

Query Match 8.3%; Score 413.6; DB 12; Length 215974;
Best Local Similarity 59.6%; Pred. No. 3.7e-66;
Matches 847; Conservative 0; Mismatches 529; Indels 46; Gaps 7;

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Db 4846 TGTCTTTTGTGTTGAGACAGGGTCTCGCTCTGTTGCCAGGCTACAGTGGCACA 4787

QY 3170 ACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCC 3229
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY 3230 CAAGTAGCTGGGACTACGAGCGTGCACACACGCTGGCTAATTAATAAAATTTTGTG 3289
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QY 3290 TAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCTGGCTTCAAGCAATC 3349
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Db 4669 -----GTCTCACTGTGTTGCCAGGCTGCTCCAAATTCCTAGGCTCAAGCAATC 4620

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QY 3470 CCTATTTTCTCTCTTTTGTGAGACAGAGTCTCACTTCAATCACCTCAACCTCCGTTTC 3529
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QY 3530 AGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGT 3589
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QY 3890 CAACTCTTGACAACTTTGCAGAAATAAATAACAATCTTGCATTTCTGCTTTTTCACCTATCACC 3949
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QY 4190 TAGAGGATGTTTGTTCATATTAATTAATAAATAAATCACTCAGTTGGCACAGTGACTCAAGCCT 4249
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QY 4370 TAGTGATGCATGCCGTGAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATGCTTGAA 4429
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Db 3512 AGAGCAAGACTCCGCTCTCAAAAAGAAACACAGAGAGGAAACAGA 3471

RESULT 27

AAAL42369/c

ID AAL42369 standard; DNA; 13670 BP.

XX AC AAL42369;

XX DT 28-JUN-2002 (first entry)

XX DE Human Guanine nucleotide binding protein gamma 7 (GNG7) gene sequence.

XX KW Human; gene; ds; guanine nucleotide binding protein gamma 7; G protein;
KW GNG7; novel polymorphic site; drug screening; gene therapy;
KW GNG7-related disease; pancreatic cancer; GNG7 haplotyping;
KW GNG7 genotyping.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT allele replace(3900, T)

FT FT /*tag= a

FT FT /note= "Single nucleotide polymorphism"

FT FT replace(3975, G)

FT FT /*tag= b

FT FT /note= "Single nucleotide polymorphism"

FT FT 4005..9671

FT FT /*tag= c

FT FT /product= "Guanine nucleotide binding protein gamma 7"

FT FT 4005..4085

FT FT /*tag= d

FT FT /number= 1

Db 4496 CAAAT 4492

RESULT 28

ABA16909

ID ABA16909 standard; DNA; 6519 BP.

XX

AC ABA16909;

XX

DT 23-JAN-2002 (first entry)

XX

DE Human nervous system related polynucleotide SEQ ID NO 9240.

XX

KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;

KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;

KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;

KW antiarheumatic; hepatotropic; cerebroprotective; antiinflammatory;

KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;

KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;

KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

XX

OS Homo sapiens.

XX

PN WO200159063-A2.

XX

PD 16-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US001334.

XX

PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

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PR 17-MAR-2000; 2000US-0190076P.

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PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

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PR 14-SEP-2000; 2000US-0233063P.

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PR 21-SEP-2000; 2000US-0234223P.

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PR 29-SEP-2000; 2000US-0236367P.

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PR 29-SEP-2000; 2000US-0236369P.

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PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

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PR 17-NOV-2000; 2000US-0249244P.

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PR 17-NOV-2000; 2000US-0249245P.
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PR 17-NOV-2000; 2000US-0249265P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-541565/60.
XX
PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system cancers
PT and metastases.
XX
PS Disclosure; SEQ ID NO 9240; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABAl1004-ABA21534) and proteins
CC (ABBl4678-ABBl8001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 6519 BP; 1661 A; 1577 C; 1542 G; 1739 T; 0 U; 0 Other;
Query Match 8.3%; Score 413.2; DB 5; Length 6519;
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Matches 865; Conservative 1; Mismatches 544; Indels 36; Gaps 9;
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QY 3561 AGYGATTCTCCTGCTAAGCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCT 3620
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QY 3921 TCTTGCACTTCTGCTTTTCACTTATCACCTTGTTTATGACTTTTTTCATATTTGCCTCAAACC 3980
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5329 CCTGGCTCTCTGGCATTTCTTAGTCTGTGTGTA-----GTGGCCCAAATC 5376
QY 3981 TTTATTGTTACTGTTTTTTCATTGTTACTATTTTATGTCAGTGAATAATATGGCTTAATTT 4040
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5377 AAATGTATTAGATTAGAAATCAGGTATTGTTTGAATAAGGCCAATTTAAGCTTTTAAAA 5436
QY 4041 GCTTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTAT 4100
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5437 TTTAAACCAATGTTGTTAAACATTTAGAAATGTGCACCTTAAAAAATACACCAATTTCTGGG 5496
QY 4101 GA-ACCTCTCCCCAGAGAAATACACACACACACACACACACTCAGTATTTTAAAAA 4159
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5497 CACAGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCAAGGCAGGATCAGTCTG 5556
QY 4160 ATGTTTGCAACTAAGACAAAGAAACCTGTCATTAGAGGATGTTTGTTCATATTAATTAATA 4219
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5557 AGGTCAGGAGGTTTCGAGACCAGTCTGGCCAAACATGGTGAAACCCCATCTCTATTAAAAA 5616
QY 4220 T----AACTCAGTTGGGCAGTGACTCAAGCCTGTAAACCACAGTACTTTTGAAGTCCAA 4275
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5617 TATAAAAAATTAGCTGGGCACGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCTGA 5676
QY 4276 GGTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAACCC 4335
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5677 CACGGGTGGATCA--TGAGGTGAGGAGATCGCGACCATCTCTGGCTAACACGGTGAAACCC 5734
QY 4336 TATCTCTACTAAAAATACAAAAAATTAGCTGGGTGAGTGATGCATGCCTGTAGTCCAGC 4395
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
5735 TGTCTCTACCAAAAAATACAAAAAATTGGCCGGCGGTGGTGAGGTGACTGTAGTCCAGC 5794
QY 4396 TACTCGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGC 4455
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db	5795	TACTCGGAGGCTGAGGCAGGAGAAATGGCGTGAACCTGGGAGCGGAGCTTGCAGTGAGC	5854
Qy	4456	CGAGATCCCACTGCACCTCCAGCCTGGCGGACACAGCGAGACTCTATCTCAAAAAAAT	4515
Db	5855	TGAGATCATGCACTGCACCTTCAGCCTGGGTGACACAGCAAGACTCCATCTCAAAAAATA	5914
Qy	4516	AAATAA	4521
Db	5915	AATAAA	5920
RESULT 29			
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ID	AAK83897 standard; DNA; 17245 BP.		
XX			
AC	AAK83897;		
XX			
DT	07-NOV-2001 (first entry)		
XX			
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38709.		
XX			
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KW	cytostatic; gene therapy; vaccine; metastasis; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WQ200157182-A2.		
XX			
PD	09-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US001354.		
XX			
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PR	01-SEP-2000; 2000US-0229343P.		
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PR	06-SEP-2000; 2000US-0230437P.
PR	06-SEP-2000; 2000US-0230438P.
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PR	26-SEP-2000; 2000US-0235484P.
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PR	29-SEP-2000; 2000US-0236327P.
PR	29-SEP-2000; 2000US-0236367P.
PR	29-SEP-2000; 2000US-0236368P.
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PR	29-SEP-2000; 2000US-0236370P.
PR	02-OCT-2000; 2000US-0236802P.
PR	02-OCT-2000; 2000US-0237037P.
PR	02-OCT-2000; 2000US-0237038P.
PR	02-OCT-2000; 2000US-0237039P.
PR	02-OCT-2000; 2000US-0237040P.
PR	13-OCT-2000; 2000US-0239935P.
PR	13-OCT-2000; 2000US-0239937P.
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PR	20-OCT-2000; 2000US-0241785P.
PR	20-OCT-2000; 2000US-0241786P.
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PR	08-NOV-2000; 2000US-0246524P.
PR	08-NOV-2000; 2000US-0246525P.
PR	08-NOV-2000; 2000US-0246526P.
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PR	08-NOV-2000; 2000US-0246609P.
PR	08-NOV-2000; 2000US-0246610P.
PR	08-NOV-2000; 2000US-0246611P.
PR	08-NOV-2000; 2000US-0246613P.
PR	17-NOV-2000; 2000US-0249207P.
PR	17-NOV-2000; 2000US-0249208P.
PR	17-NOV-2000; 2000US-0249209P.
PR	17-NOV-2000; 2000US-0249210P.
PR	17-NOV-2000; 2000US-0249211P.
PR	17-NOV-2000; 2000US-0249212P.
PR	17-NOV-2000; 2000US-0249213P.
PR	17-NOV-2000; 2000US-0249214P.
PR	17-NOV-2000; 2000US-0249215P.
PR	17-NOV-2000; 2000US-0249216P.

QY	4412	GCAAGAGAAATTGCTTGAACCTGGGAGGACAGAGGTTGCAGTGAGCGGAGATCCCACTG	4471
Db	9479	GCAGGAAAATCGCTTGAATCCAGGAGGACAGAGATTGCAGTGAGCTGAGATTGTGCCACTG	9538
QY	4472	CACCTCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAAAAA	4527
Db	9539	TACTCCAGCCTGAGCAACACAGAGTGAGACTCCATCTCCAAAAAATAAGTGGAA	9594
RESULT 30			
ADQ97146			
ID	ADQ97146	standard; DNA; 348101 BP.	
XX	AC	ADQ97146;	
XX	DT	07-OCT-2004 (first entry)	
XX	XX		
DE	Human	cancer associated sequence HD08-007, SEQ ID 122.	
XX			
KW	Cytostatic;	Gene Therapy; cancer; leukemia; lymphoma; Human; ds.	
XX			
OS	Homo sapiens.		
XX			
PN	WO2004060304-A2.		
XX			
PD	22-JUL-2004.		
XX			
PF	22-DEC-2003; 2003WO-US041389.		
XX			
PR	27-DEC-2002; 2002US-00330773.		
XX			
PA	(SAGR-) SAGRES DISCOVERY INC.		
XX			
PI	Morris DW, Malandro MS;		
XX			
DR	WPI; 2004-543781/52.		
XX			
PT	New isolated cancer associated nucleic acids comprising at least 10		
PT	contiguous nucleotides, useful for diagnosing, preventing and/or treating		
PT	cancers such as leukemia and lymphoma.		
XX			
PS	Claim 1; SEQ ID NO 122; 199pp; English.		
XX			
CC	The present invention relates to cancer associated sequences (ADQ97025-		
CC	ADQ98004). The sequences are useful for the diagnosis, prevention and/or		
CC	treatment of cancer, such as leukemia and lymphoma. Note: The sequence		
CC	data for this patent did not form part of the printed specification, but		
CC	was obtained in electronic formate directly from WIPO at		
CC	ftp.wipo.int/pub/published_pct_sequences.		
XX			
SQ	Sequence 348101 BP; 82707 A; 86009 C; 87698 G; 88942 T; 0 U; 2745 Other;		
Query Match 8.1%; Score 406.2; DB 12; Length 348101;			
Best Local Similarity 58.2%; Pred. No. 9e-65;			
Matches 895; Conservative 1; Mismatches 579; Indels 62; Gaps 8;			
QY	3029	GATAAGAAAACGTGAGGCTCAGAAGGCTGAGCTATTTGCCCAAGATCACACAGCTTGTAAAG	3088
Db	97262	GATTACAGGCTGAGCCACCGCGCCGCCACATTGTCTTTATTCTAATGAAATTGAAT	97321
QY	3089	TGGTGACAGTTTGGGTTTTTTTTTGTGTGTTTAGAGACAGGCTCTTGCTGTCAACC	3148
Db	97322	TACCAATCTTTTATTCTTTTCTTTTCTTTTCTTTTGTGAGATGAGCTTGCACTATCGCCC	97381
QY	3149	AGGCATGACACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGG	3208
Db	97382	GGGCTAGATTGCCATGGCATGTCTCTGGCTCACTGCAACCTCTGCCTCCCAGGTTCAAAGT	97441
QY	3209	GATCTGCTGACCTCAGCCTCCCAAAGTAGTGGGACTACGAGCGGTGCACCAACCGCCTGG	3268
Db	97442	GATTCTCCTGCTCAGCCTCCCAAATAGCTGGGATTACAGGCGGTGTGTACCACGCCTGG	97501
QY	3269	CTAATTAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTA	3328

Db	97502	CTAATTTTTTTGTA-TTTTGTAGAGACGGAGTTTCACTATGTTGGCCAGGCTGGTGTG	97560
QY	3329	AACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGG	3388
Db	97561	AATGCCTGACTT-----GTGATCCCCTCCCATGGCTCCCAAAGTCTGGGATTACAGTCA	97616
QY	3389	TGAGCCACCATGTGCGGCTACTTATTCTTTTACATTCCATCTTTCCAATAGAAATGTAAGA	3448
Db	97617	TGAGCCACCGCACCTGGCCGTTTTTTTTTTGTTTTTTTTTTTT-----	97660
QY	3449	TCCACAGAACAGGGATTACTGCCTATTTTCTTCTTCTTCTTTTGTAGACAGAGTCTCACT	3508
Db	97661	-----TTTGTAGACAAAAGTTTGTCTTGTGTCGAGGCTGGAGTGC AATG	97706
QY	3509	TCATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTC AAGYGATTC	3568
Db	97707	GTGTGATCTTGA-----CTCAGTGC AACCTCTGCCTCCCGGGTTC AAGCGATTC	97755
QY	3569	TCCTGCCTAAGCCTCCTGAGTAGTGGAAATTACAAGCGTGCACCAACCATGCTTGGCTAAT	3628
Db	97756	TCCTGCCTCAGCCTCCGAGTAGCTGTGATTACAGGTGCCTGCCACCATGCTTGGCTAAT	97815
QY	3629	TTTTTGTATTTTTAGCAGAGATGGGGTTTTTACCATTGTTGCCCAGGCTGGTCTCAAACTCC	3688
Db	97816	TTTTTGTATTTTTAGTAAAGACAGGGTTTTACCAATTTTGGCCAGACTTGTCTTGAACTCC	97875
QY	3689	TGACCTCAAGTGATCGCCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGCGGTGAGTC	3748
Db	97876	TGACCTCAGGTGATCACCCCTGCTCGGCCCTCCCAAAGTGTGGGATTACAGGCTGAGCC	97935
QY	3749	ACTGTGCCTGGCCGATTACTGTCTATT--TTCTTTATTGCTATATCCCCAGATCTAGAGC	3806
Db	97936	ACTGTGCCTGGCCACCAATTACTTTTTTAATAGGATAAAAATTTTATTTTCTCAAAGTAAACA	97995
QY	3807	AGTGCTGACATATAGTAGGTGCTCAATAATAATGATGAATGCACAGCCTAGATATAA	3866
Db	97996	ATTGGAAAAACAGAGGCAAGTGAAAAATGGAAAAAATCATTTTATGGCAACTAATATAA	98055
QY	3867	ACTTCTCTTTTCTTTTAAACAATCTTTGACAACTT-----TGCAGAATAAAATACA	3919
Db	98056	TTTTTGTGCATCATTTTTTAAACATCTTTTACAAAAGTTGTACTTCTAGCATACATGTAAG	98115
QY	3920	ATCTTGCATTCGTCTTTTCACTTATCACTTGTATGACTTTTTCATATTTGCCTCAAAC	3979
Db	98116	TTTTATGATCTGTAGGTTTTAATGATCTCCCTAGACATGTTTGGTGGTGTTTTAGCAT	98175
QY	3980	CTTTATTGTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATT	4039
Db	98176	AAAGTGTAACATATTTAAATTTGCTCTTTTCTGTAGGTGGTAAAAATATAATAGAAATGAA	98235
QY	4040	TGCTTATACATCCTCCTGCTCCACTTATCACTTGTATGACTTTTTCATATTTGCCTCAAAC	4099
Db	98236	AGCTAACATTTATTCAATTCAGGCTCTTTTGTAGGCTCAGGGGGCAAAGTCAAGAACAAAA	98295
QY	4100	TGAACCCCTCTC-----CCCAGAGAAATACACACACACACACTCACACACAGTTTTT	4154
Db	98296	CAACCATGATCTCTGTCTCAGTTTCTCACAGGGGAAAGACAGACAATAGAGGGGAGAGGAA	98355
QY	4155	TTTTAATGTTTGCAACTAAGACAAGAAACCTGCAT--TAGAGGATGTTTTTGTTCATATTAA	4212
Db	98356	ATGGGATGTTAGAAGGTGATGAATGCATGAGGGAGGCAGGAAGTGAGTGGGGAAGGCTCG	98415
QY	4213	TTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACTACTTTTGGGAAGTC	4272
Db	98416	CTTAGGAGTGAGGATTTGGGCAAGGTGACTCACGCTGTAAATCCCAGCACTTTTAGAAATC	98475
QY	4273	CAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGFTGAAA	4332
Db	98476	TGAGACAGGTGGATCACTTGAGCCCAAGGATTCGAGGCCAGCCTGGGCAACATGFTGAAA	98535
QY	4333	CCCTATCTCTACTAAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCC	4392

Db	98536	CTCAGTCTCTACTATAAATACAAAATTAGCTGGGCATGATGGTGCATGCCCTGTGATCCC	98595
Qy	4393	AGTACTCGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGAGGCAGAGGTTGCAGTG	4452
Db	98596	AGTACTGGGAGGCTGAGGTGGAGGATCACCTGAGCCAGGACCCAGAGGTTGCAGTG	98655
Qy	4453	AGCCGAGATCCCACCACTGCACTCCAGCCTGGCGACACAGCGAGACTCTATCTCAAAA	4512
Db	98656	AGCTGAGATCACACCCCTTCACTCCAGCCTGGCAAGAGATGAGACCCCTGTCTCAAAAC	98715
Qy	4513	AATAAATAAATAAAATAAAGGATCGGAGAGAAACAAA	4549
Db	98716	AAACAACAAAACAGAAAGAAAGAAAAAGAAAGAA	98752
RESULT 31			
ABD33272/c			
ID	ABD33272	standard; DNA; 227246 BP.	
XX	AC	ABD33272;	
XX	DT	18-NOV-2004 (first entry)	
XX	DE	Human cancer-associated (CA) gene HD07-047.	
XX	DE	Human cancer-associated protein; CAP; cancer-associated gene; CA; gene;	
KW	ds;	cancer; cytosstatic.	
XX	OS	Homo sapiens.	
XX	PN	WO2004058146-A2.	
XX	PD	15-JUL-2004.	
XX	PF	15-DEC-2003; 2003WO-US040081.	
XX	PR	17-DEC-2002; 2002US-00322281.	
XX	PA	(SAGR-) SAGRES DISCOVERY INC.	
XX	PI	Morris DW, Malandro MS;	
XX	WPI;	2004-499109/47.	
DR	XX	Novel human cancer associated protein encoded within open reading frame	
PT	PT	of cancer associated gene, useful as targets for diagnosing cancer.	
XX	PS	Claim 16; SEQ ID NO 314; 182pp; English.	
XX	CC	The invention relates to cancer-associated proteins (CAP) and the cancer-	
CC	CC	associated (CA) nucleic acids encoding them. The invention also relates	
CC	CC	to a method for treating cancers involving administering to a patient an	
CC	CC	inhibitor of CAP, and a method of screening for anticancer activity in a	
CC	CC	potential drug involving providing a cell that expresses a CA gene,	
CC	CC	contacting a tissue sample derived from a cancer cell with an anticancer	
CC	CC	drug candidate and monitoring the effect of the anticancer drug candidate	
CC	CC	on expression of the CA gene. The CAP proteins are useful for detecting	
CC	CC	cancer associated with expression of a CAP protein in a test cell sample	
CC	CC	and for screening for a bioactive agent capable of modulating the	
CC	CC	activity of a CAP protein. The CA nucleic acids are useful for diagnosing	
CC	CC	cancer, involving determining the expression of a CA nucleic acid in a	
CC	CC	tissue. This sequence represents a human CA gene of the invention. Note:	
CC	CC	The sequence data for this patent did not form part of the printed	
CC	CC	specification, but was obtained in electronic format directly from WIPO	
CC	CC	at ftp.wipo.int/pub/published_pct_sequences	
XX	Sequence	227246 BP; 57720 A; 53838 C; 54924 G; 60744 T; 0 U; 20 Other;	
Qy	Query Match	8.1%; Score 405.8; DB 13; Length 227246;	
	Best Local Similarity	59.7%; Pred. No. 1e-64;	
	Matches	898; Conservative 1; Mismatches 558; Indels 48; Gaps 11;	
Qy	3082	TTGTAAGTGGTGACAGTTTGGGTTTTTTTTTTGTTGTTTGTAGACAGAGGGTCTTGC-TC	3140

Db	140336	TGGTAATTGFAACTTTTTTTTCTCTCTTTTTTTTATATTTCTGAGACGGAGTTTGTCTC	140277
Qy	3141	TGTCACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGA	3200
Db	140276	TGTCACCCAGGCTGGAGTGAATGGCATGATCTTGGCTCACTGCAACCTCTGCACTCCCG	140217
Qy	3201	GCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCAACACC	3260
Db	140216	GTTCAAGCAATTCTCCTCGCTCAGCCACCTGAGTATCTGGGATTACAGGCACGTGCCACC	140157
Qy	3261	ACGCCTGGCTAATTAAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGC	3320
Db	140156	ACACCTGGCTAATTTTTTGTA--TTTAAGTAGGGACAGGGTTTCGCAATGTTGGCCAGGC	140099
Qy	3321	TTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTCTGGGAT	3380
Db	140098	TGGTTTCAAACTCCTGACCTCAGGTGATCCGCCCGCTCGGCCTCCCAAAGTCTGGGAT	140039
Qy	3381	TACAGGGGTGAGCCACCATGTGCGGTACTTATTTCTTTTACATTCCTTCCAATAGA	3440
Db	140038	TACAGGCGTGAGCCACCACACTTGGCCTACTTTTTTTTGTGTTTCTTTTT-----	139988
Qy	3441	ATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCTCTTTTGTAGACAGA	3500
Db	139987	-----GAGATAAGGTCTCACTTGTGCCCCAGGCTGGAGTGCAGTG	139947
Qy	3501	GTCTCACTTCATCACCTCAACCTCCGTTCACTGCAACCTCTGCCTCCCGGGTTCA	3560
Db	139946	GTGTAATCTTGGCTCAGTAGCATGATCTTGGCTCACTGCAACCTCTGCATCCCAGGTTCA	139887
Qy	3561	AGYGATTCTCTGCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCATGCT	3620
Db	139886	AGCAATTCTCTGCCTCAGCCACCTGAGTATCTGGGATTACAGGCACGTGCCACCAACC	139827
Qy	3621	TGGCTAAATTTTTGTATTTTAGCAGAGATGGGGTTTACCATGTTGCCCAGGCTGGTCT	3680
Db	139826	TGGCTAA--TTTTTGTAATTTAAAGTAGGGACAGGGTTTCGCAATGTTGGCCAGGCTGGTT	139768
Qy	3681	CAAACTCCTGACCTCAAGTGATCTGCCCTCAGTCAGTCTCCCAAAAGTCTGGAATTATAGG	3740
Db	139767	CAAACTCCTGACCTCAGGTGATCCGCCCGCTCGGCCTCCCAAAGTCTGGGATTACAGG	139708
Qy	3741	CGTGAGTCACTGTGCCCTGGCCGA--TTACTGTCTATTTTCTTTTATGCTATATCCCCAGA	3798
Db	139707	CGTGAGCCACCACACTTGGCCTACTTTTTTGTGTTTCTTTTTTGAGATAAGGCTCTCAC	139648
Qy	3799	TCTAGAGCAGTGTCTGCATATAGTAG--GTGCTCAATAAATAATTGATGAATGCACAGCC	3857
Db	139647	TTTGTGCCCAGGCTGGAGTGCAGTGGTGTAGTCTTGGCTCAGTAGCATGATCTTGGCTC	139588
Qy	3858	TAGATATAAACTTTCTTTTCTTTTAAACAAATCTTGACAACTTTGCAGATAAATA	3917
Db	139587	ACTGCAACCTCTGCCTCTCGGGTTCAAGTAATTCCTCGCCTCAGCCTCCAGAGTAGCTG	139528
Qy	3918	CAATCT-TGCATTCTGCTTTTTCACCTTATCACCTTGTATGACTTTTTTCATATTGCCTCA	3976
Db	139527	GAATTACAGGCGCCGCCACCATACCTAGATAATTTTATATTTTAGTAGAGATTTCAC	139468
Qy	3977	AACCTTTATTGTTACTGTTTTCATTGTTACTATTTTAGTCACCTGAATAATATGCTTA	4036
Db	139467	CATGTTGGCCAGGCTAGTCTCGACATCCGACCTCAGGTATGCTGCCTCAGCCTCCCA	139408
Qy	4037	ATTGCTTATACATCCTCTGCTCCACTTTTAGAAGGCCAAAATTTACAAATCTGATGAAG	4096
Db	139407	AAATGCTGAGATTACAGCATGTGCCACCCGACCCAGCCTATGTTTGTATTTTTTGAGGAAC	139348
Qy	4097	CTATGAACCTCTCTCCCCAGAGAAA---TACACACACACACACACTCACACACAGTTTT	4153
Db	139347	CACCATGCTTGTTTCCACAGTGACTTCACCATTTTACGTTCTCTACCAGTGGTGATGAA	139288
Qy	4154	TTTTTAATGTTTGCAACTAAGACAAGAAACCTTGCAATTAGAGGATGTTTGTTCATATTAAT	4213

Db	139287	GGCTCCAATTTCTCCACATCCTCACCAACACTTATTATCTGTCTGTTTGGTTATAGTCCT	139228
QY	4214	TAAAAATAACTCAGTTG-----GSCACAGTGACTCAAGCCCTGTPAACCCACAGTACTTTTG	4266
Db	139227	AAGAAAGTGGTATCTCAGGGGCCAGGTGCAGTGGCTCATGCTCTGTAATCCAGGAGTTTG	139168
QY	4267	GAAGTCCAAGTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCCAGCCTGGTCAATATG	4326
Db	139167	GGAGGCCAAGGTGGACAGATCACTTTAGGTCAGGAGTTCGAGACCCAGCCTGGCCCAACATG	139108
QY	4327	GTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGT	4386
Db	139107	GTGAAACAGCATCTCTACT-AAAAACAAAAATTAGCTGGGTGTGGGGGCAGGCACCTGT	139049
QY	4387	AGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAG-GCAGAGGT	4445
Db	139048	AATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTAAATCTGGGGGTGCGGAGGT	138989
QY	4446	TGCAGTGAGCCGAGATCCCACTGCCACTGCCAGCCTGGGCGACACAGCGAGACTCTATC	4505
Db	138988	TGCAGTGAGCCAAAGATCGGCCACTGCACTCCAGCCTGGGAGACAGACAAGACTCCGTC	138929
QY	4506	TCAAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAACTAATAAGATTCCTG	4565
Db	138928	TTGGAAAAAANAANAANAANAAGAGAAAAAGAAAAAGTGGTATCTCATTTAGTG	138869
QY	4566	AAGGT 4570	
Db	138868	ATGAT 138864	

RESULT 32
AAK84027/c
ID AAK84027 standard; DNA; 11872 BP.

XX	AAK84027;
DT	07-NOV-2001 (first entry)
XX	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38839.
DE	
XX	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW	cytostatic; gene therapy; vaccine; metastasis; ds.
XX	Homo sapiens.
OS	
XX	WO200157182-A2.
PN	
XX	09-AUG-2001.
PD	
XX	17-JAN-2001; 2001WO-US001354.
PF	
XX	31-JAN-2000; 2000US-0179065P.
PR	04-FEB-2000; 2000US-0180628P.
PR	24-FEB-2000; 2000US-0184664P.
PR	02-MAR-2000; 2000US-0186350P.
PR	16-MAR-2000; 2000US-0189874P.
PR	17-MAR-2000; 2000US-0190076P.
PR	18-APR-2000; 2000US-0198123P.
PR	19-MAY-2000; 2000US-0205515P.
PR	07-JUN-2000; 2000US-0209467P.
PR	28-JUN-2000; 2000US-0214886P.
PR	30-JUN-2000; 2000US-0215135P.
PR	07-JUL-2000; 2000US-0216647P.
PR	07-JUL-2000; 2000US-0216880P.
PR	11-JUL-2000; 2000US-0217487P.
PR	11-JUL-2000; 2000US-0217496P.
PR	14-JUL-2000; 2000US-0218290P.
PR	26-JUL-2000; 2000US-0220963P.
PR	26-JUL-2000; 2000US-0220964P.
PR	14-AUG-2000; 2000US-0224518P.
PR	14-AUG-2000; 2000US-0224519P.
PR	14-AUG-2000; 2000US-0225213P.

PR	14-AUG-2000; 2000US-0225214P.
PR	14-AUG-2000; 2000US-0225266P.
PR	14-AUG-2000; 2000US-0225267P.
PR	14-AUG-2000; 2000US-0225268P.
PR	14-AUG-2000; 2000US-0225270P.
PR	14-AUG-2000; 2000US-0225447P.
PR	14-AUG-2000; 2000US-0225757P.
PR	14-AUG-2000; 2000US-0225758P.
PR	14-AUG-2000; 2000US-0225759P.
PR	18-AUG-2000; 2000US-0226279P.
PR	22-AUG-2000; 2000US-0226681P.
PR	22-AUG-2000; 2000US-0226868P.
PR	22-AUG-2000; 2000US-0227182P.
PR	23-AUG-2000; 2000US-0227009P.
PR	30-AUG-2000; 2000US-0228924P.
PR	01-SEP-2000; 2000US-0229287P.
PR	01-SEP-2000; 2000US-0229343P.
PR	01-SEP-2000; 2000US-0229344P.
PR	01-SEP-2000; 2000US-0229345P.
PR	05-SEP-2000; 2000US-0229509P.
PR	05-SEP-2000; 2000US-0229513P.
PR	06-SEP-2000; 2000US-0230437P.
PR	06-SEP-2000; 2000US-0230438P.
PR	08-SEP-2000; 2000US-0231242P.
PR	08-SEP-2000; 2000US-0231243P.
PR	08-SEP-2000; 2000US-0231244P.
PR	08-SEP-2000; 2000US-0231413P.
PR	08-SEP-2000; 2000US-0231414P.
PR	08-SEP-2000; 2000US-0232080P.
PR	08-SEP-2000; 2000US-0232081P.
PR	12-SEP-2000; 2000US-0231968P.
PR	14-SEP-2000; 2000US-0232397P.
PR	14-SEP-2000; 2000US-0232398P.
PR	14-SEP-2000; 2000US-0232399P.
PR	14-SEP-2000; 2000US-0232400P.
PR	14-SEP-2000; 2000US-0232401P.
PR	14-SEP-2000; 2000US-0233063P.
PR	14-SEP-2000; 2000US-0233064P.
PR	14-SEP-2000; 2000US-0233065P.
PR	21-SEP-2000; 2000US-0234223P.
PR	21-SEP-2000; 2000US-0234274P.
PR	25-SEP-2000; 2000US-0234997P.
PR	25-SEP-2000; 2000US-0234998P.
PR	26-SEP-2000; 2000US-0235484P.
PR	27-SEP-2000; 2000US-0235834P.
PR	27-SEP-2000; 2000US-0235836P.
PR	29-SEP-2000; 2000US-0236327P.
PR	29-SEP-2000; 2000US-0236367P.
PR	29-SEP-2000; 2000US-0236368P.
PR	29-SEP-2000; 2000US-0236369P.
PR	29-SEP-2000; 2000US-0236370P.
PR	02-OCT-2000; 2000US-0236802P.
PR	02-OCT-2000; 2000US-0237037P.
PR	02-OCT-2000; 2000US-0237038P.
PR	02-OCT-2000; 2000US-0237039P.
PR	02-OCT-2000; 2000US-0237040P.
PR	13-OCT-2000; 2000US-0239935P.
PR	13-OCT-2000; 2000US-0239937P.
PR	20-OCT-2000; 2000US-0240960P.
PR	20-OCT-2000; 2000US-0241221P.
PR	20-OCT-2000; 2000US-0241785P.
PR	20-OCT-2000; 2000US-0241786P.
PR	20-OCT-2000; 2000US-0241787P.
PR	20-OCT-2000; 2000US-0241808P.
PR	20-OCT-2000; 2000US-0241809P.
PR	20-OCT-2000; 2000US-0241826P.
PR	01-NOV-2000; 2000US-0244617P.
PR	08-NOV-2000; 2000US-0246474P.
PR	08-NOV-2000; 2000US-0246475P.
PR	08-NOV-2000; 2000US-0246476P.
PR	08-NOV-2000; 2000US-0246477P.
PR	08-NOV-2000; 2000US-0246478P.
PR	08-NOV-2000; 2000US-0246523P.

QY 1480 ATCTAGCTGAGGCGGTAGGGTCCCAAGAAGAAGAAGAAAAAGAAAGATATAT 1539
Db 4371 CATGCTCATGAAAAATGAAATTCATCAAAACAGTTTTATTATTTTAGAGAGAGGTCITG 4312
QY 1540 ATATATATACACACACACAAAGATATAAACTTTATATATATAAAGTTTTTCATTAAAAAAA 1599
Db 4311 CTCTGTTACCGGGCTGGAGTGCAGTGGTACAATTATAAATCAACACAGACTTGAATTC 4252
QY 1600 AAAAAAACCTCTACCCACT--TTCACTTTACCAGGTTCCCTGGGTCCAACGGTCTTCAGA 1657
Db 4251 TGAGCGCAAGTATCCTCCTGCTTCAGCTTCCCAGGTAGCCGGACTACAGGCATGCACC 4192
QY 1658 GGAGGCAGCTGGCAGGGGTTCAGGGAGGCAGCGTGGGACCCGAGGAGCAGGAAGGCAGTG 1717
Db 4191 ATGAGGCTGGCTAAATTTTTTCTTTAAAAAATTAAATAAAATTTTAAAGAAAAAGTTTTT 4132
QY 1718 --TGTCCCGGGGTGCTGGCAGACCGAATTGAACCTCTGGCTATGCTTCTTGCAGTGGCC 1775
Db 4131 AAAGATGGCTGGGCACAGTGACTCAGCGCTGTAATCCCAACACTTTGGGAGCCGAGACG 4072
QY 1776 GCCGCGMCAGCGGCATCAGCCCTCGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGC 1835
Db 4071 GGTGGATCACTGAGGTCAGGAGTTTGAGAG-CAGCCTGGCCAAACATGGTGAAACTGCGC 4013
QY 1836 GTGATCCCGGGGAGTGACCCCTTYTTGGAATACAACAACACTACGGCTGCTACTGTGGCTTG 1895
Db 4012 CTCTACTAAAAATACAAAAAATTAGCCAAGCATGGTGGCAGGCACCTGTAATCCCAGCTA 3953
QY 1896 GGGGGCTCAGGCACCCCGTGGATGAACTGGACAAGTAAGTATCGCCTGCAGGAAAT 1955
Db 3952 TTCGGGAGGCTAAGGCAGGAGAAATCGCTTGAACCTCGCGGTGGAGGATGCAGTGAGCCAA 3893
QY 1956 TGGAGTGCTGCCGGGGCGGGGTGGGGCACACGCCAAGGATCTCACGAGGCATACAAAG 2015
Db 3892 GATTGCACCATTGCACCTCCAGCCTGGGCAACGAGATCAAAACTCCGTCTCCAAAAA 3833
QY 2016 GGGACTTGCATATCTGTAAGGATAACATATTTTCACTCTTTGTCAAAATAAACAAATATG 2075
Db 3832 AAAAAAGTTTTTTTAGAGATGCAGTCTCACATATGTTGCCTAGGCTGGTCTCAAACTCCT 3773
QY 2076 TTCCAAGAGGACCCCTGTAGCGAACCGCACCCCGTTAGAGATGGAACAATGACCGACGTGC 2135
Db 3772 GGCCTCAAGTGATCCTCCTGCCTCCTGAGTAGCTAGGATTACAGGCATAAGCCACAGCAC 3713
QY 2136 AAAACAGTGGGCGATGCTGCCCTCCAGTGGCAGAAATGTAGCRAACAGTAAACATCACAGCA 2195
Db 3712 CAGGCAAAAAAANAATTTTTTAATTGTACCTTAAATCCCATTTCCCAAAAATAACTACC 3653
QY 2196 ACTATCCACGTGTCATTTTCTAGCAGTGGTTGTCACTGCACTGCACCTTCTGAATACAGGATTTT 2255
Db 3652 ATTAGCATTTGGTGAAACATTATTCAAGACGTCTCTCAATGCAATTTATAAAAAAACACTGA 3593
QY 2256 ACTGTATCTTGC-----AACCATGTTAAAAAATCGCTTTCAGGCCAGGCGCGGTGGC 2307
Db 3592 GACATAGACTAACTTTAACTGCTTCCCTAAAAAATAAAAAGTATTCAGTCGGGCGCAGTGGC 3533
QY 2308 TCATGCCTGTAATCCCAGCACCTTTGGAGGCCGAGGCGGGCGGATCACTTTGAGGTCAGGA 2367
Db 3532 TCACGCCTGTAGTCCCAGCACCTTTGGGAGGCTGAGGCGGATGGATTGCCTGAGGTCAGGA 3473
QY 2368 GTTCGAGACCAGCCTTGGCCAACATGGTGAACCCCTGTCTCTACTAAAAAATACAAAAATT 2427
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QY 2428 AGCCGGACATGGTGGCGAGCGCCTGTAAACCCAGCTACTTTGGGAGACTGA-GTTGGAGGT 2486
Db 3413 AGCCGGGATGGTGGTACGTGCTGTAAATCCAGCTACTCAGGGGCTGAGGCAGGAGAA 3354
QY 2487 TTCAGTGAGCCAAGGTGCTGTCACTGCTGTCCAGCCTGGGTAAC-----AGAGCAACT 2539
Db 3353 TTGCTTGAAACCCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCATTCCACCAACTCAAGC 3294
QY 2540 CTGCTCTCAAAAAAANAANAATGCTTTTCAATAAAATATATGATAAAAGGACTTATATTTTTTC 2599

Db 3293 CTGGGTGACAGAGCGAGACTCCATCTCAAAAAAGTAATAAAAAATATATATAATTAA 3234
QY 2600 AAGCCATAGGATCATTTCTCTCTGAAGCATCTTTGGGAAGTCAATCCCCACCTGTTCTTGAG 2659
Db 3233 ATAAAAATAAAAAGTATTCAAATATAAATTTTATT--TGAATTTACATATTATAGTTTCAGAA 3176
QY 2660 AGTGGCAGGTGAGGCTGACCTATTGCTCTGCACTTACTCTATCTCAGTGTCCCTCC 2719
Db 3175 AAAAACTCAATTATTAGAACATGTTGAGGTTTCAGATACACATCTTTCTTTTATGAAAA 3116
QY 2720 CACTTTCCAGGTGCTGCCAGACACATGACAACTGCTAYGACCAGGCCAAGAAGCTGGACA 2779
Db 3115 CTATGAC----TTAAAAATATACTTGTACAAGCTGTTGAGGTAGCTCTAGACGGACAAAA 3060
QY 2780 GCTGTAAATTTCTGCTGCACAMMCCGTACACCCACACCTATTTCATACCTCGTGTCTGGCT 2839
Db 3059 GCCAGAAATACTGTCTTGACAA-----AGACAGATCTCATGACACAAATTTGTTTGGC- 3008
QY 2840 CGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTTGACCTATGAATTTCTAGTTGGTTC 2899
Db 3007 -----AATTTTGTGTTTTTCTTCTTATTTTAAAAAGGTCAAAAATCCCA 2962
QY 2900 TCAGTAGGCCGGGGGAAATAAATAGTAACAACAGCCATGATTTAGTGTAAATTTCTTGG 2959
Db 2961 GGGTCTTGATATCTGGCAGTTGGTTTCAGCAGTGTGAGACAGTTACTTATACTTCTTGT 2902
QY 2960 TTCTGGCAGTGTCTCCTTTAAATCCTCAGAAACAACACTATGGGATAGGTACAAATATCCT 3019
Db 2901 CTATGACTGTTAACGTTCTCGCACAGCAGAAAAATGCAAAAGTAATCTTGAAGCTTTTCATACT 2842
QY 3020 C-ACTTAACAGATAAGAAAACTGAGGCTCAGAGSCTGAGCTATTTGCCCCAAGATCACAC 3078
Db 2841 CTGCAATTCACTGTTCTTCATCCCAGCTCATTTGCCCTGTGGAAGAAATTCACACAGAACTC 2782
QY 3079 AGCTTGTAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTTTGTAGAGACAGGGTCTTGC 3138
Db 2781 TAACTCT-AGACTTGTGTTCTCTTGCAATTTACTTTTTTTTTTTTGTGAGATGGAGTCTCGC 2723
QY 3139 TCTGTCACCCAGGATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCT 3198
Db 2722 TCTGTTGCCAGGCTGGAGTGCAGTGGTGTGCAATCTTGGCTCACTGCAAGCTCTGCCTCCT 2663
QY 3199 GAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGCTTACTACGTTGGCCAG 3258
Db 2662 GGGTTCACGCCAATTCCTCGCTCAGCCTCCGAGTACCTGGGACTACAGGAGCCCGCCA 2603
QY 3259 CCACGCCTGGCTAAATTAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAG 3318
Db 2602 CCACGCTTGGCTAAATTTTTTGTA-TTTTTAGTAGAGATGGGTTTTTCAACCGTGTAGCCAG 2544
QY 3319 GCTTGTCTTAAACCTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAAGTG---- 3373
Db 2543 GATGGTCTCGATCTCCTGACCTC--GTGATCCACCCGTCTTGGCCTCCCAAAAGTGTAAA 2486
QY 3374 ---CTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTCATCT 3430
Db 2485 GTACTGGGATTACAGGCGTGAGCCACCGCGCCACGCCCTATTTTTTATTATTATTATTTT 2426
QY 3431 TTCCAATAGAATGTAAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCTTTTCTTTT 3490
Db 2425 TCGAGATCAA-----GTCTCACITTTGTGCGC 2401
QY 3491 TTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTCAGCTCACTGCAACCTCTGCCT 3550
Db 2400 CCAGGCTGGAGTGCCATGGCACAATC-----TAGGCCAGTGCACACCTCGCCT 2352
QY 3551 CCCGGGTTCAAGYGATTTCTCTGCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCTGCA 3610
Db 2351 CCTGAGTTCAAGTGATTTCTCTGTCTCAGCCTCCCATGTAGCTGGGACTACAGGTCCTG 2292
QY 3611 CCACCATGCTTGGCTAAATTTTGTATTTTTTAGCAGAGATGGGTTTTTACCATGTTGCC 3670

PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0251479P.
PR 06-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure; SEQ ID NO 21705; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosstatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 11872 BP; 3363 A; 2615 C; 2631 G; 3263 T; 0 U; 0 Other;
Query Match 8.1%; Score 404; DB 4; Length 11872;
Best Local Similarity 50.7%; Pred. No. 1.4e-64;
Matches 1695; Conservative 4; Mismatches 1484; Indels 163; Gaps 24;
QY 464 AATTTTATTTTATTTTACTTTTATTTTATTTTGTGAGACGGGGTCACTCTGTCGCCCAG 523
DB 5342 AGTTTTAGAAAATATTTATTTGTTTTTTTTTTTGAGACAGAGTCTCGTCTGCACCCAG 5283
QY 524 GCTGGAGTGGCGTGGTATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAATAA 583
DB 5282 GCTGGAGTGCAGTGGCGTGATCTTGGCTCACTGCAAGCTCTGCCTCCCGGTTACGCCA 5223
QY 584 TTCTCTTGCCTCAGCCTCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACA 643
DB 5222 TTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGCT-----ACAGGCACCTG 5178
QY 644 CCACCATGCCAGCTAATTTTTTGTGTTTGTGGTAGACACAGGTTTTTCACCATGT 703
DB 5177 CCACCACACCCGGCTAATTTTTTG-----TATTTTGTAGATAGATGGGTTTCACCATGT 5123

QY 704 TGGCCAGGCTGGGTGACCTCCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCCTTT 763
DB 5122 TAGCCAGGATGGTCTTGATCTCTGACCCGCGTGATCCGCCCATCTCGGCCCTCCCAAAGTG 5063
QY 764 CTAATGCAGTATCCAGTTTCCTTACTTATCATCATTTATTATTATTCTTATTATTAG 823
DB 5062 CTGGGATTACAGGCATGAGCCACCGTGCCCCAGCCT-----TTGTTTTTTTTTTGAG 5011
QY 824 ACAGAGTCTTGTGTCGCCAAGGCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAA 883
DB 5010 ACAGAGTTTCACTCTGTGCCCCAGGCTGGAGTGCACTGGCGCGATCTTGGCTCACTGCAA 4951
QY 884 GCTCCACCTGCTGGGTTACGCCCATTTCTCCCGCCTCAGCCTCCCCAGTAGCTGGACTAA 943
DB 4950 GCTCCGCCTCCCGGGTTCACGGCATTTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGCTAT 4891
QY 944 AGCGCCTGCCACCCAGCCCGCTAAATTTTTTGTGATTTTAAATAAAGACGGGTTTCAT 1003
DB 4890 AGCACCTGCCACCATGCTCAGCTATATTTTTTGTGATTTTAGTAAAGACGGGTTTCAC 4831
QY 1004 CGTGTAGCCAGGATGGTCTCGATCTCATGACCTTGTGATCCGCCCTGCCCTCGGCCTCCCA 1063
DB 4830 CGTGTAGCCAGGATGGTCTTGATCTCTGACCTCGTGATCCGCCCATCTCGGCCTCCCA 4771
QY 1064 AAGTGCTGGGATTACAGGCATGAGCCACCGTGCCCGGCCTTATCACATTTATTATTATT 1123
DB 4770 ACGTGCTGGGATCACAGGCATAAGCCACCGTGCCCGCCAAATTTTTTTTTTTTGAGACG 4711
QY 1124 GTTTTTCTCTCCCAGTGGTTGTAAGCTCCATGAGGTAGAGATTATTATTATTATTATT 1183
DB 4710 GAGTCTTGCTCCGTCGCCCAGACTGGAGTGAATGGCATGATCTCGGCTCACTTGCCTC 4651
QY 1184 ATTATTATTATTATTATTATTATTATTATATATCTGTTCACTGCTGTATCTCTAGTCTCTAG 1243
DB 4650 CCGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTATACGCATGTAC 4591
QY 1244 GACAGAGCCTGGCACATAGTAAGTGCTCAATAAATATTCACTGGATAAACAGTGCAGATA 1303
DB 4590 CACCAGGCCTGGC-----TAATTTTGTATTTTGTAGTAAATG 4552
QY 1304 GTTTAAAACTATCTGACCTAGGGAGGCTGAGGAGGAGAATGGCGTGAACCCGGGAAGCA 1363
DB 4551 GGGTTTCACTTGTGGTCAGGCTGGTCTCGAACTCCTGACCTCGTGATCTGCCTGCCTC 4492
QY 1364 GAGTTTGCAGTGAGCTGAAATCGTGTCACTGCACTCCAACCTGGGCAACAGAGCAAGACT 1423
DB 4491 AGCCTCCCAAAGTGTGGGATTACAGGAGTGAGCCACCGCCCCGGATTTCAGAAAAATA 4432
QY 1424 CCATCTCAAAAAAATAAACTATCA---GGCCTAGCTGGGTGGCACATGCCTGTA 1479
DB 4431 TTTATAGAAAAAGTAGTACATGGTTTATTTTACAGCTTTATTGTTTCGTAAAACTTATA 4372
QY 1480 ATCTTAGCTGAGGCGGTAGGTTCCCAAGAAAGAAAGAAAAAGAAAGAAAGATATAT 1539
DB 4371 CATGCTCATTAGAAAAATGAAATTCAAATCAAAACAGTTTATTTTATAGAGAGAGGTCTTG 4312
QY 1540 ATATATATACACACACAAAGATATAAACTTTATATATATAAAGTTTTCATTAAAAAAA 1599
DB 4311 CTCTGTTACCCGGGCTGGAGTGCAGTGGTACAATATAACTCACACAGACTTGAATTC 4252
QY 1600 AAAAAAACCTCTACCCACT--TTCACTTTACCAGGTTCCTGGGTCCAACGGTCTTCAGA 1657
DB 4251 TGAGCGCAAGTGATCCTCTGCTTCAGCTTCCCAGGTAGCCGGGACTACAGGCATGCACC 4192
QY 1658 GGAGGCAGCTGGCAGGGTCAAGGAGGCAGCGTGGGACCCGAGGAGCAGGAAGGCAGTG 1717
DB 4191 ATGAGGCCTGGCTAATTTTCTTTTAAAAAATTAAATAAAATTTTAAAGAAAAAGTTTT 4132
QY 1718 --TGTCCCCGGGTGCTGGCAGACCGATTGTGAACCTGGCTATGTCTTCTTTCAGTGGCC 1775
DB 4131 AAAGATGGCTGGGCACAGTGACTCAGCGCTGTAATCCCAACACTTTGGGAGGCCGAGACG 4072

Qy	4511	AAATATAATAATAATAAGGATCGGAGAGAAACAAACTAA	4554
Db	11359	AAAAAAAAAAAAAAAAAAAAAAAAAGATAACAAAAGAACAAA	11316
RESULT 35			
AAK77881			
ID	AAK77881 standard; DNA; 17173 BP.		
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AC	AAK77881;		
XX			
DT	07-NOV-2001 (first entry)		
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32693.		
XX			
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KW	cytostatic; gene therapy; vaccine; metastasis; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200157182-A2.		
XX			
PD	09-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US001354.		
XX			
PR	31-JAN-2000; 2000US-0179065P.		
PR	04-FEB-2000; 2000US-0180628P.		
PR	24-FEB-2000; 2000US-0184664P.		
PR	02-MAR-2000; 2000US-0186350P.		
PR	16-MAR-2000; 2000US-0189874P.		
PR	17-MAR-2000; 2000US-0190076P.		
PR	18-APR-2000; 2000US-0198123P.		
PR	19-MAY-2000; 2000US-0205515P.		
PR	07-JUN-2000; 2000US-0209467P.		
PR	28-JUN-2000; 2000US-0214886P.		
PR	30-JUN-2000; 2000US-0215135P.		
PR	07-JUL-2000; 2000US-0216647P.		
PR	07-JUL-2000; 2000US-0216880P.		
PR	11-JUL-2000; 2000US-0217487P.		
PR	11-JUL-2000; 2000US-0217496P.		
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PR	26-JUL-2000; 2000US-0220963P.		
PR	26-JUL-2000; 2000US-0220964P.		
PR	14-AUG-2000; 2000US-0224518P.		
PR	14-AUG-2000; 2000US-0224519P.		
PR	14-AUG-2000; 2000US-0225213P.		
PR	14-AUG-2000; 2000US-0225214P.		
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DT XX 05-NOV-2002 (first entry)
XX XX Human phosphodiesterase genomic sequence.
DE XX
KW XX Human; phosphodiesterase; PDE; phosphoinositide-specific phospholipase C;
KW KW gene therapy; vaccine; protein therapy; inflammatory disease; asthma;
KW KW chronic obstructive pulmonary disease; rheumatoid arthritis; atopy;
XX XX chromosome 2; gene; ds; enzyme; SNP; single nucleotide polymorphism.
OS XX Homo sapiens.
XX XX
FH XX
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Db	9433	TTTTCATGAGGCGAGTGTCTTGCTGATCTAGGCACCTAAATGATGTCTGGTGCCTAGCAT	9374
Qy	3900	AACTTTGCAGAAATAAATACAATCTTGCAATCTGCTTTTTCACCTATATCACCTTGTATGAC	3959
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Qy	4080	TACAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAAATACACACACACACACAC	4139
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Qy	4260	TACTTTGGAGTCCAAGGTGGTGGATCACTTGAGGTGAGAGTTTCGAGACCCAGCCTGGT	4319
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DT	07-NOV-2001 (first entry)		
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KW	Human; immunosuppressive; antiarthritic; ds; antirheumatic; cytostatic;		
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KW	antibacterial; virucide; fungicide; opthalmological; vulnerary;		
KW	secreted protein; rheumatoid arthritis; hyperproliferative disorder;		
KW	cardiovascular disorder; cardiac arrest; cerebrovascular disorder;		
KW	cerebral ischaemia; angiogenesis; nervous system disorder;		
KW	Alzheimer's disease; infection; ocular disorder; corneal infection;		
KW	wound healing; epithelial cell proliferation; skin ageing; food additive;		
KW	preservative; antiproliferative.		
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PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-488783/53.
DR
XX
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Disclosure; SEQ ID NO 1644; 980pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence is a genomic DNA encoding a partial novel secreted protein of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format

Query Match 8.0%; Score 400.4; DB 4; Length 14176;
Best Local Similarity 60.5%; Pred. No. 6.6e-64;

Matches 859; Conservative 1; Mismatches 477; Indels 83; Gaps 9;			
QY	3104	TTTTTTTTTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCAGGCATGAGCACAGT	3163
Db	4608	TTGACTTCTTTGTTTTTTTGAGATGGAGTCTCGTGTGTGCCAGGCTGGAGTGCAGT	4549
QY	3164	GGTGCAACATAGGTCACTGCAGCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA	3223
Db	4548	GGCGCAATCTTGGCTCACTGCAACCTCTGCTCTTGGGTTCAAGCAATTCTCTG-CCTCA	4490
QY	3224	GCCTCCCAAGTAGCTGGACTAC-GAGCGTGCACCACCGCTGGCTAATTAAAAAAT	3282
Db	4489	GCCTCTGGAGTAGCTGTGATTACAGGCAACCCACCACCATGCCAGCTAATTTTTGTA--	4432
QY	3283	TTTTTTTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCA	3342
Db	4431	TTTTTTAGTAGATGGGTTTCACTGTCTTGGTCAGGCTGGTCTTGAATTCCTGACCTC-	4373
QY	3343	AGCAATCCTCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTG	3402
Db	4372	-GTGATCCACCCACCTCGGCTTCCCAAAGTTCTGGGATTACAGCGTGAGCCACCTGCAC	4314
QY	3403	CGGCTACTTATTTCTTTACATTCATCTTTCCAATAGAAATGTAAGATCCACAGAACAGG	3462
Db	4313	CCGGCCTTTTTTTTTT-----	4298
QY	3463	ATTACTGCTATTTTCTTCTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACC	3522
Db	4297	-----TTTTTTTTTGAGATGGAGTCTTGCTGTTGCCAGGCTGGAGTGCAATGGCG	4247
QY	3523	TCCGTTCACTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCT	3582
Db	4246	CAGTCTCGGCTCACTGCAACCTCAGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCT	4187
QY	3583	CCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTTA	3642
Db	4186	CCTGAGTAGCTGGGATTACAGGCGCCGCCACCATGCCCCAGCTAATTTTTGTATTTTAG	4127
QY	3643	GCAGAGATGGGTTTTTACCANGTGCCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTAT	3702
Db	4126	TAGAGATGTGGGTTTCACCATGTTGGCAGGCTGGTTTCGAACCTCCTGACCTCAGGTGAT	4067
QY	3703	CTGCCTGCCTCAGTCTCCCAAAGTGTCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCG	3762
Db	4066	CTGCCCGCCTCGGCCCTCCCATAGTGTGGGATTACAGGTGTGAGCCACCAACGCCGCGCT	4007
QY	3763	ATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAG	3822
Db	4006	TTTGACTTC-----TTAATAATGGCCATTCTTGCAAGGAGTAAGCAGTACCT-----	3960
QY	3823	TAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTCTTTTCTTTT	3882
Db	3959	TATTGTGGCTTTAAATTTTGCAACCTTCCTGATGATTAGTGATGTTTCAGCATTTTTCATGT	3900
QY	3883	TTTAAACAATCTTGACAACTTTTGCAGAATAAATACAATCTTGCAATCTGCTTTTTCAT	3942
Db	3899	TTGTTGGTCATTTGTATATATATTTTGGAGAACTGTCTCCAATGTCATTTGCCTACTTTT	3840
QY	3943	TATCACCTTGTTATGACTTTTTCATATGCTCCTCAAACCTTTATGTTACTGTTTTTTCAT	4002
Db	3839	GATGGGATTTTTTTTCTTGTGTGACTTG-----TTAGAGTTACTTGTAGATTCT	3790
QY	4003	TGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCA	4062
Db	3789	GGATATTAGTCTTTGTCTGTATGCATAGTTTGCAATAATTTTCTGCCATCCTGTGGATGA	3730
QY	4063	CTTTAGAAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCCCCAGAGAAATA	4122
Db	3729	GTCTTGCTCTTTTCGTCAGAAAAATTCAAAAAGTTTGTGTTTACATTCCTGTTGGCATCA	3670
QY	4123	CACACACACACACACTCACACAGTTTTTTTTTAAATGTTTGCACATAAGACAAGAAA	4182
Db	3669	AGTACACACACACATCCACCTCTGTGTACTCCCGTTACATCATAGTTTC-ATCTGATGAAC	3611

QY	4183	CCTGCATTAGAGGATGTTTGTTCATATTAATTTAAAAATAAAGTCACTGTTGGGCAGTGACT	4242
Db	3610	ATTTTTTATGACAGTTATTTTTCTTTTATAAAAGAACTGATGGCCAGGCACGTGGCT	3551
QY	4243	CAAGCCTGTAACCAACAGTACTTTTGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAG	4302
Db	3550	TAAACCTGTAATCCACAGCACTTTGGAGGCTGAGCGGTTGGATCACCCAAAGTCAGGAG	3491
QY	4303	TTGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAG	4362
Db	3490	TTTGAGACCAGCCTGGCCAACATGGCAAAACCCCATCTCTACTAAACATACAAAAATTAG	3431
QY	4363	CTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAAATT	4422
Db	3430	CTGGGTGTGTCATGCACGCCTGTAGTCTCAGCTACTTGAGAGGCTGAGGCAGAGAAATC	3371
QY	4423	GCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACCTGCACCTCAGCCT	4482
Db	3370	ACTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAGATCGCATCATTTGCACCTCTAGCCT	3311
QY	4483	GGCGGACACAGCGAGACTCTATCTCAAAAAATAATAAAA 4522	
Db	3310	GGCGGACAGAGCAAGACCCCATCTCAAAAAAAGAA 3271	

RESULT 38
ABX74019/c

ID ABX74019 standard; DNA; 14176 BP.

XX AC ABX74019;

XX AC ABX74019;

DT 18-MAR-2003 (first entry)

XX Human novel polynucleotide #847.

KW Human; gene; ds; neural disorder; immune system disorder; renal disorder;
KW muscular disorder; respiratory disease; reproductive disorder;
KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;
KW hyperproliferative disorder; inflammatory disease; allergic reaction;
KW blood related disorder; cancer; immunosuppressive; antiinflammatory;
KW cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
KW haemostatic; antiarteriosclerotic.

XX OS Homo sapiens.

XX US2002132753-A1.

PD 19-SEP-2002.

XX 17-JAN-2001; 2001US-00764864.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 28-JUN-2000; 2000US-0214886P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 22-AUG-2000; 2000US-0226868P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

Db	165136	AGTACACACACATCCACCTCTGTACTCCCGTTACATCATAGTTTC-ATCTGATGAAC	165078
Qy	4183	CCTGCATTAGAGGATGTTTGTTCATATTAATAAAAAAATACTCAGTTGGGCACAGTGACT	4242
Db	165077	ATTTTTATGACAGTTATTTTTTCCTTTATAAAGAACAAGTGGCCAGGCACGGTGGCT	165018
Qy	4243	CAAGCCTGTAACACAGTACTTTGGAAAGTCCAAGGTGGGTGGATCATTGAGGTGAGAAG	4302
Db	165017	TAAACCTGTAATCCCAAGCACTTTGGGAGGCTGAGCGGGTGGATCACCCAAAGTCAGGAG	164958
Qy	4303	TTGAGACCAGCCTGGTCAATATGGTGAACCCATCTCTACTAAAAATACAAAAATTAG	4362
Db	164957	TTTGAGACCAGCCTGGCCAAACATGGCAAAACCCCATCTCTACTAAACATACAAAAATTAG	164898
Qy	4363	CTGGGTGTAGTGATGCAATGCCTGTAGTCCACGCTACTCGGAGGCTGAGGCAAGAGAATT	4422
Db	164897	CTGGGTGTGGTCATGCACGCCCTGTAGTCTCAGCTACTTTGAGAGGCTGAGGCAGGAGAATC	164838
Qy	4423	GCTTGAACTTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACACTGCACCTCCAGCCT	4482
Db	164837	ACTTGAACTCCAGGAGGCAGAGGTTGCAGTGAGCCGAGATCGCATCATTTGCACTCTAGCCT	164778
Qy	4483	GGCGCACACAGCGAGACTCTATCTCAAAAAAATAAATAAA	4522
Db	164777	GGCGCACAGAGCAAGACCCCATCTCAAAAAAATAAATAAA	164738

RESULT 40
ADB20847/C
ID ADB20847 standard; DNA; 177531 BP.
XX
AC ADB20847;
XX
DT 20-NOV-2003 (first entry)
XX
DE MRP1 based cancer related nucleic acid SEQ ID NO:660.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KW ds.

can be used for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject, where the subject is a human (preferably African or Asian) or a mouse. The present sequence represents a sequence which is used in the exemplification of the present invention.

Sequence 177531 BP; 51602 A; 39077 C; 38304 G; 48548 T; 0 U; 0 Other;

Query Match 8.0%; Score 400.4; DB 8; Length 177531;
 Best Local Similarity 60.5%; Pred. No. 9.5e-64;
 Matches 859; Conservative 1; Mismatches 477; Indels 83; Gaps 9;

Qy	3104	TTTTTTTTTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCTCACCCAGGCATGAGCACAGT	3163
Db	166075	TTGACTTCTTTGTTTTTTGAGATGGAGTCTCGTGTGTTGCCAGGCTGGAGTGCAGT	166016
Qy	3164	GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA	3223
Db	166015	GGCGCAATCTTGGCTCACTGCAACCTCTGCCTCTTGGGTTCAAGCAATCTCTG-CCTCA	165957
Qy	3224	GCCTCCCAAGTAGCTGGGACTAC-GAGCGTGCAACCAACCCAGCGCTGGCTAATTAATAAAT	3282
Db	165956	GCCTCTGGAGTAGCTGTGATTACAGGGCAACCCACCACCATGCCAGCTAATTTTGTGA--	165899
Qy	3283	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCA	3342
Db	165898	TTTTTAGTAGAGATGGGTTTCACTGTCTTGGTCAGGCTGGTCTTGAATTCCTGACCTC-	165840
Qy	3343	AGCAATCCTCCTACCTTGGCATCCCAAAAGTCTGGGATTACAGGGTGAGCCACCATGTG	3402
Db	165839	-GTGATCCACCCACCTCGGCTTCCCAAAAGTCTGGGATTACAGGCGTGAGCCCTGCAC	165781
Qy	3403	CGGCTACTTATTTCTTTTACATTCCTATCTTTCCAATAGAATGTAAGATCCACAGAACAGG	3462
Db	165780	CCGGCCTTTTTTTTTT-----	165765
Qy	3463	ATTACTGCCTATTTCTTCTCTTTTGTGAGACAGAGTCTCACTTCACTCAACCAACC	3522
Db	165764	-----TTTTTTTTTTGAGATGGAGTCTTGTGTGCCAGGCTGGAGTGCAATGGCG	165714
Qy	3523	TCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGTTTCAAGYGATTCTCCTGCCTAAGCCT	3582
Db	165713	CAGTCTCGGCTCACTGCAACCTCAGCCCTCCTGGGTTCAAGCGATTCTCCTGCCCTCAGCCT	165654
Qy	3583	CCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTTAATTTTGTATTTTATA	3642
Db	165653	CCTGAGTAGCTGGGATTACAGGCGCCCGCCACCATGCCAGCTAATTTTGTATTTTATAG	165594
Qy	3643	GCAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGAT	3702
Db	165593	TAGAGATGTGGGTTTACACCAATGTTGGCCAGGCTGGTTTCGAACTCCTGACCTCAGGTGAT	165534
Qy	3703	CTGCCCTGCCTCAGTCTCCAAAGTGCTGGAATTATAGGCGTGAGTCACCTGTGCCCTGGCCG	3762
Db	165533	CTGCCCGCCTCGGCCTCCCATAGTGTCTGGGATTACAGGTGTGAGCCACACCGCCCGCCT	165474
Qy	3763	ATTACTGTCTATTTTCTTTATTTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAG	3822
Db	165473	TTTGACTTC----TTAATAATGGCCATTCTTGCAAGGATGAAGGCAGTACCT-----	165427
Qy	3823	TAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTT	3882
Db	165426	TATTGTGGCTTTAATTGCACCTTCCTCATGATTAGTGTGTTGAGCATTTTTCATGT	165367
Qy	3883	TTTAAACAATCTTGACAACTTTTGCAGAAATAAATACAATCTTGCATTCTGCTTTTTCAC	3942
Db	165366	TTGTTGGTCATTGTATATATATTATTTTGAAGAACTGTCTCCATGTCAATTTGCCTACTTTT	165307
Qy	3943	TATCACCTTGTATGACTTTTTCATATATGCGCTCAAACTTTTATTTGTTACTGTTTTTTCAT	4002
Db	165306	GATGGGATTTTTTTTTTCTTGTGTGACTTG-----TTAGAGTTACTTTGTAGATTCT	165257
Qy	4003	TGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCA	4062

Db 165366 TTGTTGGTCAATTGTATATATATATTTTGAGAACTGTCTCCAATGTCATTTGGCCTACTTTTT 165307
QY 3943 TATCACCTTGTTATGACTTTTTTCATATGTCCTCAAACCTTTTATGTTACTGTTTTTTCAT 4002
Db 165306 GATGGGATTTTTTTTCTTGTGACTG-----TTAGAGTTACTTGTAGATTCT 165257
QY 4003 TGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCA 4062
Db 165256 GGATATTAGTCCTTGTCTGATGCATAGTTTGCAAATATTTTCTGCCATCCTGTGGATGA 165197
QY 4063 CTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCTCCCGAGAGAAATA 4122
Db 165196 GTCTTGCTCTTTTCGTCAGAAATTCCAAAGTTTGTGTTTACATTCTCTGTTGGCATCA 165137
QY 4123 CACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAA 4182
Db 165136 AGTACACACACACATCCACCTCTGTTACTCCCGTTACATCATAGTTTC-ATCTGATGAAC 165078
QY 4183 CCTGCATTAGAGGATGTTTGTTCATATTAATTAATAAATAAATCACTAGTTGGGCACAGTACT 4242
Db 165077 ATTTTTTATGACAGTTTATTTTTTCCTTTATAAAGAACTGATGGGCCAGGCACGGTGGCT 165018
QY 4243 CAAGCCTGTAACACAGTACTTTTGGAGTCCAAAGGTGGGTGGATCACTTGAGGTGAGAAG 4302
Db 165017 TAAACCTGTAATPCCAGCACCTTTGGGAGGCTGAGGCGGTGGATCACCCAAAGTCAGGAG 164958
QY 4303 TTCGAGACCAAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAAATACAAAAATTAG 4362
Db 164957 TTTGAGACCAAGCCTGGCCAAACATGGCAAAACCCCATCTCTACTAAACATACAAAAATTAG 164898
QY 4363 CTGGGTGTAGTGATGCATGCCGTGTAGTCCAGCTACTCGGGAGGCTGAGGCCAAGAGAAAT 4422
Db 164897 CTGGGTGTGTGTCATGCACGCCTGTAGTCTCAGCTACTTTGAGAGGCTGAGGCAGGAGATC 164838
QY 4423 GCTTGAACCTGGGAGGCAGAGTTTGCAGTGAGCCGAGATCCCACCCTGCACTCCAGCCT 4482
Db 164837 ACTTGAACCCAGGAGGCAGAGTTTGCAGTGAGCCGAGATCGCATCATTTGCACCTCTAGCCT 164778
QY 4483 GGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAA 4522
Db 164777 GGGCGACAGAGCAAGACCCCATCTCAAAAAAATAAAGAA 164738

RESULT 42
ADB96919/c
ID ADB96919 standard; DNA; 177531 BP.
XX
AC ADB96919;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MDR1 related DNA sequence SEQ ID NO:660.
XX
KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytosstatic; human; Cyp3A5; MRP1; MDR1;
KW TOP1; ds.
XX
OS Homo sapiens.
XX
PN WO2003013537-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008218.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;

XX
DR WPI; 2003-268145/26.
XX
PT New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; SEQ ID NO 660; 130pp; English.
XX
CC The invention relates to the novel use of irinotecan or its derivative
CC for the preparation of pharmaceutical compositions for treating
CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
CC malignant glioma in a subject having a genome with a variant allele which
CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
CC of the invention has cytostatic activity. The invention is useful for the
CC preparation of pharmaceutical compositions for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject (preferably human, more preferably African or Asian)
CC or a mouse. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 177531 BP; 51602 A; 39077 C; 38304 G; 48548 T; 0 U; 0 Other;

Query Match 8.0%; Score 400.4; DB 10; Length 177531;
Best Local Similarity 60.5%; Pred. No. 9.5e-64;
Matches 859; Conservative 1; Mismatches 477; Indels 83; Gaps 9;
QY 3104 TTTTTTTTTTGTGTTGTAGAGACAGGGTCTTGCTCTGTACCCAGGCATGAGCACAGT 3163
Db 166075 TTGACTTCTTTGTTTTTTTGAGATGGAGTCTCGCTGTGTGCCAGGCTGGAGTGCAGT 166016
QY 3164 GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 3223
Db 166015 GGCGCAATCTTGGCTCAGTCAACCTCTGCCTCTTGGGTTCAAGCAATTCTCTG-CCTCA 165957
QY 3224 GCCTCCCAAGTAGCTGGGACTAC-GAGCGTGCACCACCACCGCCTGGCTAATTTAAAAAAT 3282
Db 165956 GCCTCTGGAGTAGCTGTGATTACAGGGCACCCACCACCATGCCCAGCTAATTTTGTA-- 165899
QY 3283 TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCA 3342
Db 165898 TTTTGTAGAGATGGGGTTTTCACTGTCTTGGTCAAGGCTGGTCTTGAATTCCTGACCTC- 165840
QY 3343 AGCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTG 3402
Db 165839 -GTGATCCACCCACCCTCGGCTTCCCAAAGTTCCTGGGATTACAGGCGTGAGCCACCTGCAC 165781
QY 3403 CGGCTACTTATTTCTTTACATTCCTATCTTTTCCAATGAATGTAAGATCCACAGAACAGGG 3462
Db 165780 CCGGCCTTTTTTTTTT-----
QY 3463 ATTACTGCCCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTTCATCACCTCAACC 3522
Db 165764 -----TTTTTTTTTGAGATGGAGTCTTGTGTTGCCAGGCTGGAGTGCAATGGCG 165714
QY 3523 TCCGTTCAGCTCAGTCGCAACCTCTGCCCTCCCGGGTTCAAGYGATTCTCCTGCCCTAAGCCT 3582
Db 165713 CAGTCTCGGCTCACTGCAACCTCAGCCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCT 165654
QY 3583 CCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTTAA 3642
Db 165653 CCTGAGTAGCTGGGATTACAGGCGCCCGCCACCATGCCCAGCTAATTTTGTATTTTAG 165594
QY 3643 GCAGAGATGGGGTTTACCATGTTGCCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTGAT 3702
Db 165593 TAGAGATGTGGGTTTTCACCATGTTGGCCAGGCTGTTTCGAACCTCCTGACCTCAGTGAT 165534
QY 3703 CTGCCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGAGTCACTGTGCTCGGCCG 3762
Db 165533 CTGCCCGCCTCGGCCCTCCCATAGTGTGGGATTACAGGTGTGAGCCACCACCGCCGCT 165474
QY 3763 ATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAG 3822

Db 165713 CAGTCTGGCTCACTGCAACCTCAGCCTCCTGGGTTCAAGCGAATTCTCCTGCCTCAGCCT 165654

QY 3583 CCTGAGTAGCTGGAATTACAAGCGTGCACCAACCATGCTTGGCTAAATTTTGTATTTTAA 3642

Db 165653 CCTGAGTAGCTGGGATTACAGGCGCCGCCACCATGCCCCAGCTAAATTTTGTATTTTAG 165594

QY 3643 GCAGAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAAGTCTCCTGACCTCAAAGTGAT 3702

Db 165593 TAGAGATGTGGGTTTACCAATGTTGGCCAGGCTGGTTTCGAATCTCTGACCTCAGGTGAT 165534

QY 3703 CTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCOG 3762

Db 165533 CTGCCCGCCTCGGCCTCCCATAGTGTGGGATTACAGGTGTGAGCCACCAACGCCCGCCT 165474

QY 3763 ATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAG 3822

Db 165473 TTTGACTTC----TTAATAATGGCCAATCTTGCAGGAGTAAGGCAGTACCT----- 165427

QY 3823 TAGGTGCTCAATAAATAATTGATGAATGCAAGCCTAGATATAAACTTCTTTTCTTTT 3882

Db 165426 TATTGTGGCTTTAATTGTCACCTTCTGTGATGATTAGTGATGTTTTCAGCATTTTTCATGT 165367

QY 3883 TTTAAACAATCTTGTGACAACTTTGCAGAAATAAATAACAATCTTGCATTTCTGTTTTCACT 3942

Db 165366 TTGTTGGTCATTTGTATATATATTATTTGAGAACTGTCTCCATGTCAATTTGCCTACTTTT 165307

QY 3943 TATCACCTTGTTATGACTTTTTCATATFTGCCTCAAACCTTTTATGTTACTGTTTTTTCAT 4002

Db 165306 GATGGGATTTTCTTTCTTGTGACTTG-----TTAGAGTTACTTGTAGATTTCT 165257

QY 4003 TGTTACTATTTTAGTCACTGAATAATATATGGCTTAATTTGCTTATACATCTCCTGCTCCA 4062

Db 165256 GGATATTAGTCTTTGTCTGATGCATAGTTTGCAAATATTTTCTGCCATCCTGTGGATGA 165197

QY 4063 CTTTAGAGGCCAAATTTTACAAATCTGATGAAAGCTATGAACCTCTCCTCCAGAGAAATA 4122

Db 165196 GTCTTGCTCTTTTCGTCAGAAAATCCAAAAGTTTGTGTTTACATTCCTGTTGGCATCA 165137

QY 4123 CACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAAGAAA 4182

Db 165136 AGTACACACACACATCCACCTCTGTTACTCCCCGTTTACATCATAGTTTTC-ATCTGATGAAC 165078

QY 4183 CTGCAATTAGAGGATGTTTGTTCATATTAATTAATAAATAACTCAGTTGGGCACAGTGACT 4242

Db 165077 ATTTTATGACAGATTTATTTTTCCTTTATATAAAGAACTGATGGGCCAGGCACGGTGGCT 165018

QY 4243 CAAGCCTGTAACCCACAGTACTTTTGGAAAGTCCAAGGTGGTGGATCACTTGAGGTGAGAAG 4302

Db 165017 TAAACCTGTAATCCCGACACTTTTGGAGGCTGAGGCGGGTGGATCACCCAAAGTCAGGAG 164958

QY 4303 TTCGAGACGAGCCTGGTCAATATGGTGAAACCCATATCTCTACTAAAAATACAAAAATTAG 4362

Db 164957 TTTGAGACGAGCCTGGCCAAACATGGCAAAACCCCATCTCTACTAAACATACAAAAATTAG 164898

QY 4363 CTGGGTGTAGTGATGATGCATGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGATT 4422

Db 164897 CTGGGTGTGTCATGCACGCGCTGTAGTCTCAGCTACTTTGAGAGGCTGAGGCAGGAGAATC 164838

QY 4423 GCTTGAACTGGGAGGCAGAGGTTTGCAGTGAGCCGAGATCCCAACCACTGCACCTCCAGCCT 4482

Db 164837 ACTTGAAACCGAGGAGCAGAGGTTTGCAGTGAGCCGAGATCGCATCATTTGCACCTTAGCCT 164778

QY 4483 GGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAA 4522

Db 164777 GGGCGACAGAGCAAGACCCCATCTCAAAAAAATAAAGAA 164738

RESULT 45
ACN45166
ID ACN45166 standard; DNA; 87687 BP.
XX
AC ACN45166;

XX 18-NOV-2004 (first entry)

DT Human genomic sequence hCG37872.

XX Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.

XX Homo sapiens.

OS WO2003073826-A2.

PN 12-SEP-2003.

XX 28-FEB-2003; 2003WO-US006235.

PR 01-MAR-2002; 2002US-00087192.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW;

PI WPI; 2003-328604/31.

DR Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.

XX Claim 1; SEQ ID NO 1978; Opp; English.

PS The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published

XX SQ Sequence 87687 BP; 23583 A; 17049 C; 18231 G; 28170 T; 0 U; 654 Other;

Query Match 8.0%; Score 399; DB 11; Length 87687;
Best Local Similarity 60.1%; Pred. No. 1.6e-63;
Matches 900; Conservative 1; Mismatches 511; Indels 85; Gaps 11;

QY 3111 TTGTTGTTGTTTAGAGACAGGGTCTTGTCTGTCAACCCAGGCATGAGCACAGTGGTGCAA 3170

Db 5754 TTTTTTTTTTTTTGACAGTCTCGCTCTGTCAACCCAGGCTGGAGTGCAGTGGCGGA 5813

QY 3171 CCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGA-TCTGCTGACCTCAGCCTCC 3229

Db 5814 TCTTGGCTCACTGCAAGCTCTGCCCTCTGGGTTACGCCATTCTCCTGTGCTCAGCCTCC 5873

QY 3230 CAAGTAGCTGGGACTACGAGCGTGCAACCCAGCCTGGCTAATTAAAAAATTTTTTG 3289

Db 5874 CGAGTAGCTGGGACTACAGGTGCCCGCCACCATGCTGGCTAATTTTGGTATTTTAG 5933

QY 3290 TAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATC 3349

Db 5934 TAGAGACTGGGTTCACCT--GTTAGCCAGGATAGTCTCGATCCCTGAC--CTTGTGATC 5989

QY 3350 CTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGCTAC 3409

Db 5990 TGCCCGCCTCAGCCTCCCAAAGTGGTGGGATTACAGGCGTGAGCCACTGCGTCTGTCCTT 6049

QY 3410 TTATTTCTTTACATTCATCTTTCCAATAGAAATGTAAGATCCACAGAACAGGGATTA--C 3467

Db 6050 ACCTTTATACAATGTATAGAAATGTATAGGAGGCTTTAGGTAAGAGACTGGCAATTAGTT 6109

Qy 3223 AGCTCCCAAGTAGCTGGGACTACGAGCGGTGCACCACCGCCTGGCTAATTAATAAAAT 3282
Db |||||
Qy 3283 TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTGTCTTAAACTCCTGGCTTCA 3342
Db |||||
Qy 3343 AGCAATCCTCTACCTTGGCATCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTG 3402
Db |||||
Qy 3403 CGGCTACTTATTTCTTTACATTCATCTTTTCCAATAGAAATGTAAGATCCACAGAACAGGG 3462
Db |||||
Qy 3463 ATTACTGCCTATTTTCTTCTTTTGGAGACAGAGTCTCACTTTCATCACTCAACC 3522
Db |||||
Qy 3523 TCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTTCTCTGCCTAAGCCT 3582
Db |||||
Qy 3583 CCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTT-TTGTATTTT 3641
Db |||||
Qy 3642 AGCAGAGATGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGA 3701
Db |||||
Qy 3702 TCTGCCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCC 3761
Db |||||
Qy 3762 GATTACTGTCTATTTTCTTTATGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATA 3821
Db |||||
Qy 3822 GTAGTGTCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTTCTTTCTTT 3881
Db |||||
Qy 3882 TTTTA---AAACAATCTTGACAACTTTGCAGAAATAAATAACAATCTTGCAATCTGCTTTT 3937
Db |||||
Qy 3937 TCACCTATCACCTTGTATGACTTTTCATATTTGCCCTCAAACTTTATTGTTACTGTTT 3997
Db |||||
Qy 3998 TTCATTGTTACTATTTTAGTCACTGA--ATAATATGGCTTAATTTGCTTATACATCCTCC 4055
Db |||||
Qy 4056 TGCTCCACTTTAGAA-----GGCCAAATTTACAAATCTGATGAAAGC 4097
Db |||||
Qy 4098 TATGAACCTCTCCCCAGAGAAATACACACACACACACACTCACACACAGTTTTTTTT 4157
Db |||||
Qy 4158 TAATGTTTGCAACTAAGACAAGAACCTTGCATTAGAGGATTTTGTTCATATTAAATAAA 4217
Db |||||
Qy 4218 AATAACTCAGTTGGCA---CAGTCACTCAAGCCTGTAAACCACAGTACTTTTGGAGTCC 4273
Db |||||
Qy 4274 AAGTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAAC 4333

Db 97088 TAGGCAGGCAGATCAC--GAGGTCAGGAGATCGAGACCATCCTGGCTAAACGGTGAAAC 97145
Qy 4334 CCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCC 4392
Db 97146 CCCATCTCTACTAAAAATACAAAAAATTAGCGTGCAATGGTGGCACACGCCCTGTAGTCCC 97205
Qy 4393 AGCTACTCGGGAGGCTGAGGCAAGAGAATTG-CTTGAACTGGGAGGCAGAGGTTGCAGT 4451
Db 97206 AGCTACTTGTGGGCTGAGCAGGAGAAATGGTTGAACCCGGGAAGCAGAGCTTGCAGT 97265
Qy 4452 GAGCCGAGATCCACCACTGCACCTCCAGCTCCAGCGCTGGCGACACAGCGAGACTCTATCTCAAAA 4511
Db 97266 AAGCCAAGATCATGCCACTGCACCTCCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAAAC 97325
Qy 4512 AAATAAAATAAATAAAAGGATCGGAGAGAGAAACAAAACTAATAAGATTCTCTGAAGGT 4570
Db 97326 AAAAAACAAAACAAAAAAACCCAAAAAACCAAAAAACAAAAAGAACACAAAAAGAAATGT 97384

RESULT 47
ACN43946
ID ACN43946 standard; DNA; 174448 BP.
XX
AC ACN43946;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genomic sequence HCG21793.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR WPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX
PS Claim 1; SEQ ID NO 148; Opp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
SQ Sequence 174448 BP; 43106 A; 40529 C; 40481 G; 47948 T; 0 U; 2384 Other;

Query Match 8.0%; Score 398.6; DB 11; Length 174448;
Best Local Similarity 59.8%; Pred. No. 2e-63;
Matches 879; Conservative 0; Mismatches 524; Indels 66; Gaps 10;

QY	3101	GGGTTTTTTTGTGTTGTTTAGAGACAGGGTCTTGTCTGTCA	CCCAGGCATGAGCAC	3160
Db	55183	GGGATCTCTTTTTTTTTTCTGAGATGGAATCTCACTCTGTAGCCCAGGCTGGAGTGC	55242	
QY	3161	AGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACC	3220	
Db	55243	AGTGGTGTGATCTCGGCTCACTGCAACCTCCGCTCTCAAGTTCAAGCGATTCTCCTGCC	55302	
QY	3221	TCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACGCTGGCTAATTAAAAAA	3280	
Db	55303	TCAGCGTCCCAAGTAGCTGGGATTACAGACGTGTGCCACCACCAACCGGCTCATTT--TTTG	55360	
QY	3281	ATTTTTTTGTAGAGACTGGGTCTTTACTACGTTGGCCAGGCTTGTCTTTAAACTCCTGGCTT	3340	
Db	55361	TGTTTTTAGTAGGACGGGGTTTCGCCGTGCTGGCCAGGCTGGTCTCGAACTCCTGACCT	55420	
QY	3341	CAAGCAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATG	3400	
Db	55421	CAGGTGATCCGCCCGCTCGGCCCTCCCAAAGTCTGGGATTACAGGCGTG-GCCACTGCG	55479	
QY	3401	TGCGGCTACTTATTTCTTTACATTCCATCTTTTCCAATAGAAATGTAAGATCCACAGAACAG	3460	
Db	55480	CCCAGCCTTCTCTTCTTCTTCTTCTCTCC-----TCCTCCTCCTC	55523	
QY	3461	GGATTACTGCCTATTTTCTTCCCTTCTTTTTTGACACAGAGTCTCACTTCATCACCTCAA	3520	
Db	55524	CTCCTCCTTTTTTTGACAGAGTCTCACTCTATTGCCCAGGCTCGAGTGCAGTGGCACAA	55583	
QY	3521	CCTCCGTTCACTCACTGCAACCTCTGCCTCCGGGTTCAAGYGATCTCCTGCCTAAGC	3580	
Db	55584	TC-----TCAGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGAGATTCTCCCACTTCAGC	55638	
QY	3581	CTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATTGCTTGGCTAATTTTTTGTATTTT	3640	
Db	55639	CTCCCGAGTAGCTGGGATTACAGGTGCGCAACACCACAGCCGGTTAA-TTTTTGTGTTTT	55697	
QY	3641	TAGCAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTG	3700	
Db	55698	TGGTAGAAACGGGGTCTCGCCACGTTGGCCAGGTTAGTCTCAAACTCCTCACCTCAAGTG	55757	
QY	3701	ATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGAGTCACTGTGCCTGGC	3760	
Db	55758	ATCCGCCCGCCTCAGCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCACTGCGCTCGGC	55817	
QY	3761	CGATTACTGTCTATTTTCTTTATTGCTA-----TATCCCCAGATCTAGAGCAGTGTCTG	3814	
Db	55818	CTGGTGAAGACCTTCTTGCCGGTGGGACTCTGCAGAGTCTCTGACAGGGAGCAGGGCATC	55877	
QY	3815	ACATATAGTAGTGCTCAATAAATAATTGATGAATGCACAGCCCTAGATATA-----AA	3867	
Db	55878	ACATGGCGAGGAGCTGAGAGTGTCAAGTCAAGGTCCTCTCTCTCTTCTTCTTATAAAACCAC	55937	
QY	3868	CTTCTCTTTTCTTTTTTAAACAATCTTGACAACTTTGCAGATAAAATACAATCTTGCA	3927	
Db	55938	CAGTCCCACCTCTATGATAAACCAATTAATCCATGAATGGATTAAATCCACTTATGAGGACA	55997	
QY	3928	TTCTGCTTTTCACTTATCACCTTGTATGACTTTTTTCATATATGCTCA-----	3976	
Db	55998	CAGCCCTTTTAATCACCTCTGAAAGGCCCACTCTCAATGCTGCCACATGAGGAATTAC	56057	
QY	3977	-----AACCTTTATTGTTACTGTTTTTTTCATTGTTACTATTTTAGTCACTGAAT	4025	
Db	56058	ATTTCAACATGAGTTTTGGAGGGGACAAATATTCAAATCATACTATTATGTTACCAGTAA	56117	
QY	4026	AATATGGCTTAATTGCTTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAATTTACAAA	4085	
Db	56118	AATTTAAANATAGGAATAATAATTGCCGATGTGTGGCAGACTTACCAAATACTAGACCC	56177	
QY	4086	TCTGATGAAGCTATGAACCTCTCCCCAGAGAAATACACACACACACACTCACAC	4145	
Db	56178	TGTGCTAAGTGTTTTATATCTATTATTTTATTTTAAATTTTCTTGGTCACTGCATGACATAT	56237	

QY	4146	ACAGTTTTTTTTTAATGTTTGTCAACTAAGACAAAGAAACCTGCATTAGAGGATGTTGTTC	4205	
Db	56238	GCTCTGTTAGTCCCAGTTTTTTCGAATGGGCATAAACAAGACCGAACCTACCTAGAGTTGGC	56297	
QY	4206	ATATTAATTAAAAATA-----ACTCAGTTGGGCACAGTGACTCAAGCCCTGTAACCAAGTA	4261	
Db	56298	ACAAGTTGTAAAAATAGGATCCGTGGCCGGGCACAGTGGCTCACACTTGTAATTCAGCA	56357	
QY	4262	CTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTTCGAGACCAGCCTGGTCA	4321	
Db	56358	CTTTAGGAGGCCAAGCGCGGAGGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGGCCA	56417	
QY	4322	ATATGGTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGCATG	4381	
Db	56418	ACATGGCGAAACCCCGTCTCTACTTAAAAATACAAAAATTAGCCAGGCGTGGTG--CGCG	56475	
QY	4382	CCTGTAGTCCCAGTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAG	4441	
Db	56476	CCTGTAGCCCCAGTCTCTCGGGAACCTGAGGTAGGAGACTCGTTTGAACCCGGAGGCGG	56535	
QY	4442	AGTTGCAGTGAGCCGAGATCCCACCACCTGCACCTCCAGCCTGGCGACACAGCGAGACTC	4501	
Db	56536	AGTTGCAGTGAGCCCAAGATCGCACCACTGCACCTCCAGGCTGGCGACAGAGCGAGACTC	56595	
QY	4502	TATCTCAAAAAAATAAATAAAATAAAATAA	4530	
Db	56596	CATCTCAAAAAATAAATAAACAACAAAAA	56624	
RESULT 48				
AAS42187				
ID	AAS42187 standard; DNA; 6131 BP.			
XX				
AC	AAS42187;			
XX				
DT	17-DEC-2001 (first entry)			
XX				
DE	Genomic sequence #503 encoding novel human enzyme polypeptide.			
XX				
KW	Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;			
KW	ligase; hyperproliferative disorder; immunodeficiency disorder;			
KW	autoimmune disorder; neurological disorder; metabolic disorder;			
KW	inflammatory disorder; cardiovascular disorder; reproductive disorder;			
KW	blood-related disorder; infectious disorder; gene therapy; cytostatic;			
KW	anti arthritic; nephrotropic; anticoagulant; ds.			
XX				
OS	Homo sapiens.			
XX				
PN	WO200155301-A2.			
PD	02-AUG-2001.			
XX				
PF	17-JAN-2001; 2001WO-US001239.			
XX				
PR	31-JAN-2000; 2000US-0179065P.			
PR	04-FEB-2000; 2000US-0180628P.			
PR	24-FEB-2000; 2000US-0184664P.			
PR	02-MAR-2000; 2000US-0186350P.			
PR	16-MAR-2000; 2000US-0189874P.			
PR	17-MAR-2000; 2000US-0190076P.			
PR	18-APR-2000; 2000US-0198123P.			
PR	19-MAY-2000; 2000US-0205515P.			
PR	07-JUN-2000; 2000US-0209467P.			
PR	28-JUN-2000; 2000US-0214886P.			
PR	30-JUN-2000; 2000US-0215135P.			
PR	07-JUL-2000; 2000US-0216647P.			
PR	07-JUL-2000; 2000US-0216880P.			
PR	11-JUL-2000; 2000US-0217487P.			
PR	11-JUL-2000; 2000US-0217496P.			
PR	14-JUL-2000; 2000US-0218290P.			
PR	26-JUL-2000; 2000US-0220963P.			
PR	26-JUL-2000; 2000US-0220964P.			
PR	14-AUG-2000; 2000US-0224518P.			

PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
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PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
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PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
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PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.

PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249300P.
PR 17-NOV-2000; 2000US-0249301P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465566/50.

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

Disclosure; SEQ ID NO 2313; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. AAS41685-AAS42192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 6131 BP; 1422 A; 1665 C; 1561 G; 1483 T; 0 U; 0 Other;

	Query Match	8.0%;	Score 398.4;	DB 4;	Length 6131;
	Best Local Similarity	54.0%;	Pred. No. 1.4e-63;		
	Matches 1259;	Conservative	3;	Mismatches 894;	Indels 176; Gaps 15;
QY	2287	TTTTAGGCCAGGCGGCTGGCTCATGCCCTGTAATCCAGCACTTTGGGAGGCCGAGCGG	2346		
DB	789	TTTTAGGCCAGGCGGCTGGCTTATGCCCTGTAATCCAGCACTTTGGGAGGCCGAGCGG	848		
QY	2347	GCGGATCACCTTGAGGTCAGGAGTTTCGAGACCAGCCCTGGCCAAACATGGTGAACCCCTGTCT	2406		
DB	849	GCGGTCACCTTGTTGTCAGGAGTTTGAGACCAGCCCTGACTAATCATGGTGAACCCCTGTCT	908		
QY	2407	CTACTAAAAAATACAAAAATTAGCCGGACATGGTGGGAGCGCCTGTAAACCCAGCTACT	2466		
DB	909	CTACTGAAAAATACAGAAAAATTAGCCAGGGGTCTGGCGGGCGTCTGTAATCCCAGCTACT	968		
QY	2467	TGGGAGACTGAGTTGGAGGTTTCAGTGAGCCAAAG-----GTCGTG	2506		
DB	969	TGGGAGGCTGAGGACGAGAGAAATCCCTTGAAACCCGAGGGGTGGAGTTGCAGTGAGCTGAG	1028		
QY	2507	TCAGTGTCTCCAGCTGGGTAAAGCACTTATATTTTTCAGCCATAGGATCATTTCTCTGAAGC	2566		
DB	1029	ATTGCAAACTCCAGCCTGGGGACAGAGCGAGATGCCGTCTTTAAAAAATAAAAAA	1088		
QY	2567	ATAAATATATGATAAAAGCACTTATATTTTTCAGCCATAGGATCATTTCTCTGAAGC	2626		
DB	1089	AGTAGCAGAAAAACTGGAGGTTGAGGGTGTTCATTTGGTAGCCCCAGAGCTGGGTTTC	1148		
QY	2627	ATCTTGGCGAAGTCATCCACCTGTTCCTGAGAGTGGGCAAGGTGAGGGCTGACCTATTG	2686		
DB	1149	AGCTAGGAGAGGTCACCCCGGCC---CTGCTGCCCTGCCAGCGTCCCTCTCTTTCT	1204		
QY	2687	CTCTGCACTTACTCCTATCTCAGCTGTCCCTCCCACTTTTCCAGGTGCTGCCAGACACATG	2746		
DB	1205	CTCTCCCGCTCTTCTGCTGGGAAAGCAGCAGACATCTCAGGGCTGTGGAGGGATGGG	1264		
QY	2747	ACAACTGCTAYGACCAGG-----CCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAM	2801		
DB	1265	GGAGGCCACAGACCCAGGACGCTCCAGGCAGCTGTGTTCAAGTGGGCATCAGCCCTGAGGA	1324		
QY	2802	MCCGTACACCCACACCTATTATCATACTCGTGTCTGGCTCGGCAATCACCTGTAGCAGTAG	2861		
DB	1325	CTCCGTGCGGGGTCTCTGCATTGGGGTTTCTCTTTGTGCCTTCAGAAACCCGATGAA	1384		
QY	2862	GTTTATCCCTTCCCTTGACCTATGAATTTCTAGTTGGTTCTCAGTAGGCCGGGGGAAATAA	2921		
DB	1385	GGCAATGTATCCAGGCACATTCTACTTCCAATTTAAAAACCTATGGGAAGCCAACATCG	1444		
QY	2922	TAGTAACAACAGCCATGATTT---AGTGTAAATTTCTTGGTTCTGGGCAGTGTCTCCTT	2978		
DB	1445	GAACGAAACTTGGCTGTGCTTCACCGTGAAGGTATAAAGCGCCGCTCAGTTGTCTCCTG	1504		
QY	2979	TAATCCTCAGAAACAACACTATGGGATAGGTACAATTTATCCTCACTTAACAGATAAGAAAA	3038		
DB	1505	GAAGACGGGCGTCTTCCGAAACACAGGTAGCACCAAGTCTTAGTTACACCCCTAAATAGGA	1564		
QY	3039	CTGAGGC-----TCAGAAGGCTGAGCTATTTGCCCAAGATCACACAGC	3081		
DB	1565	GCTAAGCAGCTGGGAATGCAGAAAAACGCAACAATAAGTATGTGCCCGGCTGGGCTCTC	1624		
QY	3082	TTGTAAG---TGGTGACAGTTTGGGTTTTTTTTTTTGTGTTGTTTAGAGACAGGGTCTT	3136		
DB	1625	CTGTGTGCACCTTTCTCGCCACATTTCTATTTTTTTTTTTTTTTTTTTTGAGATGGAGTCTC	1684		
QY	3137	GCTCTGTCAACCCAGGCTAGAGCACAGTGGTGCAAACCATAGGTCACTGCAGCCTCAACCTC	3196		
DB	1685	GCTGTGTCAACCCAGGCTGGAAATGCAGTGGTCTGATTTTCACTCACGGCAACCTCTGCTTT	1744		

Db 2743 GGCTCATGCTGTAAATCCAGCACCTTTGGAGGCTGAGGCAGCGGATCA--TGAGGTTG 2800
QY 4299 GAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATACAAAAA 4358
Db 2801 GGAGTTCGAGACCAGCCTGGCTAACATGATGAAACCCAGTCTCTACTAAAAATACAAAGA 2860
QY 4359 TTAGCTGGGTGTAGTGATGCATGCGCTGCTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAG 4418
Db 2861 TTAGCCAGGTGTGGGGTGCATGCGCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAG 2920
QY 4419 AATTGCTTGAACTGGGAGGCAGAGGTGCAGTGAGCCGAGATCCCACCCTGCACTCCA 4478
Db 2921 AATTGCTTGAACTGGGAGGCAGAGGTGCAGTGAGCCGAGATGTGCCACTGCACTCCA 2980
QY 4479 GCCTGGCGACACAGCGAGACTCTATCTCAAAAAAATAAAATAAAATAA 4530
Db 2981 GCCTTGGCGACAGAGCAAGACTCCATCTTTGAAAAAATAAAAAATAAAAGAA 3032

RESULT 49
AAK69784
ID AAK69784 standard; DNA; 6131 BP.
XX
AC AAK69784;
XX
DT 06-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24596.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
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PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
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PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
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PR 14-AUG-2000; 2000US-0225266P.
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PR 14-AUG-2000; 2000US-0225447P.
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PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.

Qy	3437	TAGAA	TGTAAGATCCACAGAACAGGGGATTACTGCC	TATTTTCTTCCTTCTTTT	TTTGAGA	3496
Db	1981	-----	-----TTATTTATTTT	TTGAGACGGAGTCT	TGCTCT	2013
Qy	3497	CAGAG	CTCACCCTTTCATCACCTCAACCTCCGTT	CAGCTCAGCTCAACCTCTGCCTCCCGGG		3556
Db	2014	ATCGCC	AGGCTGGAGTGAGTGGACAATCTCAGCTCACTGCAAGCTCCGCTCCCGGG			2073
Qy	3557	TTCAAG	YGATTTCTCCTGCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCA			3616
Db	2074	TTACGG	CCATTTCTCCTGCCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGCCCAACCA			2133
Qy	3617	TGCTT	GGCTAAATTTTGTGA-----	TTTTTAGCAGAGATGGGTTTT		3658
Db	2134	TGCCCA	GCTAAATTTTCTTTTTTCTTTTTT	TTTAGTAGAGACGGGGTTTC		2193
Qy	3659	ACCAT	GTGCCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCT			3718
Db	2194	ATGGT	GTAGCCCAAGATGGTCTCGATCTCCTGACCTCA--TGATCCGCGCCCTTGSCCT			2251
Qy	3719	CCCAA	AGTGTGGAATTATAGGCGTGAGTCACTGTGCTGCGCGGATTACTGTCIATTTTC			3778
Db	2252	CCCAA	AGTGTGGGATTACAGGCATGAGCCA	CTGTGCCCCGCTCCCCACATTTTTTAAAG		2311
Qy	3779	TTTAT	TGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTCTCAATAAAT			3838
Db	2312	TCCAT	GG-----CCCAGATCTTCCTCCCTGACTCTCCTGTGATC-----			2350
Qy	3839	AATTG	ATGAATGCACAGCCTAGATATAAACTTTTCTTTTT	CTTTTTTAAACAATCTTGA		3898
Db	2351	-----	-----AGATCGTGGAGGGGTTTGCTTCCTCCCAAAAGGCCTGT			2390
Qy	3899	CAACT	TTGCAGAAATAAATACAATCTTGCAATCTGCTTTT	CTACTTATCACCTTGTATGA		3958
Db	2391	TTAGC	GCCAG-----CACCTCACTCTTGACTTTGTTTCCCAAAATCTTGTATGG			2442
Qy	3959	CTTTT	TCATATTGCTCAAACTTTATTTGTTACTGTTTTTTCATTTGTTACTATTTAGTC			4018
Db	2443	AGCTG	TGCGTCCGGCAGTCTCGGGAATCAGCAGCTGTGGGAAGCGGGGGTGTGTGTC			2502
Qy	4019	ACTGA	ATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAAT			4078
Db	2503	CAGCG	CTGTGCTGGGCCAGTGACTGCGGGCTGGTGGGGCGCGCCCTGACCTGCCCTGA			2562
Qy	4079	TTACA	AAATCTGATGAAAGCTATGAA-----	CCCTCTCCCAAGAGAAATACACACACA		4132
Db	2563	TTCTC	CAGCAGAAGGCAGGCAGGGAACAAAGCTGACCCCAAGAGAGCCAGGCCATAGCAGG			2622
Qy	4133	CACAC	ACTCACACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAG			4192
Db	2623	GGCTG	AGGATGCCCTGGTGAATGGATGCTGGGAGAAAAGATGGCAGAAATTCACACATGAG			2682
Qy	4193	AGGAT	GTTGTTTCATATTAATTAANAATA-----	ACTCAGTTGGGCACAGT		4238
Db	2683	TCTAT	GAGACAGGGGAAAGAATCAATAAATAAAGAAGGAAGGGCCGGGCACGGCGCGT			2742
Qy	4239	GACTC	AAGCCTGTAACCAACAGTACTTTGGAAGTCCAAGGTGGTGGATCAGTTGAGGTGA			4298
Db	2743	GGCTC	ATGCCTGTAATCCCAGCACTTTGGGAGGCTTGAGGAGCGCGATCA--TGAGGTG			2800
Qy	4299	GAAGT	TCGAGACCAGCCTGGTCAATATGTTGGAACCCCTATCTCTACTAAAAATACAAAAA			4358
Db	2801	GGAGT	TCGAGACCAGCCTGGCTAATCATGATGAACCCAGTCTCTACTAAAAATACAAAGA			2860
Qy	4359	TTAGT	GGGTAGTATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCGAAGAG			4418
Db	2861	TTAGC	CAAGTGTGGGGGTGCATGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAAGAG			2920
Qy	4419	AATTG	CTTGAACCTGGGAGGCAGAGTTGCAGTGAGCCGAGATCCACCACTGCCTCCA			4478
Db	2921	AATTG	CTTGAACCTGGGAGGCAGAGTTGCAGTGAGCCGAGATTGTGCCACTGCCTCCA			2980

Qy	4479	GCCTGGCGACACAGCGAGACTCTATCTCAAAAAAATAAAATAAAATAA	4530
Db	2981	GCCTTGGCGACAGAGCAAGACTCCATCTTTGAAAAAATAAAATAAAAGAA	3032
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ID	ABL64403/c		
XX	ABL64403 standard; DNA; 167343 BP.		
AC	ABL64403;		
XX	DT 15-MAY-2002 (first entry)		
XX	Stomach cancer related gene sequence SEQ ID NO:2740.		
DE	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;		
XX	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;		
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;		
KW	gene; ds.		
XX	Homo sapiens.		
OS	WO200194629-A2.		
XX	PN 13-DEC-2001.		
XX	PD 30-MAY-2001; 2001WO-US010838.		
PR	05-JUN-2000; 2000US-0209473P.		
PR	05-JUN-2000; 2000US-0209531P.		
PR	18-SEP-2000; 2000US-0233133P.		
PR	18-SEP-2000; 2000US-0233617P.		
PR	20-SEP-2000; 2000US-0234009P.		
PR	20-SEP-2000; 2000US-0234034P.		
PR	20-SEP-2000; 2000US-0234052P.		
PR	22-SEP-2000; 2000US-0234509P.		
PR	22-SEP-2000; 2000US-0234567P.		
PR	25-SEP-2000; 2000US-0234923P.		
PR	25-SEP-2000; 2000US-0234924P.		
PR	25-SEP-2000; 2000US-0235077P.		
PR	25-SEP-2000; 2000US-0235082P.		
PR	25-SEP-2000; 2000US-0235134P.		
PR	25-SEP-2000; 2000US-0235280P.		
PR	26-SEP-2000; 2000US-0235637P.		
PR	26-SEP-2000; 2000US-0235638P.		
PR	27-SEP-2000; 2000US-0235711P.		
PR	27-SEP-2000; 2000US-0235720P.		
PR	27-SEP-2000; 2000US-0235840P.		
PR	27-SEP-2000; 2000US-0235863P.		
PR	28-SEP-2000; 2000US-0236028P.		
PR	28-SEP-2000; 2000US-0236032P.		
PR	28-SEP-2000; 2000US-0236033P.		
PR	28-SEP-2000; 2000US-0236034P.		
PR	28-SEP-2000; 2000US-0236109P.		
PR	28-SEP-2000; 2000US-0236111P.		
PR	29-SEP-2000; 2000US-0236842P.		
PR	29-SEP-2000; 2000US-0236891P.		
PR	02-OCT-2000; 2000US-0237172P.		
PR	02-OCT-2000; 2000US-0237173P.		
PR	02-OCT-2000; 2000US-0237278P.		
PR	02-OCT-2000; 2000US-0237294P.		
PR	02-OCT-2000; 2000US-0237295P.		
PR	02-OCT-2000; 2000US-0237316P.		
PR	03-OCT-2000; 2000US-0237425P.		
PR	03-OCT-2000; 2000US-0237598P.		
PR	03-OCT-2000; 2000US-0237604P.		
PR	03-OCT-2000; 2000US-0237606P.		
PR	03-OCT-2000; 2000US-0237608P.		
PR	01-NOV-2000; 2000US-0244867P.		
PR	01-NOV-2000; 2000US-0245084P.		
XX	(AVAL-) AVALON PHARM.		
PA			
XX			

KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;	CC	comprises a sequence (S) selected from 8447 sequences (given in ABL61664
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;	CC	to ABL70110), or is at least 95% identical to (S), where a change in
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;	CC	expression is indicative of anti-neoplastic activity. (I) has cytostatic
KW	gene; ds.	CC	activity and can be used in gene therapy. M1 can be used for screening an
XX		CC	anti-neoplastic agent, and can be used for producing a product which is
OS	Homo sapiens.	CC	the data collected with respect to the anti-neoplastic agent as a result
XX		CC	of M1, and the data is sufficient to convey the chemical structure and/or
PN	WO200194629-A2.	CC	properties of the agent. M1 can be used in the treatment of cancer such
XX		CC	as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
PD	13-DEC-2001.	CC	prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
XX		CC	cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
PF	30-MAY-2001; 2001WO-US010838.	CC	cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
XX		XX	tumour
PR	05-JUN-2000; 2000US-0209473P.	SQ	Sequence 167343 BP; 49550 A; 37098 C; 35753 G; 44929 T; 0 U; 13 Other;
PR	05-JUN-2000; 2000US-0209531P.		
PR	18-SEP-2000; 2000US-0233133P.		Query Match 8.0%; Score 398.4; DB 6; Length 167343;
PR	18-SEP-2000; 2000US-0233617P.		Best Local Similarity 60.1%; Pred. No. 2.2e-63;
PR	20-SEP-2000; 2000US-0234009P.		Matches 872; Conservative 1; Mismatches 532; Indels 45; Gaps 11;
PR	20-SEP-2000; 2000US-0234034P.		
PR	20-SEP-2000; 2000US-0234052P.	Qy	3098 TTTGGGTTTTTTTTTTGTTGTTGTTTATAGAGACAGGGTCTTGCTGTCAACCCAGGCATGAG 3157
PR	22-SEP-2000; 2000US-0234509P.	Db	147653 TTTTNTTTTAAATTAATTTATTTTGTGACGCGAGTCTGTCTGTCACTAGGCTGGAG 147594
PR	25-SEP-2000; 2000US-0234567P.		
PR	25-SEP-2000; 2000US-0234923P.	Qy	3158 CACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTG 3217
PR	25-SEP-2000; 2000US-0234924P.	Db	147593 TGCAGTGGCACAAATCTTGGCTCACTGCAGCCTCCGCCTCCGGGTTGAAGCGATTCTCCT 147534
PR	25-SEP-2000; 2000US-0235077P.	Qy	3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACCCAGCCTGGCTAATTA 3277
PR	25-SEP-2000; 2000US-0235134P.	Db	147533 GCCTCTGCCTCGCCAGTAGTTGGGATTACAGGTGTGTGCTACCAACCCAGCTAATTTT 147474
PR	26-SEP-2000; 2000US-0235637P.	Qy	3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGG 3337
PR	26-SEP-2000; 2000US-0235638P.	Db	147473 TGTA-TTTTGTAGAGACGGAGTTTCACCATGTTGGCTAGGCTAGTCTTGA 147415
PR	27-SEP-2000; 2000US-0235711P.	Qy	3338 CTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGTGAGCCACC 3397
PR	27-SEP-2000; 2000US-0235720P.	Db	147414 CCTCAGGTGATATGCCACCTTGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACT 147355
PR	27-SEP-2000; 2000US-0235840P.	Qy	3398 ATGTGCGG-CTACTTAATTTCTTTACATTCCTTCCAAATAGAAATGAAGATCCACAGA 3456
PR	27-SEP-2000; 2000US-0235863P.	Db	147354 GTGCCCTGGCCTAATTTTATTTTATGTTTGTGTTTTTGTGTTTTTTTTTTTGA 147295
PR	28-SEP-2000; 2000US-0236028P.	Qy	3457 ACAGGGATTACTGCCATTTTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACC 3516
PR	28-SEP-2000; 2000US-0236032P.	Db	147294 GACCGACTCTCTCTCTGTTGCCTAGGCTGGAGTGAGTGTCACGATCTCTGCTCACTCTC 147235
PR	28-SEP-2000; 2000US-0236033P.	Qy	3517 TCAACC---TCCGTTACAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCCT 3572
PR	28-SEP-2000; 2000US-0236034P.	Db	147234 TCCTCCGCAACCTCTCAAGATTTCGGCAACCTCTGCCTCCTGAGTTCAAGCGATTCTGT 147175
PR	28-SEP-2000; 2000US-0236109P.	Qy	3573 GCCTAAGCCTCCTGAGTAGTGGAATTACAAGCGTGCACCAACCATGCTTGGCTAATTTT 3632
PR	29-SEP-2000; 2000US-0236842P.	Db	147174 GCTTCAACCTCTGGAGTAGGTGAGATTACAGGTGTGTGCCACCATGCCTGGCTAA-TTTT 147116
PR	29-SEP-2000; 2000US-0236891P.	Qy	3633 TGTATTTTTTAGCAGATGGGGTTTTTACCATGTTGCCCCAGGCTGGTCTCAAACCTCCTGAC 3692
PR	02-OCT-2000; 2000US-0237173P.	Db	147115 TGTGTTTTTTAGTAGAGATGGGGTTTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGAC 147056
PR	02-OCT-2000; 2000US-0237278P.	Qy	3693 CTCAAAGTGATCGCCTGCCTCAGTCTCCCAAAGTGTGGGAATTATAGGCGTGAATCACTG 3752
PR	02-OCT-2000; 2000US-0237294P.	Db	147055 CTCAGGTGGTC-ACCTGCTTTCGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCTCCA 146997
PR	02-OCT-2000; 2000US-0237295P.	Qy	3753 TGCCTGGCCGA-----TTACTGTCTATTTTCTTTATTTGCTATATCCCCAGATC 3800
PR	03-OCT-2000; 2000US-0237316P.	Db	146996 TGCCAGCCCATAGCTCCTATTTTAAATTGTACCTGTAATGTTGGCTGCCCTTTAATC 146937
PR	03-OCT-2000; 2000US-0237425P.	Qy	3801 TAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTTGATGAATGCACAGCCTAG 3860
PR	03-OCT-2000; 2000US-0237598P.	Db	146936 AAACCTACCCCCATGTTAATGCATCAGTCACCTAAACTAGGATAAAGGTAGGATTACTGAA 146877
PR	03-OCT-2000; 2000US-0237604P.	Qy	3861 ATATAAACTTTTCTTTTCTTTTAAAAACAATCTTGCACAACTTTTGCAGAAATAATA--- 3917
PR	03-OCT-2000; 2000US-0237606P.		
PR	03-OCT-2000; 2000US-0237608P.		
PR	01-NOV-2000; 2000US-0244867P.		
PR	01-NOV-2000; 2000US-0245084P.		
XX			
PA	(AVAL-) AVALON PHARM.		
XX			
PI	Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;		
PI	Soppet DR, Weaver Z;		
XX			
DR	WPI; 2002-188264/24.		
XX			
PT	Screening for anti-neoplastic agent involves exposing cells to a chemical		
PT	agent to be tested for anti-neoplastic activity, and determining a change		
PT	in expression of a gene of a signature gene set.		
XX			
PS	Claim 1; SEQ ID NO 5576; 44pp; English.		
XX			
CC	The present invention describes a method (M1) for screening for an anti-		
CC	neoplastic agent. The method involves exposing cells to a chemical agent		
CC	to be tested for anti-neoplastic activity, determining a change in		
CC	expression of at least one gene (I) of a signature gene set, where (I)		

Db 146876 ATGCTGCTTCCACTGGCACCACCTTTGTGAGGAAAAGGGAACCCCTAGAAAAATAACATTG 146817
QY 3918 ---CAATCTTGCAATCTGCTTTTTCACCTTATCACCTTGTTATGACTTTTTCATATGCC 3973
Db 146816 TGGGCATGATTTCTTTATCGTACGGTGAATTCAGCCTTGCAGTGATTTTTTCAGAGATGA 146757
QY 3974 TCAAAACCTTTATTTGTTACTGTTTTCATGTTTACTATTTTATGTCACCTGAATAATATGGC 4033
Db 146756 ACAGAAATTTAAAGTGTTAGAACTCAITTTGGGAGGCTAAGGCAGGTAAAGTGTCTTGAGCCC 146697
QY 4034 TTAATTTGCTTATACATCTCCTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGA 4093
Db 146696 AGGAGTTTGAGACA-AGGCTGGGTAACATAATGAGAACCCCTGTCTCTACAAACAAACAA 146638
QY 4094 AAGCTATGAACCCCTCTCCCCAGAGAGAAATACACACACACACACTCACACAGTTT 4153
Db 146637 AAACCTTATGTTCTCCGCTTTCCCAACATTTAACTTTTACATACACAGTTGATGTTTCA 146578
QY 4154 TTTTAAATGTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATA----- 4208
Db 146577 TCCCTTAAG-TAGCAAAGAGGAGATGGAGGTTGCTGAAGTGTGTAATTGTGATAACTGTT 146519
QY 4209 -----TTAATTAAAAATAACTCAGTTGGGCACACAGTGAACCTGTAAACCACAG 4259
Db 146518 TGCTTTCCTTAGAATATGTTTTCTGGCCAGGAGCGTTTTGGTGCACGCCTGTAATCCCAG 146459
QY 4260 TACTTTGGAAGTCCAAGGTGGTGGATCACTTGAGGTGAGAAGTTCGAGACCCAGCCTGGT 4319
Db 146458 CAGTTTGGGAGGCCAAGGTGGTGGATCACGTGAGGTCAAGGATCGAGACCATCCTGGC 146399
QY 4320 CAATATGGTGAAACCCCTATCTCTACTAAAAAATAC--AAAAATTAGCTGGGTGTAGTGATG 4377
Db 146398 TAACATGGTGAAACCCCTGTCTCTACTAAAAAATACAAAAAATTAGCCGGCATGTTGGTG 146339
QY 4378 CATGCCTGTACTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATGCTTGAACCTGGGAG 4437
Db 146338 GGCACCTATAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGATGGCATGAAACCAGGAG 146279
QY 4438 GCAGAGTTGCAGTGAGCCGAGATCCACCACCTGCACCTCCAGCCTGGCGGACACAGCCGAG 4497
Db 146278 GCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCACCTCCAGTCTGGGCAACCGAGCGAG 146219
QY 4498 ACTCTATCTC 4507
Db 146218 ACTCCTTCTC 146209

RESULT 52
ABK83568
ID ABK83568 standard; DNA; 201143 BP.
XX
AC
XX ABK83568;
XX

DT 29-AUG-2002 (first entry)
XX
DE Human DNA differentially expressed in granulocytic cells #139.
XX

KW Human; ds; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.
OS
XX WO200228999-A2.
PN

XX 11-APR-2002..
PD
XX

PF 03-OCT-2001; 2001WO-US030821.
XX
PR 03-OCT-2000; 2000US-0237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
XX WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.
XX
PS Claim 1; SEQ ID NO 139; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 201143 BP; 50606 A; 49308 C; 49683 G; 51546 T; 0 U; 0 Other;

Query Match 8.0%; Score 398.4; DB 6; Length 201143;
Best Local Similarity 54.0%; Pred. No. 2.3e-63;
Matches 1259; Conservative 3; Mismatches 894; Indels 176; Gaps 15;

QY 2287 TTTCAGGCCAGGCGGTGGCTCATGCCCTGTAATCCAGCACTTTGGGAGGCCGCGG 2346
Db 130818 TTTTAGGCCAGGCACGTTGGCTTATGCCCTGTAATCCTAGCACTTTGGGAGGCTGAGCGG 130877
QY 2347 GCGGATCACTTGAGGTCAGGAGTTTCGAGACCAGCCTGGCCAAACATGGTGAACCCCTGTCT 2406
Db 130878 GCGGGTCACCTGTGGTCAGGAGTTTGAGACCAGCCTGACTAACATGGTGAACCCCTGTCT 130937
QY 2407 CTACTAAAAAATACAAAATTAGCCGGACATGGTGGCGAGCGCTGTAAACCCAGCTACT 2466
Db 130938 CTACTGAAAATACAGAAAATTAGCCAGGGGTGCTGCGGGCGTCTGTATATCCAGCTACT 130997
QY 2467 TGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCCAAG-----GTCGTG 2506
Db 130998 TGGGAGGCTGAGGCAGGAGAAATCCCTTGAACCCGAGGGGTGGAGGTTGCAGTGAGCTGAG 131057

Qy	2507	TCACTGCTGTCCAGCCTGGGTAACAGAGCAAACTCTGTCTCAAAAAAATAATGCTTTCA	2566
Db	131058	ATTGCAAACTCCAGCCTGGGGACAGAGCGAGATGCCGTCCTTAAAAAATAAAAAA	131117
Qy	2567	ATAAATATATGATAAAAGGACTTATATTTTCAAGCCATAGGATCATTTCTCCTGAAGC	2626
Db	131118	AGTAGCAAAAAACTGGAGGTTGAGGGTGTTCATTGGTAGCCCCAGAGCTGGGGTTCC	131177
Qy	2627	ATCTTGGCGAAGTCATCCCCACCTGTTCCTGAGAGTGGGAGGTGAGGGCTGACCTATTG	2686
Db	131178	AGCTAGGAGAGGTCACCCCGGCC----CTGCTGCCCTGCCAGCGTCCCCCTCCTCTTTCT	131233
Qy	2687	CTCTGCACTTACTCCTATCTCAGCTGTTCCTCCCTCCACATTTCCAGGTGCTGCCAGACATG	2746
Db	131234	CTCTCCCGTCTTCTCTGCCCTGGGAAAGCAGCAGACATTTCTCAGGGCTGTGGAGGGATGGG	131293
Qy	2747	ACAACCTGCTAYGACCAGG-----CCAAGAAGCTGGACAGCTGTAAATTTTCTGCTGGACAM	2801
Db	131294	GGAGGCCAGAGCCCCAGGGACGCTCCAGGCAGCTGTGTTTCAGTGGGCATCAGCCCTGAGGA	131353
Qy	2802	MCCGTACACCCACACCTATTTCATACTCGTGTCTCTGGCTCGGCAATCACCTGTAGCAGTAG	2861
Db	131354	CTCCGGTGGGGGGTCTCTGCATTTGGGGTTTCTCTCTTTGTGCTTCAGAAACCCGATGAA	131413
Qy	2862	GTTTATCCCTTCCCTTGACCTATGAATTCATGTTGGTTCTCAGTAGGCCGGGGAAATAA	2921
Db	131414	GGCAATGTATCCAGGCACATTTCTACTTCCAATTTAAAAAACCTATGGGAAGCCAAACGATCG	131473
Qy	2922	TAGTAACAACAGCCATGATTT---AGTGTTAATTTTCTTGGTCTGGCAGTGTCTCCTT	2978
Db	131474	GAACGAACTTGGCTGTGCTTCACCGTGGGAAGGTATAAAGCGCGCTCAGTTGTCTCCTG	131533
Qy	2979	TAATCCTCAGAAACAACACTATGGGATAGGTACAATTATCCTCACTTAACAGATAAGAAAA	3038
Db	131534	GAAGACGGCGTCTTCCGAAACCAGGTAGCACCAAAGTCCTAGTTACACCCTAATAAGGA	131593
Qy	3039	CTGAGGC-----TCAGAAGGCTGAGCTATTTGCCCAAGATCACACAGC	3081
Db	131594	GCTAAGCAGCTGGGAATGCAGAAAAACGCAACAATAAGTGATGTGCCCGCGTGGGCTCTC	131653
Qy	3082	TTGTAAG-----TGGTGACAGTTTGGGTTTTTTTTTGTGTGTTTAGAGACAGGGTCTT	3136
Db	131654	CTGTGTGCACTTCTCTGCCACATTTCTATTTTTTTTTTTTTTTTTTTTGAGATGGAGTCTC	131713
Qy	3137	GCTCTGTCACCCAGGCATGAGCACAGTGGTGCAACCATAGTCACTGCAGCCTCAACCTC	3196
Db	131714	GCTCTGTCACCCAGGCTGGAATGCAGTGGTCTGATTTTCAGCTCACGGCAACCTCTGCTTT	131773
Qy	3197	CTGAGCTCAAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCAC	3256
Db	131774	CCAGGTTACGCGGATTTCTCTGCCTCAGTCTCCCGAGTAGCTGGGATTACAGGCACCTGC	131833
Qy	3257	CACCACGCTGGCTAATTAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCC	3316
Db	131834	CACCATGCCAGCCAAATTCCTTTTGATTTTGTAGTAAAAACAGGATTTTGCCATGTTGGCC	131893
Qy	3317	AGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGCTG	3376
Db	131894	AGGCTGGTTTCGAACTCCTGACCTCAAGTGATCCACCAGCCTTGGCCTCCCAAGTGCTA	131953
Qy	3377	GGATTACAGGGGTGAGCCACCATGTGGGGCTACTTATTTTCTTACATTCCATCTTTCCAA	3436
Db	131954	GGATTACATCGTGAGACACCATGCCCTCGCCCTCTCCCCACATTTATTTAT----	132009
Qy	3437	TAGAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCTTTTGTGAGA	3496
Db	132010	-----TTATTTATTTTGTAGACGGAGTCTTGTCTCT	132042
Qy	3497	CAGAGTCTCACTTCATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCTCCCGGG	3556
Db	132043	ATCGCCAGGCTGGAGTGCAGTGGCACAAATCTCAGCTCACTGCAAGCTCCGCTCCCGGG	132102

Qy	3557	TTCAAGYGATTCTCTGCTTAAGCCTCCTGAGTAGTGGAAATTACAAGCGTGCACCACCA	3616
Db	132103	TTCACGCCATTCTCTGCTCAGCCTCCCAAGTAGTGGGACTACAGGCGCCACCACCA	132162
Qy	3617	TGCTTGGCTAAATTTTTTGTATA-----TTTTTAGCAGAGATGGGTTTTT	3658
Db	132163	TGCCCAGCTAAATTTTCTTTTTTCTTTTTTTTTTTTTTTTAGTAGAGACGGGTTTC	132222
Qy	3659	ACCATGTTGCCAGGCTGGTCTCAAACTCCTGACTCAAGTGTATCTGCCCTGCCTCAGTCT	3718
Db	132223	ATGGTGTTAGCCAAGATGGTCTCGATCTCCTGACTCA--TGATCCGCCCGCTTGGCCT	132280
Qy	3719	CCCAAAGTCTGGAAATTATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTC	3778
Db	132281	CCCAAAGTCTGGGATTACAGGCATGAGCCACTGTGCCCGGCTCCCCACATTTTTTAAG	132340
Qy	3779	TTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAAT	3838
Db	132341	TCCATGG-----CCCAGATCTTCTCTCCTGACTCTCCTGTGATC-----	132379
Qy	3839	AATTGATGAATGCACAGCCTAGATATAAACCTTCTTTTTTCTTTTTTAAAAACAATCTTGA	3898
Db	132380	-----AGATCGTGGAGGGGTTTGTCTCTCCCAAAAGGCTTGT	132419
Qy	3899	CAACTTTGCAGAAATAAATACAATCTTGCATTCCTGTTTTTCACTTATCACCTTGTATGA	3958
Db	132420	TTAGCGCCAG-----CACCTCACTCTTGACTTGTTTCCCAAAATCTTGTATGG	132471
Qy	3959	CTTTTTCATATTGCCCTCAAAACCTTTATTGTTACTGTTTTTTTCACTTGTACTATTTAGTC	4018
Db	132472	AGCTGTGCGTCCGGCAGTCTCGGGAATCAGCAGCTGTGGAAAGCGGGGGTGTGTGTC	132531
Qy	4019	ACTGAATAATATGCGTTAATTTGCTTATACATCCTCTCTGCCACTTTTAGAAGGCCAAAT	4078
Db	132532	CAGCGCTGTGCTGGGCCAGTGACTGCGGGCTGGTGGGGCGCCCCCGCCACTGCCCCTGA	132591
Qy	4079	TTACAAATCTGATGAAAGCTATGAA-----CCCTCTCCCCAGAGAAATACACACACA	4132
Db	132592	TTCTTCAGCAGAAAGCAGGCAGGGAAACAAAGCTGACCCCCAGAGAGCCAGGCCATAGCAGG	132651
Qy	4133	CACACACTCACACACAGTTTTTTTTTAAATGTTTGCAACTAAGACAAGAAACCTGCATTAG	4192
Db	132652	GGCTGAGGATGCCTGGTGAATGGATGCCTGGGAGAAAAGATGGCAGAAATTCACACATGAG	132711
Qy	4193	AGGATGTTTGTTCATATAATTAATAAATA-----ACTCAGTTGGGCACAGT	4238
Db	132712	TCTATGAGACAGGGAAGAATCAATAAAATAAAGAAGGAAGGGCCGCGCGCGGT	132771
Qy	4239	GACTCAAGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAAGGTGGTGGATCACTTGAGGTGA	4298
Db	132772	GGCTCATGCCTGTAATCCCAGCACCTTTGGGAGGCTGAGGCAGCGCGGATCA--TGAGGTTG	132829
Qy	4299	GAAGTTCGAGACCGCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAATACAAAAA	4358
Db	132830	GGAGTTCGAGACCGCTGGCTAACAATGATGAAAACCCAGTCTCTACTAAAAATACAAAGA	132889
Qy	4359	TTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAG	4418
Db	132890	TTAGCCAGGTGTGGGGTGCATGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGCAGGAG	132949
Qy	4419	AATTGCTTGAACCTGGAGGCAGAGGTTTGCAGTGAGCCGAGATCCCACCCTGCACCTCCA	4478
Db	132950	AATTGCTTGAACCTGGAGGCAGAGGTTTGCAGTGAGCCGAGATTTGTGCCACTGCACCTCCA	133009
Qy	4479	GCCTGGCGCACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAATAA	4530
Db	133010	GCCTTGGCGACAGCAAGACTCCATCTCTTTGAAAAAATAAATAAATAAAGAA	133061

AC ABN97454;
XX 13-AUG-2002 (first entry)
DT XX
DE Gene #3952 used to diagnose liver cancer.
XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
PN WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030589.
XX
PR 02-OCT-2000; 2000US-0237054P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR WPI; 2002-426119/45.
XX
XX Diagnosing and detecting the progression of liver cancer, hepatocellular
PT carcinoma or metastatic liver tumor in a patient, involves detecting the
PT level of expression of two or more genes in a liver tissue sample.
XX
PS Claim 1; SEQ ID NO 3952; 298pp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 76798 BP; 19630 A; 19179 C; 19394 G; 18595 T; 0 U; 0 Other;

Query Match 7.9%; Score 396; DB 6; Length 76798;
Best Local Similarity 53.6%; Pred. No. 5.4e-63;
Matches 1300; Conservative 2; Mismatches 942; Indels 180; Gaps 16;

QY 2278 AAAAAATCGTTTCAGGCCAGGCGGGTGCTCATGCCCTGTAATCCAGCACTTTGGGAGG 2337
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2338 CCGAGGCGGGCGGATCACTTGAGGTCAGGATTCGAGACCGAGCTGGCCCAACATGGTGAA 2397
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2398 ACCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCTGTAAACC 2457
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2458 CCAGCTACTTGGGAGACT-----GAGTTGGAGGTTTCAG 2491
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2492 TGAGCCAAAGTCGTGTCACTGTCTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAA 2551
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2552 AAAAAAATGCTTTCAATAAATATATGATAAAAGGACTTATATTTTTTCAAGCCATAGGAT 2611
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2612 CATTTCTCCTGAAGCATCTTGGC-----GAAGTCATCCCC 2646
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2647 ACCTGTTCCCTGAGAGTGGGCGAGGTGAGGGCTGACCTATTGCTCTGCACCTTACTCCTATCT 2706
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2707 CAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGCTAYGACCCAGGCC 2766
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2767 AAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMCCGTACACCCACACCTATTTCATAC 2826
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2827 TCGTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCCTTGACCTATGAA 2886
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2887 TTCTAGTTGGTTCCTCAGTAGGCCGGGGGAAATAATAGTAACAACAGCCATGATTTAGTG 2946
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3007 GTACAATTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAAGCTGA----- 3057
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3058 -----GCTATTTGCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTT 3111
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3112 TGTGTTGTTTAGACAGGGTCTTGCTCTGTCACCCAGGCGATGAGCACAGTGGTGCAAC 3171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3172 CATAGGTCACATGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGCCTCCCA 3231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3232 AGTAGCTGGGACTACGAGCGTGCACCACCGCTGGCTAAATTAATAAATTTTTTTGTA 3291
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3292 GAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCT 3351
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3352 CCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGGTGAGCCACCATTGTGCGG----- 3405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3406 -----CTACTTATTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGA 3456
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3457 ACAGGGATTACTGCCTAT-----TTTCTTCTTTTCTTTTTTGGACAGAGTCTCACT 3508
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3509 TCATCACCTCAACCTCCGTTCA-----GCTCACTGCAACCTCTGCCTCCCG 3554
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 12497 AAAAAAAGCGACTATGTATGAAATACCCAGCACAGTGCCCTTCCCTTACCCATCAT 12556
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2612 CATTTCTCCTGAAGCATCTTGGC-----GAAGTCATCCCC 2646
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2647 ACCTGTTCCCTGAGAGTGGGCGAGGTGAGGGCTGACCTATTGCTCTGCACCTTACTCCTATCT 2706
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2707 CAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGCTAYGACCCAGGCC 2766
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2767 AAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMCCGTACACCCACACCTATTTCATAC 2826
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2827 TCGTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCCTTGACCTATGAA 2886
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2887 TTCTAGTTGGTTCCTCAGTAGGCCGGGGGAAATAATAGTAACAACAGCCATGATTTAGTG 2946
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3007 GTACAATTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAAGCTGA----- 3057
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3058 -----GCTATTTGCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTT 3111
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3112 TGTGTTGTTTAGACAGGGTCTTGCTCTGTCACCCAGGCGATGAGCACAGTGGTGCAAC 3171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3172 CATAGGTCACATGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGCCTCCCA 3231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3232 AGTAGCTGGGACTACGAGCGTGCACCACCGCTGGCTAAATTAATAAATTTTTTTGTA 3291
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3292 GAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCT 3351
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3352 CCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGGTGAGCCACCATTGTGCGG----- 3405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3406 -----CTACTTATTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCACAGA 3456
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3457 ACAGGGATTACTGCCTAT-----TTTCTTCTTTTCTTTTTTGGACAGAGTCTCACT 3508
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QY 3509 TCATCACCTCAACCTCCGTTCA-----GCTCACTGCAACCTCTGCCTCCCG 3554
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XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX PN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001354.
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XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure; SEQ ID NO 21743; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 30620 BP; 7407 A; 7216 C; 7192 G; 8805 T; 0 U; 0 Other;
Query Match 7.9%; Score 394.8; DB 4; Length 30620;
Best Local Similarity 60.1%; Pred. No. 7.9e-63;
Matches 863; Conservative 1; Mismatches 508; Indels 64; Gaps 10;
QY 3110 TTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCACAGTGGTGCA 3169
Dd ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 1490 TTTTTTTTTTTTGAGATAAGAGTCTTGCTCTGTCGCCCCAGACTGGAGTGCGACACA 1549
QY 3170 ACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCC 3229
Dd ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 1550 ATCTCGGCTCACTCCAACCTCCACCTCCTAGGTTCAAGTGATCTCATGCTCAGCCTCC 1609
QY 3230 CAAGTAGCTGGGACTACGAGCGGTGCACACCACCGCTGGCTAATTAATAAATTTTTTTG 3289
Dd ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 1610 TGAGTAGCTGGGATTACAGGCATGCATCAACATGTCCAGCTAGTTTATGTA--TTTTAG 1667
QY 3290 TAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCAAGCAATC 3349
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Dd 2701 AAAATTAGCTGGATGTGGTGGCGCACACCTGTAAACGCCAGCTACGTGGGAGGCTGAGGCA 2760
QY 4415 AGAGAAATTGCTTGAACTGGGAGGCGAGAGTTTGCAGTGAGCCGAGATCCCACCACCTGCAC 4474
Dd ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dd 2761 GGAGAAATTGCTGGAAACCCGGGAGGCGAGAGGCTGCAGTGGGCTGAGATCGCACCACTGCAC 2820
QY 4475 TCCAGCCTGGGCGACACAGCGGAGACTCTATCTCAAAAAAATAAATAAATAAATAA 4530
```

Db	2821	TCCAGCCTGGGTGACAGACGAGACTCCATCTCAAAAAAAAAAAAAATAATAATAA	2876
RESULT 56			
ADP74371			
ID	ADP74371 standard; DNA; 19300 BP.		
XX	AC ADP74371;		
XX	DT 26-AUG-2004 (first entry)		
XX	DE Human X chromosome nucleotides 469701-489000.		
XX	KW Human; ds; antisense; NRF; NF-kappaB repressing factor;		
KW	nuclear factor kappaB; immune response; inflammatory response;		
KW	oncogenesis; apoptosis; cell cycle; differentiation; cell migration;		
KW	chromosome Xq24-25.		
XX	OS Homo sapiens.		
XX	PN US2004110156-A1.		
XX	PD 10-JUN-2004.		
XX	PF 10-DEC-2002; 2002US-00317271.		
XX	PR 10-DEC-2002; 2002US-00317271.		
XX	PA (ISIS-) ISIS PHARM INC.		
XX	PI Dobie KW;		
XX	DR WPI; 2004-440344/41.		
XX	PT New antisense oligonucleotides for modulating NF-kappaB repressing factor		
PPT	expression, useful for diagnosing, preventing or treating diseases or		
PPT	conditions involving an immune response.		
XX	PS Claim 1; SEQ ID NO 4; 61pp; English.		
XX	CC The invention relates to a compound 8-80 nucleobases in length targeted		
CC	to a nucleic acid molecule encoding NF-kappaB repressing factor (NRF). NF		
CC	-kappaB (nuclear factor kappaB) is involved in such cellular processes as		
CC	the immune response, inflammatory response, oncogenesis, apoptosis, cell		
CC	cycle, differentiation and cell migration. The compound (an antisense		
CC	oligonucleotide) specifically hybridises with the nucleic acid molecule		
CC	encoding NRF (which appears as ADP74371 and comprises nucleotides 469701-		
CC	489000 of the X chromosome containing the NRF gene at Xq24-25) and		
CC	inhibits the expression of NRF. Also included are inhibiting the		
CC	expression of NRF in cells or tissues, screening for a modulator of NRF,		
CC	a diagnostic method for identifying a disease state, a kit or assay		
CC	device comprising the above compound, and treating an animal having a		
CC	disease or condition associated with NRF. The antisense oligonucleotide		
CC	is useful for inhibiting the expression of NRF in cells or tissues to		
CC	prevent or treat diseases associated with aberrant NRF expression, such		
CC	as diseases or conditions involving an immune response. In addition, the		
CC	compound is used for diagnostics, prophylaxis, or as research reagents or		
CC	kits. The present sequence comprises nucleotides 469701-489000 of the X		
CC	chromosome containing the NRF gene at Xq24-25, and is a target for the		
CC	antisense oligonucleotides.		
XX	SQ Sequence 19300 BP; 4979 A; 4025 C; 4288 G; 6008 T; 0 U; 0 Other;		
Query Match			
Best Local Similarity 7.9%; Score 394.6; DB 12; Length 19300;			
Matches 908; Conservative 1; Mismatches 520; Indels 82; Gaps 12;			
QY	3099	TTGGGTTTTTTTTTGTGTTAGACAGGGTCTTGCTC-TGTCACCCAGGCATGAG	3157
Db	8747	TTTTTTTTTTTTTTTTTTTGAGATGGAGTTTCACTCTTGTTGCCAGGCTGGAA	8806
QY	3158	CACAGTGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTG	3217

Db	8807	GGCAATGGTGGATCTCGGCTCACTAAACCTCTGCCTCCAGGTTCAAGCGATTCCT	8866
Qy	3218	ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACCGCTGCTAAATAA	3277
Db	8867	GTCTCAGCCTCCCAAGTAGCTGGATTACAGGCATGCGCCATCACACCCGCTAATTTT	8926
Qy	3278	AAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGG	3337
Db	8927	GTATTTTGTAGAGACA--GGTTTCTCTATGTGGTCAGGCTGGTCTCGAATCCCGA	8983
Qy	3338	CTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGTCTGGATTACAGGGTGAGCCACC	3397
Db	8984	CCTCAGGTGATCTGCGCTTGGCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCACA	9043
Qy	3398	ATGTGCGGCTACTTATTCT-----TTACATTCCATCTTTTCCAATA	3438
Db	9044	CGGCCCCGGCTTTTGTTTTATCTCATACTTTGGAAATATGTACTCCCAAATTTGAATGG	9103
Qy	3439	GAATGTAAGATCCACAGAACAGGGATTACTGCTTATTTTCTTCTTTTGTGAGACA	3498
Db	9104	AAGTGATATGTAGATGTATTGTGTTATTATTATTTATTATTATTATTGTGAGACA	9163
Qy	3499	GAGTCTCATTTCATCACCTCAACCT-----CCGTTCAGCTCACTGCAACC	3543
Db	9164	GAGTCTCGCTCTTGTCTCCAGGCTGGAGTGCAGTGGTGCAATCTCAGCTCACTGCAACC	9223
Qy	3544	TCTGCCTCCCGGTTCAAGYGATTCTCCTGCTTAAGCCTCCTGAGTAGTGGAAATTACAA	3603
Db	9224	TCCGCTCCCGGTTCAAGCAATTTCTCCTGCTCAGCCTCCTGAGTAGCTGGGATTACAG	9283
Qy	3604	GCGTGCAACCACCATGCTTGGCTAAATTTTTGTATTTTGTAGCAGAGATGGGGTTTACCAT	3663
Db	9284	GCGCTGTGTACCACACCCAGCTAA-TTTTTGTATTTTAGTAGAGACGGGGTTTACCAT	9342
Qy	3664	GTTGCCCAGGCTGCTCAAACTCCTGACCTCAAGTGATCTGCCCTGCCTCAGTCTCCCAA	3723
Db	9343	GTTGGGTAAGTGTCTTGAACTCCTGACCTCAGGTGATCTGCCACCTCAGCCTCCCAA	9402
Qy	3724	AGTGCTGGAATTATAGGCGTGAGTCACTGTGCTGCGCCGATTACTGTCTATTTTCTTTAT	3783
Db	9403	AATGTTGGATTACAGGTGTGAGCCACCCCGCCAGCCATATTGTGT-TTTAGACTGTGC	9461
Qy	3784	TGCTATATCCCCAGATCTAGAGCAGTGTCTGCACATATAGTAGGTGCTCAATAAATAATG	3843
Db	9462	TTTCTGATGTTCAGATAAGAGTCAATGAAATAAAATACTCTTGGTATTTAATACTCG	9521
Qy	3844	ATGAATGCACAGCCTAGATAT-----AAACTTCTTTTTTCTTTTAAACAAT	3893
Db	9522	TGCTAGCTTTAGCAGCAACAGTTGTAGTGGGAAGTACAGGTACAAACAGAGTAGCTTC	9581
Qy	3894	CTTGACAACTTTGCAGAAATAAATAACAATCTTGCAATCTGCTTTTCTACTTACTATT	3952
Db	9582	CAGCAGTCTGTGCGGGAGGCCACCGTGCTTGAATCTGCTTTGCGTGGAAATGATACGTG	9641
Qy	3953	TTATGACTTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTTTCAITGTTACTATT	4012
Db	9642	ATGGGTGTGCAACCTGTTCTACTGAAAATGGAAAATGTTACCCCTCCTCTGTTTCAGAAC	9701
Qy	4013	TTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTC-----	4060
Db	9702	TGATTCATGTAAGGTATGATAGTTACTCAATTTTCAGAACTTCTTCCCAAATGCTACCAG	9761
Qy	4061	----CACTTTAGAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCCCAGA	4116
Db	9762	GAATCTCTTTTGGTCTTAGGCTGGGGAAGGCTCTGAAGGTAGGAAGGAGACAGGTA	9821
Qy	4117	GAAATACACACACACACACTCACACAGTTTTTTTTTT-----AATGTTT	4165
Db	9822	ACCGTCATAACCAACACTTCACTTGAGCTCCTGTTCTGTCTCTGTAGTAAATGTTA	9881
Qy	4166	GCAACTAAGACAAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAAATAAATA---A	4222

Db 9882 TTCTATCAAGCAGCCAATCTTTCATAAGGAGCCTTTTTTTTTTTTTTTTTTTTAAAGAGACCGT 9941

QY 4223 CTCAGTTGGSCACAGTGACTCAAGCCTGTCTAACCACAGTACTTTTGGAAGTCCAAGGTGGST 4282

Db 9942 CTCAGCCGGTGCAGTTGCTCACACCTGTAATCCTAGCACCTTTGGGAGGCTGAGGCAGGT 10001

QY 4283 GGATCACTTGAGGTGAGAAGTTTCGAGACCAGCCTGGTCAATATGGTGAAACCCATCTCT 4342

Db 10002 GGATTACCTGAGGTCAGGAGTTTCAAGGTCAGCCTGGCCAAACATGGCAAACCCCTGTCTCT 10061

QY 4343 ACT-AATAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCG 4401

Db 10062 ACTAAAAATACAAAAATTAGCCAGCGCTGGTGGCGCATGCCTGTAAATCCCAGCTACTTG 10121

QY 4402 GGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGTTGCAGTGAGCCGAGAT 4461

Db 10122 GGAGGCTGAGGCAGGAGAAGTGCTTGAACCCGGGAGGTGGAGTTGCAGTGAGCTGATAT 10181

QY 4462 CCCACCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAATAATAA 4521

Db 10182 TGTGCCACTGCACCTCCAGCCTGGGAGACAGAGCAAGACTCCCTCTCAAAAAAATAAAAAA 10241

QY 4522 ATAAAAATAAG 4532

Db 10242 AAAAAAAAAG 10252

RESULT 57

ADE84033
ID ADE84033 standard; DNA; 9289 BP.

XX AC ADE84033;

XX DT 29-JAN-2004 (first entry)

XX DE 5' regulatory region of human gene RBL2.

XX KW ds; lymphoid cell proliferative disorder; methylation;
KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW diffuse large B-cell lymphoma; mantle cell lymphoma;
KW chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW follicular lymphoma; diagnosis; prognosis.

XX OS Homo sapiens.

XX PN WO2003044226-A2.

XX PD 30-MAY-2003.

XX PF 25-NOV-2002; 2002WO-EP013265.

XX PR 23-NOV-2001; 2001DE-01057491.

XX PR 28-DEC-2001; 2001DE-01064501.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;

XX DR WPI; 2003-457621/43.

XX PT Detecting and differentiating between lymphoid cell proliferative
PT disorders comprises contacting a target nucleic acid with at least one
PT reagent that distinguishes between methylated and non-methylated CpG
PT dinucleotides.

XX PS Disclosure; SEQ ID NO 29; 448pp; English.

XX CC The invention relates to a method of detecting and differentiating
CC between lymphoid cell proliferative disorders associated with at least
CC one gene and/or their regulatory regions in a subject by contacting a
CC target nucleic acid in a biological sample obtained from the subject with
CC at least one reagent or series of reagents that distinguish between
CC methylated and non-methylated CpG dinucleotides within the target nucleic

CC acid. The genes and/or their regulatory regions are preferably selected
CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYO1, CDH3,
CC MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2a, CDKN2B, FOS,
CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFB2, TP73, CDKNIC,
CC GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
CC of the genes are useful for detecting the methylation state of all the
CC CpG dinucleotides within one or more the sequences, or their complements,
CC for determining the cytosine methylation state and or single nucleotide
CC polymorphisms (SNPs), and for differentiating at least two of the medical
CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
CC lymphoma. They are also useful for detecting of a predisposition to,
CC differentiation between subclasses, diagnosis, prognosis, treating and/or
CC monitoring of lymphoid cell proliferative disorder. This sequence
CC represents the 5' and/or regulatory region from one of the above
CC mentioned genes.

XX SQ Sequence 9289 BP; 2515 A; 1963 C; 2097 G; 2714 T; 0 U; 0 Other;

Query Match 7.9%; Score 392.4; DB 10; Length 9289;
Best Local Similarity 57.9%; Pred. No. 1.8e-62;
Matches 832; Conservative 1; Mismatches 532; Indels 71; Gaps 5;

QY 3094 ACAGTTTGGGTTTTTTTGTGTTGTTTAGAGACAGGGTCTTGCTGTCAACCAGGCA 3153

Db 2360 ACACTTATTATTATAATTATTATTATTATGAGATGGATTGCTGTGCGCCAGGCT 2419

QY 3154 TGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCT 3213

Db 2420 GGAGTGCAGTGGCATGATCCCAGCTAACTGCAGTCTTTGCCTCCTGGGTCCAGCAATC 2479

QY 3214 GCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGACCACCAGCCTGGCTAAT 3273

Db 2480 TCCTGCCTCAGCCTCCTGAGTAGTGGGATTACTGGCACCAACCACCTCCTGGCTAAT 2539

QY 3274 TAAAAAAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTC 3333

Db 2540 TTTTGTGA-TTTTGTAGAGAAATGGGTTTTCACAATGTTGCCAGGCTGGTCTTAAACTC 2598

QY 3334 CTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGC 3393

Db 2599 CTAACCTTAAGTGATCTGCCCGCCTTGGCCTCCCAAGTGTAGGATTACAGGCGTGAGC 2658

QY 3394 CACCATGTGCGGCTACTTATTCTTTACATTCCTTCCAATAGAATGTAAGATCCAC 3453

Db 2659 CACCGGCTTGGCCAAATTATTATTA----- 2685

QY 3454 AGAACAGGGATTACTGCCTATTTCTTCCTTTCTTTTGTAGACAGAGTCTCAGTTCATC 3513

Db 2686 -----TTATTTTGTGACAGGGTCTCTGTGCCC 2716

QY 3514 ACCTCAACCTCCGTTCAGCTCACTGCAAACCTCTGCCTCCCGGTTCAAGYGATTCCTCTG 3573

Db 2717 AAGCTGTAGTGGCATGGTCACAGTTCACCTGCAGACTCCCAGGCTTAGGCGTTCCTCCA 2776

QY 3574 CCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCACCATGCTTGGCTAATTTT 3633

Db 2777 CCTCAGTCTCCCAAGTAGTAGGATTACAGGCGTGACCACTCTGGGTAA-TTTT 2835

QY 3634 GTATTTTGTAGCAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACC 3693

Db 2836 CTATTTTGTAGAGACAGGGTTTCACTATGTGCCCAGGCTGGTCTCGAACTCCTGTAC 2895

QY 3694 TCAAGTGATCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGAGTCACTGT 3753

Db 2896 TCAAGCAGTCTCCCACTTGACCTCCCAAAGTGTGGATTACAGGTGTGATCCACAAC 2955

QY 3754 GCCTGGCCGATTACTGTCTATTTTCTTTTATTGCTAT----ATCCCCAGATCTAGAGCAGT 3809

Db 2956 GTCCAGCCTATATACTTAAAGATACTTCTAAACCACTTGTGTTCAACTTCTGTCTTGCCC 3015

QY 3810 GTCTGACATATAGTAGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACT 3869

Db 3016 CATAGTCACCTTGAGACTCATCTAGCTTAGCCAACTCCAAAAGCATTTGCTGATTACTGTGAA 3075
Qy 3870 TTCTTTTCTTTTTTAAACAATCTTTGACAACCTTTGCAGAATAAATACAATCTTGCATT 3929
Db 3076 TTTTACTAAGGTTTTCTTAAAGAGGTTCCATTGTCTCAAAATGTTTCTCCTGAAATATCCTG 3135
Qy 3930 CTGCTTTTTCACCT--TATACCTTGTTATGACTTTTTCATATATGCTTCAAAACCTTTATT 3986
Db 3136 TTACCTGTCTACCTGATTTTCTCCTATCTTTCAGAGTTCCTGCTCCTCCCGCCTGT 3195
Qy 3987 GTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTAT 4046
Db 3196 CATATACCTTCCATAAGCCCTACTTTTGTCCAGCACTTTTCCCTCTGTCTCAGTTTACA 3255
Qy 4047 ACATCTCTCTCTCCACCTTTAGAAGGCCAAAATTTACAAATCTGATGAAAGCTATGAACCC 4106
Db 3256 TATCCCAACCAAGCAAAACAATAATAGCAAAACAGTAATGCCTTCTGAATCCTCAAAATGC 3315
Qy 4107 TCTCCCCAGAGAAATACACACACACACACACTCACACACAGTTTTTTTTTTAATGTTTG 4166
Db 3316 TCAATCCTCAGATTGCTCCTCAATCTGGAAAATGTTTTATATCAAGCCCATTTATAAATC 3375
Qy 4167 CAACTAAGACAAGAAACCTGCAATTAGAGGATGTTTGTTCATATTAATTAATAAATAACTCA 4226
Db 3376 AAGGATTGGCAATTTAAAAAATTAAAAATAAAGAGGAATTGGAATAAATAAATGAATTG 3435
Qy 4227 GTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAAGTCCAAGGTGGTGGAT 4286
Db 3436 GCTGGGCACGGTGGCTCACGCCTGTAATCCAGAACTTTTGGAGGCCGAGGTGGTGGAT 3495
Qy 4287 CACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGTGAAACCCCTATCTCTACTA 4346
Db 3496 CACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGTTGAAACCCCTGCCTGTACTG 3555
Qy 4347 AAAATACAAAAATTAGCTGGGTGAGTGATGCATGCCCTGAGTCCCAGCTACTCGGAGG 4406
Db 3556 AAAATACAAAAATTAGCTGGGTGGGTGGCGCACACCTGTAATCCCAGATACTCAGGAGG 3615
Qy 4407 CTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCAC 4466
Db 3616 CTGAGGCAGGAGAAATCGCTTGAACCCAGGAGCGGAGGTTGCAGTGAGCCGAGATCGTGC 3675
Qy 4467 CACTGCACTCCAGCCTGGCGCACACAGCGAGACTCTATCTCAAAAAAATAAATAA 4522
Db 3676 CACTACACTCCAGCCTGGGCAACAGAGCCAGACTCTGTCTCAAAAAAAAAAAAAA 3731

RESULT 58
AAS00624

ID AAS00624 standard; DNA; 36221 BP.

XX AC AAS00624;

XX DT 07-SEP-2001 (first entry)

XX DE Human death-associated protein 6 (DAXX) gene.

XX KW Death-associated protein 6; DAXX; polymorphism; haplotype pair; human; immune disorder; autoimmune disease; population diversity; ds; paternity testing; anthropological lineage; forensic application.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT variation replace(26869,G)

FT FT variation replace(26870,T)

FT FT variation replace(27145,A)

FT FT variation replace(27239,G)

FT FT variation /*tag= d

FT variation replace(27620,T)
FT /*tag= e
FT variation replace(27788,G)
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FT variation replace(30752,T)
FT /*tag= s
FT variation replace(31916,T)
FT /*tag= t

FT WO200125245-A2.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US027487.

XX PR 06-OCT-1999; 99US-0157909P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Chew A, Choi JY, Denton RR, Nandabalan K, Stephens JC;

XX DR WPI; 2001-308220/32.

XX PT New human death-associated protein 6 (DAXX) gene variants comprising 19 polymorphic sites useful in studying the effect of variation on the biological activity of DAXX and in developing drugs targeting the protein.

XX PS Claim 1; Fig 1; 97pp; English.

XX CC The sequence represents a DNA encoding human death-associated protein 6 (DAXX). This gene may comprise one or more polymorphisms at specific nucleotide positions to form one of nineteen possible polymorphic variants. Associations between a trait and a genotype or a haplotype of the DAXX gene can be identified by comparing the frequency of the genotype or haplotype in a population exhibiting the trait with that of a reference population. A higher frequency in the trait population indicates an association. Methods involving genotyping or haplotyping of the DAXX gene of an individual can lead to prediction of haplotype pairs for the DAXX gene of related individuals, and may be useful in studying the expression and biological function of DAXX, as well as in developing drugs targeting this protein. Polymorphic variants of DAXX are useful in studying the effect of the variation on the biological activity of DAXX as well as on the binding affinity of candidate drugs targeting DAXX for the treatment of autoimmune diseases and other immune disorders.

XX CC Polymorphism is also useful for studying population diversity, anthropological lineage, paternity testing, forensic applications, and for identifying associations between the DAXX genetic variation and a trait such as level of drug response or susceptibility to disease. DAXX

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2006, 07:28:08 ; Search time 12140 Seconds
(without alignments)
19273.657 Million cell updates/sec

Title: SEQ1-4500-9500-7328G
Perfect score: 4997.8
Sequence: 1 ctggtcatctcagttctttt.....tttgagaccagcctggacaa 5001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gssl:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	505.4	10.1	507	5	BU785040
3	349	7.0	349	9	AQ017732
4	344.2	6.9	4087	4	BC024593
5	341	6.8	3990	4	HSM803026
6	337.2	6.7	15970	9	AQ839852
7	334	6.7	347	1	AL708471
8	315.8	6.3	897	6	CD557847
9	311	6.2	3095	4	CR858326
10	309.8	6.2	3775	4	CR627381
11	308	6.2	891	5	BU174155
12	307.2	6.1	5797	4	CR749233
13	307	6.1	1654	4	CR591254
14	306.6	6.1	777	8	DR761502
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16	305.2	6.1	935	5	BU838401
17	303.2	6.1	910	5	BO722917
18	301.8	6.0	627	6	CD702127
19	301.2	6.0	1605	4	CR860521
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22	300	6.0	820	5	BU568843

96	269.8	5.4	1036	3	BQ070834	BQ070834	AGENCOURT
c 97	269.6	5.4	763	8	CX871744	CX871744	HESC4_60
98	269	5.4	5155	4	HSM809074	BM648923	Homo sapi
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101	268.8	5.4	1108	3	BM806595	BM806595	AGENCOURT
c 102	268.6	5.4	3179	4	HSM804145	AL832834	Homo sapi
c 103	268.4	5.4	923	6	CD518127	CD518127	AGENCOURT
c 104	268.4	5.4	8488	4	CR933654	CR933654	Homo sapi
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c 106	267.8	5.4	586	1	AL701696	AL701696	DKFZp686D
c 107	267.8	5.4	697	5	BU930659	BU930659	AGENCOURT
108	267.8	5.4	3146	4	BC036603	BC036603	Homo sapi
109	267.8	5.4	6181	4	HSM803508	AL832201	Homo sapi
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112	267.4	5.4	3287	4	CR858848	CR858848	Pongo pyg
113	267.4	5.4	5404	4	HSM808938	BM648787	Homo sapi
114	267	5.3	858	5	BQ422295	BQ422295	AGENCOURT
c 115	266.8	5.3	722	9	AQ583981	AQ583981	RPCI-11-4
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121	266.2	5.3	988	3	BM905391	BM905391	AGENCOURT
122	266	5.3	671	6	CB270192	CB270192	1009099 H
c 123	266	5.3	877	6	CD515864	CD515864	AGENCOURT
c 124	265.8	5.3	443	9	AQ164853	AQ164853	HS_2180_A
c 125	265.8	5.3	970	3	BM468547	BM468547	AGENCOURT
c 126	265.8	5.3	1921	4	AF370377	AF370377	Homo sapi
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129	265.2	5.3	626	3	BM990577	BM990577	UI-H-DI0-
130	265.2	5.3	820	6	CD653272	CD653272	AGENCOURT
c 131	265	5.3	4087	4	BC024593	BC024593	Homo sapi
132	265	5.3	4756	4	CR857077	CR857077	Pongo pyg
c 133	264.8	5.3	622	5	BX505562	BX505562	DKFZp686P
c 134	264.8	5.3	788	3	BM013486	BM013486	603638941
c 135	264.8	5.3	835	5	BU933013	BU933013	AGENCOURT
136	264.8	5.3	3804	4	HSM802182	AL137707	Homo sapi
c 137	264.6	5.3	600	5	BX507478	BX507478	DKFZp686A
c 138	264.6	5.3	680	9	AQ356404	AQ356404	CITBI-E1-
c 139	264.6	5.3	1345	1	AV762220	AV762220	AV762220
c 140	264.6	5.3	3204	4	CR858951	CR858951	Pongo pyg
141	264.6	5.3	4071	4	HSM804424	AL833113	Homo sapi
c 142	264.4	5.3	714	8	CX872940	CX872940	HESC4_74
143	264.4	5.3	729	6	CF127074	CF127074	UI-HF-ET0
c 144	264.4	5.3	778	1	AV764490	AV764490	AV764490
c 145	264.2	5.3	872	9	BZ608878	BZ608878	WHABK92TR
146	264.2	5.3	910	5	BQ681678	BQ681678	AGENCOURT
c 147	264	5.3	1033	3	BM456793	BM456793	AGENCOURT
148	263.6	5.3	712	6	CF146965	CF146965	UI-HF-CB0
c 149	263.6	5.3	3466	4	HSM803362	AL832055	Homo sapi
150	263.4	5.3	857	9	AQ896568	AQ896568	HS_3134_A

ALIGNMENTS

RESULT 1	BU785306	BU785306	599 bp	mRNA	linear	EST 11-OCT-2002
LOCUS	in43g09.y1	HR85 islet	Homo sapiens	CDNA	clone	IMAGE:6125008 5'
DEFINITION	similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ; , mRNA sequence.					
ACCESSION	BU785306	EST.				
VERSION	BU785306.1	GI:23831050				
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;					

REFERENCE	Hominidae; Homo.				
AUTHORS	1 (bases 1 to 599) Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y. Endocrine Pancreas Consortium Unpublished (2000) Other_ESTs: in43g09.xl Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 448.				
FEATURES	Location/Qualifiers 1..599 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6125008" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /clone_lib="HR85 islet" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."				
source					
ORIGIN	Query Match 10.4%; Score 520.2; DB 5; Length 599; Best Local Similarity 98.7%; Pred. No. 3.7e-34; Matches 522; Conservative 2; Mismatches 5; Indels 0; Gaps 0;				
QY	1761	CTTCTTGAGTGGCGCGCCGCGM	CAGCGGCATCAGCCCTCGGGCCGTGTGGCAGTTC	CGC	1820
Db	10	CTGCTCACAGTGGCGCGCCGCG	CACGCGGCATCAGCCCTCGGGCCGTGTGGCAGTTC	CGC	69
QY	1821	AAAATGATCAAGTGGTGGTATCC	CGGGGAGTGACCCCTT	YTTTGGAAATACAACTACGGC	1880
Db	70	AAAATGATCAAGTGGTGGTATCC	CGGGGAGTGACCCCTT	CTTTGGAAATACAACTACGGC	129
QY	1881	TGCTACTGTGGGTGGGGGCTC	AGGCACCCCGTGGATGAAC	TGGACAAGTAAGTGATC	1940
Db	130	TGCTACTGTGGCTTGGGGGGCT	CAGGCACCCCGTGGATGAAC	TGGACAAGTAAGTGATC	189
QY	1941	CGCCTGCAGGAAATTGGAGTGC	CTGCCGGGGGGGTGGGCACAC	CGCCAAGGATCTC	2000
Db	190	CGCCTGCAGGAAATTGGAGTGC	CTGCCGGGGGGGTGGGCACAC	CGCCAAGGATCTC	249
QY	2001	ACGAGGCATACAAAGGGGACTT	TGCATATCTGCTAAAGGATAA	CATATTTTTCACCTCTTGTC	2060
Db	250	ACGAGGCATACAAAGGGGACTT	TGCATATCTGCTAAAGGATAA	CATATTTTTCACCTCTTGTC	309
QY	2061	AAATAAACAAATATGTTCCAAG	GAGGACCCCTGTAGCGAACGC	ACCCCGTTAGAGATGGAAA	2120
Db	310	AAATAAACAAATATGTTCCAAG	GAGGACCCCTGTAGCGAACGC	ACCCCGTTAGAGATGGAAA	369

QY 2121 CAATGACCGACGTGCAAAACAGTGGGCGATGCTGCCCTCCAGTGGCAGAATGTAGCAACA 2180
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Db 370 CAATGACCGACGTGCAAAACAGTGGGCGATGCTGCCCTCCAGTGGCAGAATGTAGCAACA 429
|||||
QY 2181 GTAACATCACAGCAACTATCCACGTGTCTATTTCTAGCAGTGGTTGTCTACTGCACCTTC 2240
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Db 430 GTAACATCACAGCAACTATCCACGTGTCTATTTCTAGCAGTGGTTGTCTACTGCACCTTC 489
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QY 2241 TGAATACAGGATTTTACTGTATTCTTGCAACCACATGTTAAAAAATCGCTTT 2289
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Db 490 TGAATACAGGATTTTACTGTATTCTTGCAACCACATGTTAAAAAATCACTGT 538
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RESULT 2
BU785040/c 507 bp mRNA linear EST 11-OCT-2002
LOCUS in43g09.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6125008 3',
mRNA sequence.

ACCESSION BU785040
VERSION BU785040.1 GI:23830576
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 507)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hallier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)

TITLE Endocrine Pancreas Consortium
JOURNAL Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 443.
Location/Qualifiers

FEATURES source
1..507
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6125008"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match 10.1%; Score 505.4; DB 5; Length 507;
Best Local Similarity 99.8%; Pred. No. 6.7e-33;
Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4006 TACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTT 4065
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Db 507 TACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTT 448
|||||
QY 4066 TAGAAGGCCAAATTTACAAATCTGATGAAGCTATGAACCCCTCTCCCAGAGAAATACAC 4125
|||||
Db 447 TAGAAGGCCAAATTTACAAATCTGATGAAGCTATGAACCCCTCTCCCAGAGAAATACAC 388
|||||
QY 4126 ACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCT 4185
|||||
Db 387 ACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCT 328
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QY 4186 GCATTAGAGGATGTTTGTTCATATTAAATTAATAAATACTCAGTTGGGCACAGTGACTCAA 4245
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Db 327 GCATTAGAGGATGTTTGTTCATATTAAATTAATAAATACTCAGTTGGGCACAGTGACTCAA 268
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QY 4246 GCCTGTAACACACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACATTGAGGTGAGAAAGTTC 4305
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Db 267 GCCTGTAACACACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACATTGAGGTGAGAAAGTTC 208
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QY 4306 GAGACCAGCCTGGTCAATATGTTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCTG 4365
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Db 207 GAGACCAGCCTGGTCAATATGTTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCTG 148
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QY 4366 GGTGTAGTATGCATGCCTGTAGTCCCAGTACTCGGAGGCTGAGGCAAGAGAATTGCT 4425
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Db 147 GGTGTAGTATGCATGCCTGTAGTCCCAGTACTCGGAGGCTGAGGCAAGAGAATTGCT 88
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QY 4426 TGAACCTGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCAGTGCACCTCCAGCCTGGG 4485
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Db 87 TGAACCTGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCAGTGCACCTCCAGCCTGGG 28
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QY 4486 CGACACAGCGAGACTCTATCTCAAAAA 4512
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Db 27 CGACACAGCGAGACTCTATCTCAAAAA 1
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RESULT 3
AQ017732 349 bp DNA linear GSS 09-JUN-1998
LOCUS CIT-HSP-2308L15.TR CIT-HSP Homo sapiens genomic clone 2308L15,
genomic survey sequence.

ACCESSION AQ017732
VERSION AQ017732.1 GI:3196468
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 349)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.

TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CIT-HSP-2308L15.TF

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse

Class: BAC ends.
Location/Qualifiers
1..349
/organism="Homo sapiens"


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/db_xref="taxon:9606"
/clone="2308L15"
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/cell_type="Sperm"
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/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"

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    Matches 349;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY 314 TTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCATGATCATAGCTCA 373
Db 1 TTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCATGATCATAGCTCA 60

QY 374 CCACAGCTTCCAACTCGTGGGCTCAAAGTGATCCTCCCACCTTACTCAACTAAGTAGTTAG 433
Db 61 CCACAGCTTCCAACTCGTGGGCTCAAAGTGATCCTCCCACCTTACTCAACTAAGTAGTTAG 120

QY 434 GCCAATCTCCCATTTATTTTATTTTAAATTTTATTTTATTTTATTTTACTTTATTTTAT 493
Db 121 GCCAATCTCCCATTTATTTTATTTTAAATTTTATTTTATTTTATTTTACTTTATTTTAT 180

QY 494 TTTTGACACGGGGCTCACTCTGTCGCCAGGCTGGAGTGGGTGGCGTGATCTCAGATCA 553
Db 181 TTTTGACACGGGGCTCACTCTGTCGCCAGGCTGGAGTGGGTGGCGTGATCTCAGATCA 240

QY 554 CTACAACCTCCATCTCCTGGGTTCAAATAATTCTCTTGCCCTCAGCCTCTCAAGTAGCTGG 613
Db 241 CTACAACCTCCATCTCCTGGGTTCAAATAATTCTCTTGCCCTCAGCCTCTCAAGTAGCTGG 300

QY 614 GACTTGTAGCTCTCAAGTAGCTGGCACACACCAACCATGCCAGCTAATT 662
Db 301 GACTTGTAGCTCTCAAGTAGCTGGCACACACCAACCATGCCAGCTAATT 349

RESULT 4
BC024593
LOCUS
DEFINITION
Homo sapiens cDNA clone IMAGE:3914314, with apparent retained
intron.
ACCESSION
BC024593
VERSION
GI:22137609
KEYWORDS
HTC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 4087)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
```

```
JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 4087)
AUTHORS
Strausberg,R.
TITLE
Direct Submission
JOURNAL
Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 22 Row: m Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis
This clone has the following problem: retained intron.

FEATURES
    Location/Qualifiers
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    /db_xref="taxon:9606"
    /clone="IMAGE:3914314"
    /tissue_type="Uterus, leiomyosarcoma"
    /clone_lib="NIH MGC_71"
    /lab_host="DH10B"
    /note="Vector: pCMV-SPORT6"

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QY 3099 TTGGGTTTTTTTTTTGTTGTTTGTAGACAGGGTCTTGCTCTGTCAACCAGGCATGAGC 3158
Db 2019 TTTGAAATTTGTTGTTGTTTGTAGACAGGGTCTGGGTCTGCCACCAGGCTGGAGT 2078

QY 3159 ACAGTGGTGCACATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGA 3218
Db 2079 GTAGTGGTGTATCATAGCTCAATGCAGCCCCAACCTTCGGGGCGCAAGTGATCTCTCA 2138

QY 3219 CCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGGCTAATAAAA 3278
Db 2139 CCTCAGCCTCCTGAGTAGCTGGGACTACAGGCATGTGCCACCACACCCCTCCTAATATA 2198

QY 3279 AAAT-----TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTC 3333
Db 2199 TTTTTTTTATTTTGTAGAGATGAGGTTTCATTATGTTGCCCAGACTGGTCTGGAACCTC 2258

QY 3334 CTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGC 3393
Db 2259 CTGGC-TCAAGTGATCCTCCCTCCTTGCCCTCCCGAAAGTGTGGGATTGCGTGCACGAGC 2317

QY 3394 CACCATGTGCGGCTACTTATTTCTTTTACATTCCTATCTTTCCAATAGAAATGAAGATCCAC 3453
Db 2318 CACCACATCTGGCCTGTTTGATTATTTAAATTTTTTTTTTT----- 2356

QY 3454 AGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTCATC 3513
Db 2357 -----TTTTTTTTTTTGAGATAGAGTCTCGCTCTGTCGCTCAGGCTGGAGT 2402
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Qy	3514	ACCTCAACCTCCGTT	CAGCTCACTGCAACCTCTGCTCCCGGGTTCAAGGATTCCTCTG	3573
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Qy	3574	CCTAAGCCTCCTGAGT	AGTGGAAATTACAAGCGTGCAACCACCATGCTTGGCTAAATTTTT	3633
Db	2463	TGTCAGCCTCCCGAGT	AGCTGGGGTTACAGGTGTCCACCACCAAGCCTGGCTAA-TTTTT	2521
Qy	3634	GTATTTTTAGCAGAGAT	GGGGTTTTTACCANGTTGCCAGGCTGGTCTCAAACTCCTGACC	3693
Db	2522	GTATTTTTAGTACAGCT	GGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACC	2581
Qy	3694	TCAAGTGATCTGCCT	GCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGT	3753
Db	2582	TC--GTGATCTGCCT	CGCCTCGCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGT	2639
Qy	3754	GCCTGGCCGATTACT	GTCTATTTTTCTTTATTGGCTATATCCCCAGATCT-AGAGCAGTGT	3812
Db	2640	GCCAGCCGATTATTT	AAATATTTTTATTGCTTCCTCTTTCAGAAATGATTGATTGCT	2699
Qy	3813	TGACATATAGTAGGT	CTCAATAAATAAATTGATGAATGCACAGCCTAGA----TATAAAC	3868
Db	2700	AGGCTTATATTCAG	CCATCATTAACCAAAATGTGTGAGCCCTGACTCAGGGCTTTTACAT	2759
Qy	3869	TTTCTTTTCTTTTT	TAATAACAATCTTGACAACTTTTGACAGATAAAT-----	3916
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Db	3117	AATTTAGGCC--	--GGGTGCAGTGACTCAGCCCTGCAGTCTTAGCCCTTTGGGAGGCCGA-	3172
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Qy	4337	ATCTCTACT-AAAA	ATACAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCCAGC	4395
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Qy	4396	TACTCGGGAGGCT	GAGGCAAGAGAATTGCTTTGAACCTGGGAGGCAGAGGTTGCAGTGAGC	4455
Db	3293	TACTTGGGAGGCT	GTGATGGGAGGATCGCTGGAGCGTGGGAGGTCAAGGCTCGCGTGGGT	3352
Qy	4456	CGAGATCCCACCAC	TGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAAT	4515
Db	3353	CATGGTTGTGCCAC	TGCACCTTACGCTGGGTGACAGAGTAAGACCCCTGTCTAAAAAGCAA	3412
Qy	4516	AAATAAATAAAATA	AGGATCGGAGAGAAACAA 4548	
Db	3413	AATAAGATGCAGTT	TGGAGTGTAAAAATAGAGAA 3445	

RESULT 5	HSM803026	3990 bp	mRNA	linear	HTC 16-APR-2005
LOCUS	Homo sapiens mRNA; cDNA DKFZp761O0217 (from clone DKFZp761O0217).				
DEFINITION	AL713681				
ACCESSION	AL713681.1	GI:19584382			
VERSION	HTC.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 3990)				
AUTHORS	Ansorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.				
CONSRIM	The German cDNA Consortium				
TITLE	Direct Submission				
JOURNAL	Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY				
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp761O0217) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp761O0217 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.				
FEATURES	Location/Qualifiers				
source	1..3990				
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	/mol_type="mRNA"				
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	/clone_lib="761 (synonym: hamy2). Vector pSport1; host DH10B; sites NotI + SalI"				
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	/protein_id="CAD28485.1"				
	/db_xref="GI:19584383"				
	/db_xref="GOA:P99999"				
	/db_xref="InterPro:IPR002327"				
	/db_xref="InterPro:IPR003088"				
	/db_xref="UniProt/Swiss-Prot:P99999"				
	/translation="MGDVEKGKKIFIMKCSQCHTVEKGGHKHTGPNLHGLFGRKTGQA PGYSYTAANKNKGIIWGEDTLMYLENPKKIIPGTMIFVGIIKKKEERADLIAYLKKA TNE"				
ORIGIN					
Query Match	6.8%;	Score 341;	DB 4;	Length 3990;	
Best Local Similarity	57.5%;	Pred. No. 5.7e-20;			
Matches	856;	Conservative 1;	Mismatches 541;	Indels 91;	Gaps 10;
Qy	3104	TTTTTTTTTTGTTGTTT	TAGAGACAGGGTCTTGCTCTGTACCCAGGCATGAGCACAGT	3163	
Db	2522	TTTTCTCATTTATTTT	TCTGAGACGGAGTTTCGCCCTTTTCGCCCAGGCTGAGTACAGT	2581	
Qy	3164	GGTGCAACCATAGGT	CACCTGCAGCCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA	3223	
Db	2582	GGTGCAATC-----	TCACCTGCAACCTCCGCCTTCAGTTGCAAGTGATTTCTCTGCTCA	2636	
Qy	3224	GCCTCCCAAGTAGCT	GGGACTACGAGCGGTGCACACCACCGCTGGCTAATTAAAAAATT	3283	

Db	2637	GCCTCCTGAGTAGCTGGGATTGCAGGCACCCGCCACACCGCTGGCTAAATTTTGTGTA--T 2694
QY	3284	TTTTTTGTAGAGACTGGGTCTTTACTACGTTGGCCAGGCTTGTCTTTAAACTCTCGGCTTCAA 3343
Db	2695	TTTTAGTGGAGATGGTGTTCACCATTGTTGCCAGACTGGTCTTGGACTCTCGACCTC-- 2752
QY	3344	GCAATCCTCFACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGC 3403
Db	2753	GTGATCCACCCACCTTGGCCTCCCAAAGTTCTAGGATTACAGGTGTGAGCCACACGTCC 2812
QY	3404	GGCTACTTATT----- 3414
Db	2813	GGCCAATTTTCTCATTTCTATGCTCCTATATTAAAGTCTGTGTTGGCACAGATGAGTA 2872
QY	3415	-----TCCTTTACATTCATCTTTCCAATAGATGTAAAGATCCACAGAACACGGGATTACT 3468
Db	2873	ACTGCCATGTTCTAGGTCAAGTTATACCCAAAGCACTTCTGGTGGTTTAAATGTGATTCTG 2932
QY	3469	GCCTATTTTCTCCTTCTTTTTTGAGACAGAGTCTCACTTCATCACC----- 3516
Db	2933	TAACTTTTTTATTATTTTTTTTGAGATAATTCACCTCTTGTGCCCAGGCTGGAGTGC 2992
QY	3517	-TCAACCTCCGTTCAAGTCACTGCAACCTCTGCTCCCGGTTCAAGYGATTCCTCTGCC 3575
Db	2993	AATGGCGTGATCGTGCTCACCGCAACCTCCGCTTCCAGGTTCAAGCGATTCTCCTGAC 3052
QY	3576	TAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCAACCATGCTTGGCTAAATTTTGT 3635
Db	3053	TCAGCCTCTCAAGTAGCTGGGATTACAAGCATGCGCCACCAATGCCAGCTTATTT--TGT 3110
QY	3636	ATTTTTAGCAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTC 3695
Db	3111	GTTTTTAGTAGACACAGGTTTCTCCATGCTGACAGGCTGGTCTTGAACTCCCGACGTC 3170
QY	3696	AAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACCTGTGC 3755
Db	3171	GGGTGATCTGCCTGCCTCGGCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACACGC 3230
QY	3756	CTGGCGGATTACTGTCTATTTTCTTTATTGCTATATATATATATATATATATATATATAT 3815
Db	3231	CTGGCCAATTA--TGTAATTTTTTAAAAAGGACATTTCTATCAGGGATATATACCTTCA 3287
QY	3816	CATATAGTAGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTTCTTT 3875
Db	3288	GAAATAAGGAAATAGGGGAAAAAAGAGCATTATAAAACCAATGTTTTTCATTTCTAGTGC 3347
QY	3876	TTCTTTTTTAAAAACAATCTTGACAACCTTTGCAGAAATAAATACAAATCTTGCATTCTGCTT 3935
Db	3348	TTGCTGTGTAAGTGGCTAGGTTGGTAGAATCAAAAAACAAGGCCAGATGTATTTAAGGGGT 3407
QY	3936	TTTCACTTATCAGCTGTTATGACTTTTTTCATATTGCTTCAAACTTTTATGTACTGTT 3995
Db	3408	ATTCAGATGCCACTACATGCTTATTTTGTCTAGAACAGTGCTGTCTAATAGAACTTTCT 3467
QY	3996	TTTTTCATTGTTACTATTTTAGTCACTGAATAATATAGGCTTAATTTGCTTATACATCCTCC 4055
Db	3468	GTGACGATGGATATTTGTAGACTTT-----TGCTGCTCAGTGTGGTAGCCACTAACCA 3521
QY	4056	TGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCTCCAG 4115
Db	3522	CATGTGGCTGTAAAGCCCTTGAATAATAGCTAGTGTGACTAGAAAAGTATTTTATTTAAA 3581
QY	4116	AGAAATACACACACACACACACTCACACACAGTTTTTTTTTAAATGTTTGCAACTAAGA 4175
Db	3582	TTTACATAGGCACAAGTGGCTAGTGGCTACTGTATTGACATTTCTGGGTCTAGGACTAGAA 3641
QY	4176	CAAGAAACCTGCATTAGAGG--ATGTTTGTTCATATTAATTAATAAATAAATACTCAGTTGGC 4233
Db	3642	CCAGTGGTCTGTAAACAAAGTACTTTCTCTTTACTCTATTAATCTAGAAATAGCCGGGC 3701
QY	4234	ACAGTGACTCAAGCCTGTAAACACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGA 4293

Db	3702	ATGTCGCTCATGCCCCTGTGGTCCCAGCACTTTGGGAGGCCAAGGCAGGCAGATCACTTGA	3761
Qy	4294	GGTGAGAAAGTTTCGAGACCAGCCCTGGTCAAATATGGTGAACCCCTATCTCTACTAAAAATAC	4353
Db	3762	GGTCGGGCGTTTGAGACCAGCCCTGGTCAACATATGGCGAAACCCCTGTCTCTACAAAAACAT	3821
Qy	4354	AAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC	4413
Db	3822	AAAAATTAGCCAGGTGTGGTGGCGGCACCTGTAGTCTCAGCTACTTTGGGAGGCTGAGGC	3881
Qy	4414	AAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCA	4473
Db	3882	ACAAGAAATCACTTGAACCTTGGGAGGTGGAGGTTGCAGTGAGCCAGGATTGTGCCCACTGCA	3941
Qy	4474	CTCAGCCTGGCGACACAGCGAGACTCTATCTCAAAAAATAAAATAAA	4522
Db	3942	CTCAAGCCTGGGTGAC-GAGTGAACCTGTCTCCAAAAATAAAAAATAAAAA	3989

RESULT 6	
AQ839852/c	
LOCUS	AQ839852 linear GSS 31-MAR-2000
DEFINITION	260L13-C56 CITB Homo sapiens genomic clone 260L13, genomic survey sequence.
ACCESSION	AQ839852
VERSION	AQ839852.1 GI:6652484
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE	A 6-Mb high-resolution physical and transcription map encompassing the hereditary prostate cancer 1 (HPC1) region
JOURNAL	Genomics 64 (1), 1-14 (2000)
PUBMED	10708513
COMMENT	Contact: Carpten JD

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FEATURES
source
1. .15970
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="260L13"
/clone_lib="CITB"

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ORIGIN

Query Match	6.7%	Score 337.2;	DB 9;	Length 15970;
Best Local Similarity	57.8%;	Pred. No. 4.7e-20;		
Matches 905: Conservative	1: Mismatches 529:			
			Indels 131:	Gaps 12:

Qy	3098	T T T G G G T T T T T T T G T T G T T A G A G A C A G G G T C T T G C T C T G T C A C C C A G G C A T G A G	3157
D _b	6787	T T T T A T T T T A T T A T T T T T T T T G A G G T G G A G T A T C G C T A T G T C A C C C A G G C T G G A G	6728
Qy	3158	C A C A G T G G T G C A A C C A T A G G T C A C T G C A G C C T C A A C C T C C T G A G C T C A A G G G A T C T G C T G	3217
D _b	6727	T G C A G T G G C A T G A T A T C A G C T C A C T G C A A C C T T C A C C T G C T A G A T T C A A G C A G T T C T C G T	6668
Qy	3218	A C T C A G C C T C C C A A G T A G C T G G G A C T A C G A G C G T G C A C C A C C A G C C T G G C T A A T T A A A	3277


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Matches 347; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1123 TGTGTTTCTCTCCACTAGGTTGTAAGCTCCATGAGGTTAGAGATTATTATTATTAT 1182
Db 347 TGTGTTTCTCTCCACTAGGTTGTAAGCTCCATGAGGTTAGAG---ATTATTATTATTAT 291
QY 1183 TATTATTATTATTATTATTATTATTATTATTATCTGTTCACTGCTGTATCTCTAGCTCCTA 1242
Db 290 TATTATTATTATTATTATTATTATTATTATTATCTGTTCACTGCTGTATCTCTAGCTCCTA 231
QY 1243 GGACAGAGCCTGGCACATAGTAAGTGCTCAATAAATATTCACTGGATAAACAGTGCAGAT 1302
Db 230 GGACAGAGCCTGGCACATAGTAAGTGCTCAATAAATATTCACTGGATAAACAGTGCAGAT 171
QY 1303 AGTTTAAACTATCTGACCTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGC 1362
Db 170 AGTTTAAACTATCTGACCTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAAGC 111
QY 1363 AGAGTTTGAGTGAGCTGAAATCGTGTCACCTGCACCTCCAACTGGGCAACAGAGCAAGAC 1422
Db 110 AGAGTTTGAGTGAGCTGAAATCGTGTCACCTGCACCTCCAACTGGGCAACAGAGCAAGAC 51
QY 1423 TCCATCTCAAAAAAAAAAAAAAACTATCAGGCCTAGCTGGTGGCACAT 1472
Db 50 TCCATCTCAAAAAAAAAAAAAAACTATCAGGCCTAGCTGGTGGCACAT 1
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RESULT 8
CD557847/c
LOCUS
DEFINITION
AGENCOURT 14423258 NIH_MGC_180 Homo sapiens cDNA clone
IMAGE:30390116 5', mRNA sequence.
CD557847
CD557847.1 GI:31583915
EST.
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 897)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM464 row: k column: 21
High quality sequence stop: 636.
Location/Qualifiers
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/clone="IMAGE:30390116"
/lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_180"
/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI;
Site 2: EcoRV (destroyed); Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.68 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."
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.ORIGIN

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Query Match
Best Local Similarity 6.3%; Score 315.8; DB 6; Length 897;
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Db 765 TGTATGCATCCCGATATTATTTATTTATTTATTTTGTAGACATGGTCTCACTCTG 706
QY 3143 TCACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGC 3202
Db 705 TTGCCCAGCCTGGAGTGCAGTGGCAGGATCTCAGCTCACTGCAACCTCCACCTCCAGGT 646
QY 3203 TCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGACCAACCAC 3262
Db 645 TCAAGCAATTCTCCACCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGCACCAACCAC 586
QY 3263 GCCTGGCTAATTAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTT 3322
Db 585 GCCCAGCTAATTTTTTGTATTTTAAGTACAGATGGGTTTTTGCCATGCTGCCAGGCTC 526
QY 3323 GTCTTAAACTCTCTGGCTTCAAGCAATCCTCTACCTTGGCATCCCCAAAGTGTGGGATTA 3382
Db 525 CTCTCAAAATTCCTGACCTCAAGTGATCTGCCACCTTGGCCTCCCAAAGTGTGGGATTA 466
QY 3383 CAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTTACATTCCATCTTTTCCAAATAGAAT 3442
Db 465 CAGGCGTGAGCCACCGTGCCAGCTGCATCCTGATATTTAATGCTTGCCAGAATTTGATT 406
QY 3443 GTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCTTTTGTAGACACAGAT 3502
Db 405 GCACCATGCTTATTGGCTTCTATCTTTTTTTTTTTTTTTTGTAGATGGAGACTCACTCTCT 346
QY 3503 CTCACCTTCATCACCCTCAACCTCCGT---TCAGCTCACTGCAACCTCTGCCTCCCGGTT 3558
Db 345 CTCCCAGGCTGGAGTGCAGTGGTGTGATCTCAGCTCACTGCAACCTCCACTTCTGGGTT 286
QY 3559 CAAGYGATTCTCTGCTCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCACCATG 3618
Db 285 CAAGCGATTCTCTGTCTCAGCCTCCAGAGTAGCTGGGACTACAGATGTGTGCCACCACA 226
QY 3619 CTTGGCTAATTTTTTGTATTTTGTAGCAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGGT 3678
Db 225 CCTGGCTAA--TTTCGTATTTTGTAGTAGAGATGGGGTTTTCACCATGTTGGCCAGACTAAT 168
QY 3679 CTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATA 3738
Db 167 CTCGAACCTCCTGACCTCAGGTGATCCGCTGCCTTGGCCTCCCAAAGTGTGGGGTTACA 108
QY 3739 GCGGTGAGTCACTGTGCCTGGCCGATTAC 3767
Db 107 GCGGTGAGCCACCAACCCAGCCGGCTTCC 79
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RESULT 9
CR858326
LOCUS
DEFINITION
Pongo pygmaeus mRNA; cDNA DKFZp469P012 (from clone DKFZp469P012).
ACCESSION
CR858326
VERSION
CR858326.1 GI:55727613
KEYWORDS
HTC.
SOURCE
Pongo pygmaeus (orangutan)
ORGANISM
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Pongo.
REFERENCE
1 (bases 1 to 3095)
AUTHORS
Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,
Osanger,A., Fobo,G., Han,M. and Wiemann,S.
CONSRM
The German cDNA Consortium
TITLE
Direct Submission
JOURNAL
Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match          6.2%; Score 308; DB 5; Length 891;
Best Local Similarity 72.0%; Pred. No. 7.8e-17;
Matches 451; Conservative 0; Mismatches 155; Indels 20; Gaps 3;

QY 476 TATTTTACTTTTATTTTGGACGGGGCTACTCTGTCGCCCAGGCTGGAGTGGG 535
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Db 4 TTTT TTTT TTTT TTTT TGAGACGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAG 63

QY 536 TGGCGTGATCTCAGATCACTACAACCTCCATCTCCTGGGGTTCAAATAATTCTTGCCTC 595
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 TGGCGGATCTCGGCTCACTGCAAGCTCCGCCCTCTCGGGTTCACGCCATTCTCCTGCCTC 123

QY 596 AGCCTCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGTGGCACACACCACCATGCCCA 655
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Db 124 AGCCTCCCAAGTAGCTCGGACT-----ACAGGCGTCTCTCCACCATGCCTG 168

QY 656 GCTAATTTTGTGTGTTTTTTTGGTAGAGACAGGTTTTTACCATGTTGGCCAGGCTGG 715
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Db 169 GCTAATATTT---TGTATTTTGTAGTAGACGGGGTTTCACCGTGTAGCCAGGATGG 224

QY 716 GTGACCTCCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCTTTTCTAATGCAGTAT 775
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Db 225 TCTCGATCTCTTAACCTGGTGATCCGCCCGCTCGGCTCCCAAAGTATTGGGATTACCC 284

QY 776 CCAGTTTCTCTACTTATACATTTATTATTATTCTTATTATTATTAGACAGAGTCTTGC 835
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Db 285 GCGTGAGCCACCGCGCGCTGCAAAATAATCTTTCTTTTCTGAGACAGAGTCTCGC 344

QY 836 TTTGTGCGCAAGGCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAAGCTCCACCTGCT 895
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Db 345 TCTGTTGCCCAGGCTGGAGTGCAGTGGCACGATCTCGGCTCACGGCACGCTCCGCTCCC 404

QY 896 GGGTTCACGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAAGCGCGCTGCCA 955
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Db 405 GGGTTCACGCCATTCTCCTGCTCAGCTTCCCGAGTAGCTGGGACTACAGGGGCCGCCCA 464

QY 956 CCACGCCCCGCTAATTTTGTATTTTAAATAAAGACGGGGTTTCATCGTGTAGCCAG 1015
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Db 465 CCACGCCCCGCTAA-CITTTTGTGTTTTTAGTAGACGGGGTTTACCGTGTAGCCAG 523

QY 1016 GATGGTCTCGATCTCATGACCTTGTGATCCGCTCGCCTGCCCTCCCAAAGTCTGGGAT 1075
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 524 GATGGTCTCGATCTCCTGACCTTGTGATCTGCCCGCTCGGCTCCCAAAGTCTGGGAT 583

QY 1076 TACAGGCATGAGCCACCGTGCCCGGC 1101
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 584 TACAGGCGTGAGCCACCGCGCCCGGC 609

RESULT 12
CR749233/c
LOCUS CR749233 Homo sapiens mRNA; cDNA DKFZp686C0331 (from clone DKFZp686C0331).
DEFINITION Homo sapiens mRNA; cDNA DKFZp686C0331 (from clone DKFZp686C0331).
ACCESSION CR749233
VERSION CR749233.1 GI:51476197
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
```

```

REFERENCE 1 (bases 1 to 5797)
AUTHORS Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
CONSRTM The German cDNA Consortium
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp686C0331) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686C0331
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES             Location/Qualifiers
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                     NGQKRGHTGKKPFKYIECGKAFKQFSTLTTHKKIHTGGKPYKCEECGKAFNHSCSLTR
                     HKKIHTGEKPYKCEECGKAFKHSSTLTTHKRNHTGEKPYKCDKCGKAFMSSSTLSKHE
                     I IHTKKPYKCEECGKAFNRSSTLTTHKIIHTGEKPYKCEECGKAFKYSYTLTTHKRI
                     HTEDPYKCEECGKAFKYSSTLTTHKRIHTGEKPYKCEECGKAFKSSDLTTHKIIHT
                     GEKPYKCEECGKAFKYSSTLTTHKIIHTGERPYKCEECGKAFNOSILTTHKRIHTGE
                     KFYKCEECGKAFKRSSHLTTHKIIHTGEKPYKCEECGKAFKHFNSLTTHKKIHTGKKP
                     YRCEECGKAFKHSSKLTTHKRFHTGEKPYRCE"

ORIGIN
Query Match          6.1%; Score 307.2; DB 4; Length 5797;
Best Local Similarity 56.9%; Pred. No. 2.7e-17;
Matches 902; Conservative 1; Mismatches 569; Indels 114; Gaps 14;

QY 3105 TTTT TTTT TTTT TTTT TAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGACACAGTG 3164
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Db 4976 TTTT TTTT TTTT TTTT TGTGACAGAGTCTTGCTCTGTGCCAGGCTGGAGTGCAGTG 4917

QY 3165 GTGCAACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAG 3224
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4916 GCACGATCTCGGTCACCTGCAACCTCTGCCTCCTGGGTTACACCATTTCTCCCG-CCTCAG 4858

QY 3225 CCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACCCAGCCTGGCTAATTAATAAAATTT 3284
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4857 CCTCTGGAGTAGCTGGGACTACAGGGCGGCCACCAACCCAGCTAATTTA-----TT 4804

QY 3285 TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCAAG 3344
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4803 TTTAGTAGAGACAGGGTTTCAACGTTGTAGCCAGGATGGTCTTGATCTCTGACCTCATG 4744

QY 3345 CAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCG 3404
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4743 --ATCCACCTGCCTGGGCCTCCCAAAGTCTGGGATTACAGGTGTGAGCCACTGTCCCTG 4686
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QY 657 CTAATTTTGTGTGTTTTTTTGGTAGAGACAGGTTTTCACCATGTTGGCCAGGCTGGG 716
Db ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
559 CTAATATTT---TGTATTTTGTAGTAGAGACGGGGTTTACCGTGTAGCCAGGATGGT 614

QY 717 TGACCTCCCTTTTAGATTTCTCCTCATCTGCTCTATTTCTTCCCTTTCTAATGCAGTATC 776
Db ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
615 CTCGATCTCTAACCCTGGTGATCCGCCCGCTCGGCCTCCCAAAGTATTGGGATTACCCG 674

QY 777 CAGTTTCCTTACTTATCACATTTATTATTATTCTTATTATTATTGAGACAGATCTTGCT 836
Db ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
675 CGTGAGCCACCGCGCCGCTGCAAAATAATCTTTCTTTTCTTGAGACAGAGTCTCGCT 734

QY 837 TTGTCGCCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGCTCCACCTGCTG 896
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
735 CTGTTGCCAGGCTGGAGTGGCAGCATCTCGGCTCACGGCACGCTCCGCTCCCG 794

QY 897 GGTTCAGCCATTCTCCCGCTCAGCCTCCCGAGTAGCTGGGACTAAAGGCGCTGCCAC 956
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
795 GGTTCAGCCATTCTCTGCCTCAGCTTCCCGAGTAGTGGGACTACAGGGGCCGCCAC 854

QY 957 CAGCCCCGCTAATTTTTTGTATTTTAAATAAAGACGGGGTTTTCATCGTGTAGCCAGG 1016
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
855 CAGCCCCGGCTAA-CTTTTGTGTTTTTGTAGTAGAGCGGGGTTTTCACCGTGTAGCCAGG 913

QY 1017 ATGGTCTCGATCTCATGACCTGTGATCCGCTCGCCTCGGCCCTCCCAAAGTGCTGGGATT 1076
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
914 ATGGTCTCGATCTCCTGACCTGTGATCTGCCCGCTCGGCCCTCCCAAAGTGCTGGGATT 973

QY 1077 ACAGGCATGAGCCACCGTGCCCGGC 1101
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
974 ACAGGCGTGAGCCACCGCGCCCGGC 998
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RESULT 14
DR761502
LOCUS
DEFINITION HESc4 129 D09.g1 A037 NIH_MGC_262 Homo sapiens cDNA clone
IMAGE:7971211 5', mRNA sequence.
DR761502
DR761502.1 GI:71054202
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 777)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: BresaGen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM 17087 row: 9 column: 17
Seq primer: JENREV (CAGGAACAGCTATGACC)
High quality sequence stop: 777.
Location/Qualifiers
1. .777
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/mol_type="mRNA"
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/clone="IMAGE:7971211"
/sex="male"
FEATURES
source
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/tissue_type="embryonic stem"
/cell_type="human embryonic stem cells"
/cell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH_MGC_262"
/note="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early neural progenitor cell type.
Cell line id and NIH Registry designation is BG01.
Positive for Nestin and Musashi expression. Passage number
18. cDNA primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGCGCCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. This primary library
is non-normalized (normalized primary library is
NIH_MGC_259). It was constructed by Express Genomics
(Frederick, MD). Sequence ends have been trimmed to
exclude vector and regions below Phred quality 16. Note:
this is a Mammalian Gene Collection library."
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ORIGIN

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Query Match 6.1%; Score 306.6; DB 8; Length 777;
Best Local Similarity 72.2%; Pred. No. 1.1e-16;
Matches 479; Conservative 0; Mismatches 129; Indels 55; Gaps 4;

QY 456 TTTATTTTAAATTTTATTTTATTTTACTTTATTTTGGAGACGG-GGCTCACTCT 514
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
145 TATTTGTGGTTTTTTTGGTTTTGTTTTGTTTTTGGAGACGGAGTCTTGCTCT 204

QY 515 GTCGCCCAGGCTGGAGTGGTGGCGTGAFTCTCAGATCACTACAACCTCCATCTCCTGGG 574
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
205 GTCGCCCAGGCTAGAGTGCAGTGGCGGATCTCGGCTCACTGCAACCTCCGCTCCCAGA 264

QY 575 TTCAAATAATTTCTTTGCCTCAGCCTCTCAAAGTAGCTGGGACTTGTAGTCTCAAGTAGC 634
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
265 TTCACACCAATTTCTCTGCCTCAGCCTCCCGAGTAGCTGGGA-----TTAC 309

QY 635 TGGCACACACCAACCATGCCAGCTAAATTTTGTGTGTTTTTTTGGTAGAGACAGGTTT 694
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
310 AGGTGCCCCACCAACCGCCAGCTAATTTTGTG-----TATTTTGTAGAGACGGGTT 364

QY 695 TCACCATGTTGCCCAGGCTGGGTGACCTCCCTTTTAGATTCTCCTCATCTGCTCTATTTC 754
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
365 TCACCATGTTAGCCAGGACGG-----TCTCC 390

QY 755 TTCCCTTTCTAATGCAGTATCCAGTTTCCTTACTTATCACATTTATTTATTCTTATT 814
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
391 ATCTCTGACCTCGTGATCCACCTGCCTCGGCTCCCAAACATATTGTGTGTTTTTTT 450

QY 815 ATTATTGAGACAGAGTCTTGCTTTGTGCCAAGGCTGGAGTACAGTGTGCGATCTCGGC 874
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
451 TTTTGTGAGACGGAGTCTCGCTCTGTGCCCAGGCTGGAGTGCAGTGGCGCTATCTCGGC 510

QY 875 TCACTGCAAGCTCCACCTGTGGGTTCAAGCCATTCTCCCGCTCAGCCTCCCCAGTAGC 934
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
511 TCACTGCAAGCTCCGCTCCCGGTTTCAGCCACTCTCCTGCCTCAGCCTCCTTAGTAGC 570

QY 935 TGGGACTAAAGCGCCTGCCACCACGCCCGCTAAATTTTGTATTATTAAAGACG 994
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
571 TGGGACTACAGGCGCCGCCACCATGCTGGCTAAATTTTGTATTATTAGTAGAGACG 630

QY 995 GGGTTTCATCGTGTAGCCAGGATGGTCTCGATCTCATGACCTTGTGATCCGCTGCCTC 1054
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
631 GGGTTTCACCGTGTGTGACAGGATGGTCTCGATTTCTGACTTCGTGATCGGCCGCTC 690

QY 1055 GGCCTCCCAAAGTCTGGGATTACAGGATGAGCCACCGTCCCGGCTTATCACATTTA 1114
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
691 GGCCTCCCAAAGTCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCACTATTGTGTTT 750

1115 TTA 1117
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751 TTA 753
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RESULT 15
BU180590
LOCUS
DEFINITION
  BU180590
  AGENCOURT_7852598 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6140102
  5', mRNA sequence.
ACCESSION
  BU180590
VERSION
  BU180590.1 GI:22694574
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominiidae; Homo.
REFERENCE
  1 (bases 1 to 832)
  NIH-MGC http://mgs.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM13458 row: c column: 15
  High quality sequence stop: 508.
FEATURES
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      /clone="IMAGE:6140102"
      /tissue_type="retinoblastoma"
      /lab_host="DH10B (phage-resistant)"
      /clone_lib="NIH_MGC_67"
      /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
      Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
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      Technologies."
ORIGIN
  Query Match 6.1%; Score 306.6; DB 5; Length 832;
  Best Local Similarity 72.2%; Pred. No. 1.1e-16;
  Matches 479; Conservative 0; Mismatches 129; Indels 55; Gaps 4;

QY 456 TTTATTTTAAATTTTATTTTATTTTACTTTATTTTATTTTATTTTGAGACGG-GGCTCACTCT 514
  ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12 TATTTGTGGTTTTTTTTTGGTTTTGTTTTGTTTTGTTTTGTTTTGAGACGGAGTCTGCTCT 71

QY 515 GTCGCCAGGCTGGAGTGGGTGGCGTGATCTCAGATCACTACAACCTCCATCTCTGGG 574
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 72 GTCGCCAGGCTAGAGTGCAGTGGCGCGATCTCGGCTCACTGCAACCTCCGCCCTCCAGA 131

QY 575 TTCAAATAATTCTCTTGCCCTCAGCCTCTCAAGTAGCTGGACTGTAGCTCTCAAGTAGC 634
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 132 TTCACACCATCTCTGCTGCCTCAGCTCCCGAGTAGCTGGGA-----TTAC 176

QY 635 TGGCACACACCACCATGCCAGCTAATTTTGTGTGTTTTTTTGGTAGACAGGTTT 694
  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177 AGGTGCCACACCACCGCCAGCTAATTTTTTG-----TATTTTAGTAGACGGGGTT 231

QY 695 TCACCATGTTGGCCAGGCTGGGTGACCTCCCTTTTAGATTCTCCTCATCCTGCTATTTC 754
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Db 232 TCACCATGTTAGCCAGGACGG-----TCTCC 257

QY 755 TTCCCTTTCTAATGCAGTATCCAGTTTCCTTACTTATACATTTATTATTATTCTATT 814
  || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 258 ATCTCTGACCTCGTGATCCACCTGCCTCGGCCTCCCAAACTATTGTGTGTTTTTTT 317

QY 815 ATTATTGAGACAGAGTCTTGTCTTGTGCGCAAGGCTGGAGTACAGTGGTCCGATCTCGGC 874
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Db 318 TTTTTTGAGACGGAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGGCGGTATCTCGGC 377
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 875 TCACTGCAAGCTCCACCTGCTGGGTTCAAGCCATTCTCCGGCCTCAGCCTCCCCAGTAGC 934
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Db 378 TCACTGCAAGCTCCGCCTCCCGGTTTCACGCCACTCTCCTGCCTCAGCCTCCTTAGTAGC 437
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QY 935 TGGGACTAAAGCGCCTGCCACCACGCCCGCTAAATTTTTTGTATTTTAAATAAGACG 994
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Db 438 TGGGACTACAGGCGCGCCACCATGCTGGCTAAATTTTTTGTATTTTAGTAGAGACG 497
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QY 995 GGGTTTCATCGTGTAGCCAGGATGGTCTCGATCTCATGACCTTGTGATCGCCTGCCTC 1054
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Db 498 GGGTTTCACCGTGTGTGACAGGATGGTCTCGATTTCCTGACTTCGTGATCCGCCGCTC 557
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QY 1055 GGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCGTGCCCGCCTTATCACATTTA 1114
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Db 558 GGCCTCCCAAAGTCTGGGATTACAGGCGTGAGCCACCGCGCCGCTATTGTGTTT 617
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QY 1115 TTA 1117
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Db 618 TTA 620
  |||||

RESULT 16
BU838401
LOCUS
DEFINITION
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  AGENCOURT_8122967 Lupski_dorsal_root_ganglion Homo sapiens cDNA
  clone IMAGE:6177002 5', mRNA sequence.
ACCESSION
  BU838401
VERSION
  BU838401.1 GI:24022796
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominiidae; Homo.
REFERENCE
  1 (bases 1 to 935)
  NIH-MGC http://mgs.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Dr. James R. Lupski
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM13554 row: e column: 03
  High quality sequence stop: 622.
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      /clone_lib="Lupski_dorsal_root_ganglion"
      /note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
      NotI; Site 2: SalI; cDNA made by oligo-dT priming.
      Directionally cloned using the following adaptors:
      5'-TCGACCATCGGTCCTCCG-3' and
      5'-GACTAGTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >
      1 kb for average insert length 1.7 kb. This is a primary
      library, non-amplified. Library constructed by Life
      Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
      College of Medicine) and is available through Life
      Technologies."
```


Db	1542	TGTAGTGGTGCAATCTCAGCTCACTGCAACATCCATCTCCGGATTCCACTTATTCTCCT	1483
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Db	1482	GCCTCAGCCTCTCAGGTAGCTGGGATTATGGGTGCCTGCCATAATGCCCAACTCAATTTT	1423
Qy	3278	AAAAATTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGG	3337
Db	1422	GTA--CTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACCTCCTGG	1365
Qy	3338	CTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACC	3397
Db	1364	CCTCAAGTGATCCACCTGCCTTGGCCTCCCAAAGTGTGGGATTACAGGTGTGACCACTG	1305
Qy	3398	ATGTGGGCTACTTATTTCTTTTACATTCCATCTTTCCAATAGAAATGTAAGATCCACAGAA	3457
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Qy	3458	CAGGGAATTACTGCCTATTTTCTTCCTTTCTTTTGTAGACAGAGTCTCATTCATCACCT	3517
Db	1249	TGATCATTGACGCTTTTCTTTTCTTTTGTAGACAGCATCTCACTGTCTCACCC	1190
Qy	3518	CAACCTCCGTTCA-----GCTCACTGCAACCTCTGCCTCCCGGGTTCAAAGY	3563
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Qy	3564	GATTCCTCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCAACCATGCTTGG	3623
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Qy	3684	ACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGT	3743
Db	1009	ATTCTGACCTCAGGTGATCCGCCACCTCAGCCTCCCAAAGTGTGGGGTTATAGGCGT	950
Qy	3744	GAGTCACGTGCTGGCCGATTACTGTCTATTTTCTTTAT	3783
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RESULT 20			
CR599842			
LOCUS			
DEFINITION	CR599842 1863 bp mRNA linear HTC 21-JUL-2004		
ACCESSION	full-length cDNA clone CS0DA002YO06 of Neuroblastoma of Homo sapiens (human).		
VERSION	CR599842		
KEYWORDS	CR599842.1 GI:50480649		
SOURCE	HTC; CNSLT_cDNA.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1863)		
JOURNAL	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.		
REMARK	Full-length cDNA libraries and normalization		
REFERENCE	Unpublished		
AUTHORS	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ invitroGen Corporation 1600 Faraday Avenue		
TITLE	2 (bases 1 to 1863)		
JOURNAL	Genoscope.		
COMMENT	Direct Submission		
	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
	- Web : www.genoscope.cns.fr)		
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a		

FEATURES	division of Invitrogen.				
source	Location/Qualifiers				
	1. .1863				
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	/db_xref="taxon:9606"				
	/clone="CS0DA002YO06"				
	/tissue type="Neuroblastoma"				
	/plasmid="pCMVSPORT_6"				
ORIGIN					
	Query Match	6.0%;	Score 301.2;	DB 4;	Length 1863;
	Best Local Similarity	56.9%;	Pred. No. 1.7e-16;		
	Matches 811;	Conservative 1;	Mismatches 509;	Indels 105;	Gaps 10;
Qy	3124	GAGACAGGGTCTTGCTCTGTTCACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTG	3183		
Db	496	GGGTCAAGTCTCACTCTGTTCACCCAGGCTGGAGTCTGTGGCACCGTGTGGCTCACTG	555		
Qy	3184	CAGCCTCAACCTCCTGAGCTCAAGGGATCTGTGACCTCAGCCTCCCRAAGTAGTGGAC	3243		
Db	556	CAACCTCCGTCTCTGGGTTCAAGCAATTCTTGCCTCAGCCTCCAGAGTAGTGGAT	615		
Qy	3244	TACGAGCGTGCACCACACGCGCTGGCTAATTAATAAAATTTTGTAGAGACTGGGTCT	3303		
Db	616	TACAGGTGCCACACACACCCGGCTAATTTTATTATATTTTAGTAGACACGGGGTTT	675		
Qy	3304	TACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCTACCTTGGCA	3363		
Db	676	CACCATGTTGGCCAGGCGGTCTTGAACTTGTGACGTCAAGTGATGCACCGCCTTGGCC	735		
Qy	3364	TCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTTACAT	3423		
Db	736	TCCCAAAGTCTGGGATTACAGGTCAGGTCAGATTTTGAACAAATCTCGCTAGAGATTGAACAG	795		
Qy	3424	TCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCT	3483		
Db	796	AGCTGCGCCTGGATCCGCCACAGTGAGGAGACCTGAAGACCAGAGAAAAACACAGCAAAC	855		
Qy	3484	TTCTTTTGTGACAGAGTCTCACTTCATCACCTCAACCTCCGTTTCACTCACTGCAA-C	3542		
Db	856	GGAGTCTTGCTCTGTTGCCAGGCTGGAGTGTAGTGTGGCGATCTCGGCTCCCTGCAAGA	915		
Qy	3543	CTCTGCCTCCCGGTTCAAGYGATTCTCTGCCTAAGCCTCCTGAGTAGTGGAATTACA	3602		
Db	916	ATCTGCCTCCACAGATTCAGCCATTTTCCACCTCAGCCCTGGAGTAGCTGGAAGTACA	975		
Qy	3603	AGCGTGCACCAACATGCTTGGCTAAT- - - - -TTTTTGTATTTTGTAGCAGAGATGGGGTTTT	3658		
Db	976	GGCTCCCGCCACACGCGCTGGCTAATTTTGTATTATTTTAGTAGAGAGGGGGTTT	1035		
Qy	3659	ACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAAGTGATCTGCCTGCCTCAGTCT	3718		
Db	1036	ACTGTGTTAGGTAGGATGGTCTCGATCTCCTGACCTCA--TGATCCATCCGCTTGGCCT	1093		
Qy	3719	CCCAAAGTCTGGAATTATAGGCGTGAGTCACTGTGCTTGGCCGATTACTGTCTATTTTC	3778		
Db	1094	CTCAAAGTCTGGGATTACAGGCATGAGCCACCGCACCTGGCTG- - - - -TTTT 1141			
Qy	3779	TTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAT	3838		
Db	1142	TTCATTTCTATATGATTTTGTCTGTGGAATGTCAGTGACTTAGCGGTGTTTTTCACATG	1201		
Qy	3839	AATTGATGAATGCACAGCCTTAGATATAAACTTTCTTTTTTTTTTAAACAATCTTGA	3898		
Db	1202	TTTATAAAGCTGAATAGTTCTGTATGTCAGTCAACCCCTAGTGTAGTCATGCTACT	1261		
Qy	3899	CAACTTTGCAGATAAAATACAATCTTGCAATCTTGCTTTTTCACTTATCACCTTGTATGA	3958		
Db	1262	CTCCTGCTGTCATAGATGGGGCCTGTCCACACCCCAAAATCTCTCGGTTCCCGCTGTCC	1321		
Qy	3959	CTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTTTCATTGTTACTATTTTAGTC	4018		

Db 1322 GCACCTGAAGGTACCCACCAGATGTGTCTGCTCACTGCCCTCCATCCACCTTTCTTGTGGT 1381

QY 4019 ACTGAATAATATGGCTTAATTTGCTTATACATCCTCTGCTCCACCTTTAGAAAGGCCAAAT 4078

Db 1382 TCTCATGTTTCTGCCTC-----CCTAGAGACCATTTCTCTCTACAGCAGTAG----- 1428

QY 4079 TTACAAATCTGATGAAGCTATGAACCTCTCTCCCCAGAGAAATACACACACACACACA 4138

Db 1429 -----TTTCCAATAGAAATACAATGCCAGACACATA 1459

QY 4139 CTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATG 4198

Db 1460 C-----GTCATTTTAGATTTTCTAGTAGTCACTTTAGAAAAAGTGAAAAAGAGGCCA 1510

QY 4199 TTTGTTCATATTAAATAATAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACACA 4258

Db 1511 GCTG-----CAGTGGCTCACACCTGTAATCCCA 1538

QY 4259 GTACTTTGGAAGTCCAAGGTGGGTGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGG 4318

Db 1539 GCACTTTGAAGGCTGAGGTGGGTGATCAC--GAGGTCAGAGATCGAGACCATCCTGG 1596

QY 4319 TCAATATGCTGAACCCCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATG 4377

Db 1597 CCAACATGGTGAACCCCTCTCTACTAAAAATACAAAAAATTAGCTGGCGTGGTGCCA 1656

QY 4378 CATGCCCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAG 4437

Db 1657 GCGCCCTGTAGTCCCAGCTACTCGAGAGGCTGAGGCGAGGAATGGCGTGAACCCGGTAG 1716

QY 4438 GCAGAGTTGCAGTGAGCCGAGATCCCACCCTGCACTGCACCTCAGCCCTGGCGACACAGGAG 4497

Db 1717 GCAGAGCTTGCAGTGAGCCGAGATAGCGCCACTGCACCTCAGCCCTGGCGACAGAGGAG 1776

QY 4498 ACTCTATCTCAAAAAAATAAATAAATAAATAAAGGATCGGAGAGA 4543

Db 1777 ACTCCATCTCAAAAAAATAAATAAAGGTTACAAAGAAACAGGTGAAA 1822

RESULT 21

BQ958903

LOCUS

DEFINITION BQ958903 946 bp mRNA linear EST 21-AUG-2002

5', mRNA sequence.

AGENCOURT_10035485 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6483214

BQ958903

EST.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 946)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLCM2667 row: g column: 23

High quality sequence stop: 534.

Location/Qualifiers

1. .946

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6483214"

FEATURES

source

/tissue_type="carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_40"

/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 6.0%; Score 300.6; DB 5; Length 946;

Best Local Similarity 69.1%; Pred. No. 3e-16;

Matches 468; Conservative 1; Mismatches 197; Indels 11; Gaps 4;

QY 3096 AGTTTGGGTTTTTTTTTGTGTTGTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATG 3155

Db 24 AGNTTTTTTTTTTTTTTTTTTTTGTGAGACAGAGTCTTGCTCTGTCAACCCAGGCTGG 83

QY 3156 AGCACAGTGGTGCAACCATAGGTCACTGAGCCCTCAACCTCCTGAGCTCAAGGGATCTGC 3215

Db 84 AGTGCAGTGGTG--CGATCGCTCACTGCAACCTCAGCCTCCTGGATTAAAGTATTCTC 140

QY 3216 TGACCTCAGCCTCCCAAGTAGTGGGACTACGAGCGTGCACCACCGCTGGCTAATTA 3275

Db 141 CTGCCTCAGCCTCCCAAGTAGTGGGATTACAGGTGTGCACCACCATGCCCGGCTAAATT 200

QY 3276 AAAAAATTTTTTGTAGAGACTGGGTCTTACTACGTGGCCAGGCTTGTCTTAAACTCCT 3335

Db 201 TTTTGTATTTTGTAGTGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCT 260

QY 3336 GGCTTCAAGCAATCCTCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCA 3395

Db 261 GACCTC--GTGATCCGCTGCCTCAGCCTCCCAAAGTGTGGGATTACAGGTGTGAGCCA 318

QY 3396 CCATGTGCGGCTACTTATTTCTTTTACATTCATCTTTTCCAATAGAATGTAAGATCCACAG 3455

Db 319 CCAGCCTGGCCCCAGTCCAAAATATTTTAAAGATTGTTTCCTTAGTGTCTTGAAGTTTG 378

QY 3456 AACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTCATCAC 3515

Db 379 CACA-----AAATTCTTTTTTTGAGATGGAGTCTCACTCTGTCACCCCAGGCTGGAGTGC 433

QY 3516 CTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCTCCCGGTTTCAAGYGATTCCTCTGCC 3575

Db 434 AGTGGCGTGATCTTGGCTCACTGCAACCTCTGCCTCCTGGGTTTCAAGCAATTCTCCCAAC 493

QY 3576 TAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGT 3635

Db 494 TCAGCCTCCCAAGTAGCTGGGATTACAGACGTGTGCCACCACCATACCTGGGTAA-TTTTTGC 552

QY 3636 ATTTTTCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTC 3695

Db 553 ATTTTTCAGAGAGGAGTTTCACCATGTTGGCCAGGTTGGTCTTTGAACCTCCTGACCTC 612

QY 3696 AAGTGATCTGCCCTGCCTCAGTCTCCCCAAAGTCTGGAATTATAGGCGTGAAGTCACTGTGC 3755

Db 613 AGGTGATCCTCTGCCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCGTGC 672

QY 3756 CTGGCCGATTACTGTCT 3772

Db 673 TCAGCCCGCANAAATTCCT 689

RESULT 22

BU568843/c

LOCUS

DEFINITION AGENCOURT_10400218 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6616116

5', mRNA sequence.

ACCESSION BU568843

VERSION BU568843.1 GI:22919143

EST 16-SEP-2002

Db 615 G-CTCCCTCGGCTCCCAAAGTGCTGGGATTACAGGATGAGCCAAAGTGCCTCGGCCAGC 673
QY 1106 TCACATTTATTATT 1119
Db 674 TGGCCTTGTTTCTT 687

RESULT 25
BP382202
LOCUS
DEFINITION BP382202 Sugano cDNA library, adipose tissue Homo sapiens cDNA
clone adSE01815, mRNA sequence.
ACCESSION BP382202
VERSION BP382202.1 GI:52417857
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 618)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
FEATURES
source
1. .618
/organism="Homo sapiens"
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/clone="adSE01815"
/tissue_type="adipose tissue"
/clone_lib="Sugano cDNA library, adipose tissue"

ORIGIN
Query Match 6.0%; Score 298.6; DB 3; Length 618;
Best Local Similarity 73.2%; Pred. No. 5.9e-16;
Matches 462; Conservative 0; Mismatches 139; Indels 30; Gaps 5;

QY 480 TTA... 539
Db 9 TTT... 68
QY 540 GTG... 599
Db 69 GCG... 128
QY 600 TCT... 659
Db 129 TCC... 173
QY 660 ATT... 719
Db 174 ATA... 229
QY 720 CCT... 770
Db 230 GAT... 288
QY 771 AGT... 830
Db 289 TGA... 348
QY 831 CTT... 890

Db 349 CTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGACAGATCTCGGCTCAGGCAGCTCCGC 408
QY 891 CTGCTGGGTTACGGCCATTCTCCCGCTCAGCCTCCCAGTAGTGGGACTAAAGCGCC 950
Db 409 CTCCCGGTTACGGCCATTCTCCTGCCTCAGCTTCCGAGTAGCTGGGACTACAGGGCC 468
QY 951 TGCCACCACGCCCGCTAAATTTTGTATTTTAAATAAGACGGGTTTCATCGTGTTA 1010
Db 469 CGCCACCACGCCCGGCTAA-CTTTTGTGTTTGTAGTAGAGACGGGATTCACCGTGTTA 527
QY 1011 GCCAGGATGGTCTCGATCTCATGACCTTGTGATCCGCCTCGCCTCCCAAAGTGCT 1070
Db 528 GCCAGGATGGTCTCGATCTCCTGACCTTGTATCTGCCCGCTCGGTCTCTCAAAGTGCT 587
QY 1071 GGGATTACAGGCATGAGCCACCGTGCCCGGC 1101
Db 588 GGGATTACAGGCGTGAGCCACCGGCCCGGC 618

RESULT 26
BQ706343/c
LOCUS
DEFINITION BQ706343 918 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8484983 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301091
5', mRNA sequence.
ACCESSION BQ706343
VERSION BQ706343.1 GI:21845242
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 918)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: g column: 12
High quality sequence stop: 632.
Location/Qualifiers
FEATURES
source
1. .918
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/mol_type="mRNA"
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/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 6.0%; Score 298; DB 5; Length 918;
Best Local Similarity 68.6%; Pred. No. 5.1e-16;
Matches 456; Conservative 1; Mismatches 197; Indels 11; Gaps 3;

QY 3098 TTTGGGTTTTTTTGTGTTGTTTAGACAGAGGGTCTTGCTCTGCACCCAGGCATGAG 3157
Db 666 TTTGGATTATGATTATTATTCTTTGAAGCCAGGGTCTCGCTCTGTCAACAGCCGGAG 607

Db	2922	CTCAGCCTCCCGAGTAGCTGGGACTACAGGTGCCCGCCACCACGCCCGGCTAATTTT	2863
Qy	977	GTATTTTAAAGACGGGGTTTCATCGTGTTAGCCAGATGGTCTCGATCTCATGACC	1036
Db	2862	GTATTTTAGTAGACACGGGGTTTCACCGTGTTAGCCAGATGGTCTCGATCTCCTGACC	2803
Qy	1037	TTGTGATCCGCCTGCCTCGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGTGC	1096
Db	2802	TCATGATCCGCCTGCCCTCGGCCTCCTAAAGTGCTGGGATTACAGGCATGAGCCACCATGC	2743
Qy	1097	CCGGCCTTATCACATTTATTATTATTATTATTATTCTCTCCCACTAGGTTGTAAGCTCCATG	1156
Db	2742	CCGGCCACATCTGGTGTGTTCAACATCATTTAACTAGGATTAAGATGTTTGGGCCAGGC	2683
Qy	1157	AGGTTAGAGATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATCT	1216
Db	2682	ACGGTGGCTCACACCTGTAATCCCAACACTTTGGGAGGCTGAGGCAGGTGGACCACTGA	2623
Qy	1217	GTTCACTGCTGTATCTCTAGCTCTAGGACAGAGCCCTGGCACATAGTAAGTGCTCA-ATA	1275
Db	2622	GGTCAGGAGTTCAAGACCAGCCTGACTAAACATGGTGAAACCCATCTCTATTAAAAATACA	2563
Qy	1276	AATATTCACTGGATAAACAGTGCAGATAGTTTAAAACTATCTGACCTAGGGAGGCTGAGG	1335
Db	2562	AAGACATTAGCCAGGTGTAGTGGCGCATGCCTGTATCCCACTACTTTGGGAGGCTGAGG	2503
Qy	1336	CAGGAGAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGAGCTGAAATCGTGTCACTGC	1395
Db	2502	CAGGAGAATTGCTTGAGCCCGGAGGTGGAGGTTGCAGTGAACCAAGATTGCGGCCACTGC	2443
Qy	1396	ACTCCAACCTGGGCAAC-AGAGCAAGACTCCATCTCAAAAAAAAAAAAAA	1446
Db	2442	ACTCCAGCCTGGGCAACAAGAGCAAAACTCTGTCTCAAAAAAAAAAAAAA	2391
RESULT 30			
CX780936			
LOCUS			
DEFINITION			
CX780936.1 GI:58297726			
EST.			
Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Homnidae; Homo.			
1 (bases 1 to 736)			
NIH-MGC http://mgc.nci.nih.gov/.			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Other ESTs: HESC3_2_B04.g1.A036			
Contact: Daniela S. Gerhard, Ph.D.			
Office of Cancer Genomics			
National Cancer Institute / NIH			
Bldg. 31 Rm10A07 Bethesda, MD 20892			
Email: cgapbs-r@mail.nih.gov			
Tissue procurement: BresaGen, Inc.			
cDNA Library Preparation: Express Genomics, Inc.			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,			
University of Georgia			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
Plate: NDAM1172 row: c column: 08			
Seq primer: M13-21 (TGAAACGACGGCCAGT)			
High quality sequence stop: 711			
POLYA=Yes.			
Location/Qualifiers			
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source			

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/clone_lib="NIH_MGC_260"			
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RNA obtained from human embryonic stem cells isolated from			
the inner cell mass of blastocyst stage embryos. Cell line			
id and NIH Registry designation is BG01. Positive for			
SSEA3, SSEA4, Tra 1-60, Tra 1-81, CD9, Alk Phos, Oct4 and			
Nanog expression; negative for SSEA1 expression. Passage			
number 21. cDNA primed using oligo-dT primer:			
5'-pGACTAGTTCTAGATCGCGAGCGCGCCCC(T)25-3' and cloned into			
the EcoRV/NotI sites of pExpress-1. This primary library			
is non-normalized (normalized primary library is			
NIH_MGC_261). It was constructed by Express Genomics			
(Frederick, MD). Sequence ends have been trimmed to			
exclude vector and regions below Phred quality 16. Note:			
this is a Mammalian Gene Collection library."			

ORIGIN

Query Match			
Best Local Similarity 5.9%; Score 293.6; DB 8; Length 736;			
Matches 464; Conservative 1; Mismatches 220; Indels 9; Gaps 3;			
Qy	3099	TTGGGTTTTTTTTTGTGTTTGTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGC	3158
Db	1	TTTTTTTTTTTTTTTTTTTTTGTAGATGGAGTCTCACTCTCTTGCCCAGGCTGAAGT	60
Qy	3159	ACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGA	3218
Db	61	GCAGTGGCGGGATCTCGGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCAGCTTCTTCTG	120
Qy	3219	CCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACCGCTGGCTAAATAAAA	3278
Db	121	CTTCAGCCCCCTGAGTAGCTGGGATTACAGGCACCCACCACCGGCTGGATACTT-TT	178
Qy	3279	AAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGC	3338
Db	179	TTGTATTTTGTAGTAAAAATGGGGTTTGCTATATATGGCCAGGCTGGTCTCAAACCTCTGAC	238
Qy	3339	TTCAAGCAATCCTCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCA	3398
Db	239	CTCAGGTGATCCACCTGCCTAAGCCTGCCAAAGTGTGGGATTACAGGCATGAACCACCA	298
Qy	3399	TGTGCGGCTACTTATTTCTTTACATTTCCATCTTTCCAATAGAAATGTAAGATCCACAGAAC	3458
Db	299	TGCCAGCCTCTTTATCTTTTAAATATATCACAAGTTATTTATTTATTATTATTA	358
Qy	3459	AGGATTACTGCCCTAATTTCTTCCTTTCTTTTTTTTGAGACAGAGTCTCACTTTCACCTC	3518
Db	359	TTTATTTATTTTGAGATGGAGTTTGTGCCCTTGTTGCCCAAGCTGGAGTGCAATGGCAC	418
Qy	3519	AACCTCCGTTTCAGCTCACTGCAACCTCTGCTCCCGGGTTCAAGYGATTCTCCTGCCTAA	3578
Db	419	GATC----TCAGCTCACTGCAACCTCCACCTCCCGGGTTCAGTGATTTCTCCTGCCTCA	473
Qy	3579	GCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATT	3638
Db	474	GCCTCCTGAGTAGCTGGGATTACAGGCACATGCCATCATGCTGGCTAA--TTTGCATT	531
Qy	3639	TTTAGCAGAGATGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACCTCCTGACCTCAAG	3698
Db	532	TTTAGTAGAGACAGAGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGG	591
Qy	3699	TGATCTGCCTGCCTCAGTCTCCCAAAGTGTCTGGAATTATAGGCGTGAGTCACTGTGCCTG	3758
Db	592	TGATCTGCCCTCCTCGGCCTCCCAAAGTGTCTGGGATTATAGGCATGAGCCACCGTGCCCA	651


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QY 3759 GCCGATTACTGTCTATTTTCTTATTGCTATATC 3792
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Db 652 GCCATTATCACAAAGTTATTATTAATCTCCTTTCTC 685

RESULT 31
CR990046/c
LOCUS
DEFINITION CR990046 RZPD no.9016 Homo sapiens cDNA clone RZPDp9016F115 5',
mRNA sequence.
ACCESSION CR990046
VERSION CR990046.1 GI:68283931
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 772)
AUTHORS Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D.
and Korn,B.
TITLE Human T-Lymphocytes library
JOURNAL Unpublished (2005)
COMMENT Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; RZPDp9016F115.
RZPDLiB; (Human T-Lymphocytes) RZPD LiB No.9016
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact:
Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp9016F115
contact RZPD (product- support@rzpd.de) for further information.
Primer name: qe3_4 , Primer sequence: CGGATAACAATTACACAG.

FEATURES
source
1..772
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/clone_lib="RZPD no.9016"
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NotI; vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
; 1st strand cDNA was prepared from mRNA obtained from
human T-Lymphocytes with a NotI - oligo(dr) primer [5'
GACTAGTTCTAGATCGCGAGCGCGCCCTTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to SalI adaptors,
digested with NotI and cloned into the NotI and SalI sites
of the pQE80LSN_cloned vector"

ORIGIN
Query Match 5.9%; Score 293.2; DB 7; Length 772;
Best Local Similarity 68.8%; Pred. No. 1.4e-15;
Matches 462; Conservative 0; Mismatches 178; Indels 32; Gaps 3;

QY 473 TTTTATTTTACTTTATTTTATTTTGAGACGGGGCTCACTCTGTGCGCCAGGCTGGAGTG 532
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 724 TTTTATTTTATTTTATTTTATTTTGAGACAGAGTCTCTGACTCTTTGTTGCCAGGCTGGAGTG 665
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 533 CGGTGGCGTGATCTCAGATCACTACAACCTCCATCTCTGGGTTCAAATAATCTCTTGC 592
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 664 CAATGGTGCAATCTTGGCTCACTGCAACCTCCGCCCTCAGGGTTCAAGCGGATTCTCCTGC 605
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QY 593 CTCAGCCTCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACCATGC 652
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 604 CTCAGCCTCTCTGAGTAGCTGGGACT-----ACAGGTGCCTGCCACCACGC 560

QY 653 CCAGCTAATTTTGTGTGTTTTTTTGGTAGAGACAGGTTTTCCACCATGTTGGCCAGGC 712
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 559 CCGGCTAATTTT-----GTATTCCTCCACTAGAGATGGGGTTTCACCACTGCGCCATGG 506

QY 713 TGGGTGACCTCCC-----TTTTAGATTCTCTCATCTGCTCTATTCTTCCCCT 761
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 505 TGGTCTCGAACTCCTGACCTCAGGTGATCCACCCGCTCGGCCTCCCAATTCGTGGGAT 446

QY 762 TTCTAATGCAGTATCCAGTTTCCTTACTTATFACATTTATTATTATTCTTATTATTG 821
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 445 TATAGGCCTGAGGCACCAAGCCAGCCCAAGAGTTTCTTTCTTTTTTTTTTTTTTTTG 386

QY 822 AGACAGAGTCTTGCTTTGTGCGCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGC 881
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Db 385 AGATGGAGTCTGGCTCTGTCAACCAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCACTGC 326

QY 882 AAGCTCCACCTGCTGGGTTCAAGCCATTCTCCGCTCAGCCTCCCCAGTAGCTGGGACT 941
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Db 325 AAGCTCTGCCTCCAGGTTACACCACTTCTTGCCTTAGCCTCCGGAGTAGCTGGGACT 266

QY 942 AAAGGCGCTGCCACCACCGCCCGCTAATTTTGTATTTTAAATAAGCGGGTTTC 1001
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Db 265 ACAGGTGCCTGCCACCATGCCGGCTAATTTTGTATTTTAGTAGAGACAGGGTTTC 206

QY 1002 ATCGTGTTAGCAGGATGGTCTCGATCTCATGACCTTGTGATCCGCTCGGCTCC 1061
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 205 ACCGTGTTGCCAGGATGGTCTCGATCTCTTGACCTTGTGATCTGCCCTGGCCTCC 146

QY 1062 CAAAGTGCTGGATTACAGGCATGAGCCACCGTCCCGCTTATCACATTTATTATTTA 1121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 CAAAGTGCTGGATTACAAGCGTGAGACACCGGCTTGCCGAGTTTCTTTCTTTCTT 86

QY 1122 TTGTTTTTCTCT 1133
||| ||| ||| |||
Db 85 TTTTTTTTTTTTT 74
|||

RESULT 32
AQ342859 666 bp DNA linear GSS 07-MAY-1999
LOCUS RPCI11-122M7.TV RPCI-11 Homo sapiens genomic clone RPCI-11-122M7,
DEFINITION genomic survey sequence.
ACCESSION AQ342859
VERSION AQ342859.1 GI:4167755
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 666)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
JOURNAL Map Building
COMMENT Unpublished (1997)
Other_GSSs: RPCI11-122M7.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@igr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
```


Db	324	TATTTGTAATTTTTTTTTTTTGAGATGGAGTCTTGCTCTGTGCCCAGGCTGGAGTGCAGT	265
Qy	861	GGTCCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGTTACAGCCATTCTCCCGCCTCA	920
Db	264	GGCGGATCTCGGCTCACTACGAGCTCCGCCTCCACAGGTTACAGCCATTCTCCTGCTCA	205
Qy	921	GCCTCCCCAGTAGCTGGGACTAAAGGCGCCTGCCACCACGCCCCCGCTAAATTTTTTGTAT	980
Db	204	GCCTCACGAGTAGCTGGGACTACAGGCGCCGCCACCACGCCCAGCTAAATTTTTTGTAT	145
Qy	981	TTTTAATAAAGACGGGTTTTTCATCGTGTTAGCCAGGATGGTCTCGATCTCATGACCTGT	1040
Db	144	TTTTAGTAGACGGAGTTTCACCGTGTTAGCCAGGATAGTCTCGATCTCCTGACCTCGT	85
Qy	1041	GATCCGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGTGCCCGG	1100
Db	84	GATCCGCCTGCCTGGCCTCCCAAAGCGCTGGGAATTACAGGCGTGAGCCACTGCACCCGG	25
Qy	1101	CCTTAT 1106	
Db	24	CCTTAT 19	

RESULT 34
HSM805110/c
LOCUS HSM805110 5326 bp mRNA linear HTC 22-SEP-2004
DEFINITION Homo sapiens mRNA; cDNA DKFZp434O1216 (from clone DKFZp434O1216).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

gene

CDS

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/db_xref="UniProt/TreMBL:Q8NDN1"
/translation="MLRTDAGEDLADAPAEELQEKSGPAGPPSPQSQPAARPPKEVPA
SRQAQLREEGNWLNQTESLTAEAVYLMGKPSKLQLEYDLWGQDQDPRPGSLPTAL
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PRNQASLRSLKTFPPSSAPCSSLGRNRPRLVPGPSSGNSDGGFLFAVPTTLPPN
SRHGKLFSPSKEAELTFROHLSISMQSDFFLPKPRKLRNRHLRKLVPVQRTLLPRPS
ENSHNVCSFSLSNSSVTGRGSRPIQSSLTKAALSRPIVPKVLPPQATSHLASAID
LAATSAGILSGNLPALDTEGLSIPLSDEVTGAI SQDSTGTGHQDGTLLPTVGG
DPFVISPRIPEQEPVADSFQGSVLSSELKAPLQNGLSIPLSSESSSTRLSPDVI
SALLDLSLGPPEDALSQGEPAHISDSII EIAISSGEGVPLSPAKNGSDSSKSLLPS
PSSSPQPHWIASPTHDPQWPSDSTDSSLSLFAFSIPEKSRKMLPTPIGTNSGTSL
LGPSLLDGNRSDFVSRLADVAEVDVDSQLVCMNNENSIDYISRFNDLAQELSIAEPG
LREALFDGGGGGPAVSDLSO"

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ORIGIN

Query Match 5.8%; Score 290.8; DB 4; Length 5326;
Best Local Similarity 71.0%; Pred. No. 6.3e-16;
Matches 470; Conservative 0; Mismatches 157; Indels 35;

Qy	469	TTATTTTATT	T T A C T T T A T T T A T T T T T G A G A C G G G C T C A C T C T G T G C C C A G G C T G G	528
Db	5326	TTTTTTTTTT	T T T T T T T T T T T T T T T T T G A G A T G G A G - T C T A G C T G T C A C C C A G G C T G G	5268
Qy	529	AGTCGGTGCG	G T A T C T C A G A T C A C T A C A A C C T C C A T C T C C T G G G T T C A A A T A A T T C T C	588
Db	5267	AGTCAGTGGCA	T G A T T T G G C T C A C T G C C A C C T C C A C C T C C C G G G C T C A A G T G A T T C T C	5208
Qy	589	TTGCCTCAGCC	T C T C A A G T A G C T G G G A C T T G T A G C T C T C A A G T A G C T G G C A C A C A C C A C C	648
Db	5207	CTGCCCTCAGCC	T C C T G A G T A G C T G G A C T - - - - - A T A G G C G T G C A C C A C C	5163
Qy	649	ATGCCAGCTAA	T T T T T T G T G T T T T T T T T T T T T G G T A G A G A C A G G T T T T C A C C A T G T T G G C C	708
Db	5162	ACACCAGCTAA	T T T T - - - - - G T A T T T T T A G T A C A G A T G G A G T C T T G C C A C G T C G G C C	5109
Qy	709	AGGCTGG--GT	A C C T T T T A G A T T C T C C T C A T C C T G C T C T A T T C T T C C C C T T T C T A	766
Db	5108	AGGCTGGTCTC	A A A A C T C C T G A C C T C A T G A T C A C C T G C C T T G G C C T C C C A A A G T G C T A G G A	5049
Qy	767	ATGCAGTATCC	A G T T T C C T T A C T T A T C A C A - - - - - T T T A T T A T T A T T C T T A T T A	815
Db	5048	TTACAGGCATG	A C C A C C A C G C C C G G C T G A G A A A C C T T T T T C T T T T T C T T T T T C T T T T T T	4989
Qy	816	TTATTGACAGA	G A T C T T G C T T T T G T G C C A A G G C T G G A G T A C A G T G G T G C G A T C T C G G C T	875
Db	4988	TTTTTGAGACG	G A G T C T G C T G T C A C C C A G G C T A G A A T G C A G T G G T G C G A T C C G G C T	4929
Qy	876	CAC TGAAGCT	C C A C C T G C T G G G T T C A C G C C A T T C T C C G C C T C A G C C T C C C A G T A G C T	935
Db	4928	CAC TGAAGCT	C C G C C T C C C G G T T C A T G C C A T T C T C C T G C C T C A G C C T C C T G A T A G C T	4869
Qy	936	GGGACTAAAGG	C G C C T G C C A C C A C G C C C G C T A A T T T T T T G T A T T T T T A A T A A A G A C G G	995
Db	4868	GGGACCACAGG	T G C C G C C A C C A C C A C G C C G G C T A A T T C T T T T T C T T T T T T A G T A G A G A T G G	4809
Qy	996	GGTTTCATCGT	G T T A G C C A G G A T G G T C T C G A T C T C A T G A C C T T G T G A T C C G C C T G C C C T C G	1055
Db	4808	GGTTTCACCGT	G T T A G C C A G G A T G G T C T C G A T C T C C T G A C C T C G T G A T C T G C A C A C C T T G	4749
Qy	1056	GCCTCCAAAAG	T G C T G G G A T T A C A G G C A T G A G C C A C C G T G C C C G G C C T T A T C A C A T T T A T	1115
Db	4748	GCCTCCAAAAG	T G C T G G G A T T A C A G G A T G A G C C A C C G C C T G G C C A A G A A A C C T T T T T	4689
Qy	1116	TA 1117		
Db	4688	CA 4687		

RESULT 35
CR613629
LOCUS
DEFINITION


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Db      518 CAGGATGGTCTCGATCTTTTGACC-TATGATCCACCTGCGCTCCCAAAGTGCTGG 576
Qy      1073 GATTACAGGCATGAGCCACCGTGCCCGGCCTTATCACATT 1112
Db      577 GATTACAGGCGTGAGCCACCATGCCCGGCCCCAGGATATT 616

RESULT 38
BQ710315/c
LOCUS   BQ710315              769 bp      mRNA      linear      EST 16-JUL-2002
DEFINITION   AGENCOURT_8351732 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282212
5', mRNA sequence.
ACCESSION   BQ710315
VERSION     BQ710315.1  GI:21849214
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 769)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LNCM2476 row: d column: 21
            High quality sequence stop: 549.
FEATURES    Location/Qualifiers
            source          1..769
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                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:6282212"
                        /lab_host="DH10B (phage-resistant)"
                        /clone_lib="NIH_MGC_113"
                        /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                        EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                        into EcoRI/XhoI sites using the following 5' adaptor:
                        GGACAGAG(G). Library constructed by Ling Hong in the
                        laboratory of Gerald M. Rubin (University of California,
                        Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                        Superscript II RT (Life Technologies). Note: this is a
                        NIH_MGC Library."

ORIGIN
Query Match      5.8%; Score 287.6; DB 5; Length 769;
Best Local Similarity 67.0%; Pred. No. 4.1e-15;
Matches 453; Conservative 1; Mismatches 215; Indels 7; Gaps 3;

Qy      3104 TTTTttttTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGT 3163
Db      768 TTTTttttTGTGTTTttTATTGAGACAGAGTCTCACTCTGTCCCCAGGCTGGAGTGCACT 709

Qy      3164 GGTGCAACCATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 3223
Db      708 GGGGTGATCTCGGCTCACTGCAACCTCTGCCTCCTGGTTCAAGCGATTCTCCTGCCTCA 649

Qy      3224 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACCGCCTGGCTAATTA AAAAATT 3283
Db      648 GCCTCCCGAGTAGCTGGGACTATAGCGCCCCGCCACTGTGCCGGCTAATTTTATA---T 592

Qy      3284 TTTTttTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTA AACTCCTGGCTTCAA 3343
Db      591 TTTTAGTAGACACGGGGTTTCCCCCATGTTGGCCAGGCTGGTCTCGAATTCCTAACCTCAG 532
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Qy      3344 GCAATCCTCCTACTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGC 3403
Db      531 GTGATCCGCGCTGGCTCAGCCTCCCAAACATGCTGGGATTACAGGTGTGAGCCACCATGCCC 472
Qy      3404 GGCTACTTATTCTTTACATTCCATCTTTTCAATAGAATGTAAGATCCACAGAACAGGGA 3463
Db      471 GGCTGTGTTACACTTTTGTGGTGTCTCACAGGCTCTCTGAGGCTCTGCTCATTTTGTGTTT 412
Qy      3464 TTACTGCCTATTTTCTTCTTTTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCT 3523
Db      411 TTGTTTTTATTTTTTTGAGACAGAGTCTCTTTCTGTCACTAGACTGGAGTGCGGTGC 352
Qy      3524 CCGTTCAGCTCACTGCAACCTCTGCCCTCCCGGGTTCAAGYGATTCTCCTGCGCTAAGCCTC 3583
Db      351 AATCTCGGCTCACTGCAACCTCTGCCCTCCAGAGTTCAAGCGATTCTCTTGCTCAGCCTC 292
Qy      3584 CTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAA--TTTTTTGTATTTT 3641
Db      291 CCAAGTAGCTGGGATTACAGGCACATGCCACCATGCCCAACTAATATTTTTTTGTATTTT 232
Qy      3642 AGCAGAGATGGGGTTTTACCATGTTGCCCGAGGCTGCTCAAACTCCTGACCTCAAGTGA 3701
Db      231 AGTAGAGATGGGGTTTGACCATGTTGGCCAGGATGGTCTAGATCTCTTGACCTC--GTGA 174
Qy      3702 TCTGCCCTGCCTCAGTCTCCCAAAGTGCTGGAAATTATAGGCGTGAGTCACTGTGCCTGGCC 3761
Db      173 TCCAAACCACCTTGGCCTCCCAAAGTGCTGAGATTACAGGCGTGAGCCACTGCGCCTGGCC 114
Qy      3762 GATTACTGTCTATTTT 3777
Db      113 GGCTCCTCCTTCTTAT 98

RESULT 39
CD516136/c
LOCUS   CD516136              688 bp      mRNA      linear      EST 06-JUN-2003
DEFINITION   AGENCOURT_14372513 NIH_MGC_181 Homo sapiens cDNA clone
IMAGE:30397717 5', mRNA sequence.
ACCESSION   CD516136
VERSION     CD516136.1  GI:31447854
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 688)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM481 row: h column: 14
            High quality sequence stop: 541.
FEATURES    Location/Qualifiers
            source          1..688
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:30397717"
                        /tissue_type="White Matter"
                        /dev_stage="Unknown"
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/lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_181"
/note="vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV
(destroyed); Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Query Match      5.7%;   Score 287;   DB 6;   Length 688;
Best Local Similarity 68.3%;   Pred. No. 4.9e-15;
Matches 428;   Conservative 0;   Mismatches 195;   Indels 4;   Gaps 2;

QY  480 TTACTTTATTTTATTTTGAGACGGGGCTCACTCTGTGCGCCAGGCTGGAGTGC-GGTGG 538
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Db  682 TTTTNTTTTTTTTTCAGATAGAGTCTTGCTTTGTTGCCCAGGCTGGAGTGCAAAATGG 623

QY  539 CGTGATCTCAGATCACTACAACTCCATCTCCTGGGTTCAAATAATTCTCTTGCTCAGC 598
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Db  622 AGCAATCTTGGCTCAATGCACCTCTGCTTCCCTAGTTCAAGCGATTCTCTTGCTCAGC 563

QY  599 CTCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGGCACACACCACATGCCAGCT 658
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  562 CTCTGGAGTAGCTGGGATTACAGGCACGCCACCAAGC---CTGGCTCATTTTGTATTTTC 506

QY  659 AATTTTTGTGTGTTTTTTTGGTAGAGACAGGTTTTTCACCATGTTGGCCAGGCTGGGTG 718
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  505 AGTAGAGTGTTCATCATTTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGATCCG 446

QY  719 ACCTCCCTTTTAGATTCTCCTCATCTGCTCTATTCTTCCCTTTTCTAATGCATATCCA 778
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  445 CCGCCTCAGCTGCCCAAGGCTGGGATTACAGGCATGAGCCACCGTGCCCGCTACT 386

QY  779 GTTTCCTTACTTATCACATTTATTATTATTCTTATTATTATTGAGACAGAGTCTTGCTTT 838
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  385 TTTTCTTTTTCGTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTGTGAGACAGAGTCTGCTCT 326

QY  839 GTCGCCAAGGCTGGAGTACAGTGGTGCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGG 898
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  325 GTTGCCCAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCACTGCAAGCTCCCGCTCCCGGG 266

QY  899 TTCAGGCCATTCTCCCGCTCAGCCTCCCCAGTAGCTGGGACTAAAGGCGCCTGCCACCA 958
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  265 TTCACACCATTCTCCTGCCTCAGCCTCCGAGTAGCTGGCACTACAGGCGCCCGCCACCA 206

QY  959 CGCCCCGCTAAATTTTTTGTATTTTAAATAAGACGGGTTTTCATCGTGTAGCCAGGAT 1018
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Db  205 CGCCTGGCTAAATTTTTTGTATTTTGTAGTAAAGACGGGTTTCACTGTGTAGCCAGGAT 146

QY  1019 GGTCTCGATCTCATGACCTTTGTGATCCGCTGCTCGGCTCCCAAGTCTGGGATTAC 1078
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Db  145 GGTCTCAATCTCCTGACCTGGTGATCCGCCTACCTCGGCCTCCCAAGTCTGGGATTAC 86

QY  1079 AGGCATGAGCCACCGTGCCCGCCTTA 1105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  85 AGGTGTGAGCCACCGTGCCCGGCCCTA 59

RESULT 40
HSM808459/c
LOCUS      HSM808459      4088 bp      mRNA      linear      HTC 22-SEP-2004
DEFINITION Homo sapiens mRNA; cDNA DKFP686I19131 (from clone DKFP686I19131).
ACCESSION  BX648311
VERSION    BX648311.1  GI:34367470
KEYWORDS   HTC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1  (bases 1 to 4088)
AUTHORS    Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,
            Osanger,A., Fobo,G., Han,M. and Wiemann,S.
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CONSRMTM      The German cDNA Consortium
TITLE          Direct Submission
JOURNAL        Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
               Neuherberg, GERMANY
COMMENT        Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
               Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
               sequenced by GBF (National Research Centre for Biotechnology Ltd.,
               Braunschweig/Germany) within the cDNA sequencing consortium of the
               German Genome Project.
               This clone (DKFP686I19131) is available at the RZPD Deutsches
               Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
               Please contact RZPD for ordering:
               http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFP686I19131
               Further information about the clone and the sequencing project is
               available at http://mips.gsf.de/projects/cdna/.

FEATURES             Location/Qualifiers
     source           1..4088
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                     /mol_type="mRNA"
                     /db_xref="RZPD:DKFP686I19131Q"
                     /db_xref="taxon:9606"
                     /clone="DKFP686I19131"
                     /tissue type="uterus"
                     /clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
                     DH10B; sites SfiIA + SfiIB"
                     /dev_stage="adult"
                     /note="unspliced mRNA, 5' and 3' truncated"

ORIGIN

Query Match      5.7%;   Score 285.2;   DB 4;   Length 4088;
Best Local Similarity 56.9%;   Pred. No. 2.2e-15;
Matches 619;   Conservative 1;   Mismatches 459;   Indels 9;   Gaps 5;

QY  3452 ACAGAACAGGGATTACTGCCTATTTTCTTCCTTTTGTGAGACAGAGTCTCACTTCA 3511
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1504 AAAAAAAGCTGCTCAGGAATTATTGATTGTTGTTTTTGAGATGGAGTCTCCCTTG 1445

QY  3512 TCACCTCAACCTCCGT---TCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAAGYGATT 3567
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1444 TCGAGTGCAGTGGTGTGATCTCGGCTCACTGCAACCTCCGCTCCCAAGGCTCAAGCGATT 1385

QY  3568 CTCCTGCCTAAGCCTCCTGAGTAGCTGGGAATTACAAGCGTGCACCACCATGCTTGGCTAA 3627
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1384 CTCCCGCTCAGCCCCCGAGCGCGCGGGATCACAGGTGTGCGCCACCAACCCAGCTAA 1325

QY  3628 TTTTGTGATTTTGTAGCAGAGATGGGGTTTACCATGTTGCCCAGGCTGGTCTCAAACTC 3687
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1324 -CCTCTGTATTCCTAGTAGAGACAGGGCTTCACCATGTTGGCCAGGCTGGTCTTGAAC 1266

QY  3688 CTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAGTGTGGAATTATAGGCGTGAGT 3747
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1265 CCGACCTCATATGATCGCCCGACCCAGCCTCCCAAGCGTTGGGATTACAGGCGTGAGC 1206

QY  3748 CACTGTGCCTGGCCGATTACTGTCTATTTTCTTTTATTGCTATATCCCCAGATCTAGAGCA 3807
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1205 CACCACACTGGGCCCAAGGCATTATTGGTTAATGCTCCAATTCCCTGGACATCCACATTC 1146

QY  3808 GTGCTGACATATAGTAGGTGCTCAATAATAATAATTGATGAATGCACAGCCTAGATATAA 3867
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1145 ATGTTCTCTCTGCAGAAATGTCTAAGAAATCTTAAAAGAAAGGAATGATT--ATGTAA 1088

QY  3868 CTTTCTTTTCTTTTAAAAACAATCTTCACAACCTTTGCAGAATAAATACAATCTTGCA 3927
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1087 CATACCTAACTATGTCTAGTTAACTTAGGCAACAACACTACGTGGCACCCAGTCAAAACAGAC 1028

QY  3928 TTCTGCTTTTTCACCTTATCACCTTGTTATGACTTTTTCATATTTGCCTCAAACCTTTATTG 3987
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  1027 ATCACTAAATCCATGGAGTAAAAAATTCCTATACCTTTAGTGATAGGAGCCTGTATTACTC 968

QY  3988 TTACT-GTTTTTTCATTTGTACTATTTTACTGCTGAATAAATATGGCTTAATTTGCTTAT 4046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  967 CTCTAGCAGTTATAAAATTTAATAAATCTAGTCTTCTACTTTCTAGTCTATATAAATTA 908
```


Db 2360 CACAATCATAGCTCACTGCAGCCTCCAAACTCCTGAGCTCAAGGATCCTTTTGCCTCAGC 2419

QY 3226 CTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGGCTAAT--TAAAAAAATT 3283

Db 2420 CTCCTGATAGCTAGGACTACAGGTGCATGCCACCATGCTTGGCTAATTGTTTTTAAAT 2479

QY 3284 TTTTGTAGAGACTGGGTCTTTACTACGTTGGCCAGGCTTGCTTAAACTCCTCGGCTCAA 3343

Db 2480 TTTGTTAGAGATGGGTCTCACTGTATTGCCAGGCTGGTCCAAACTCCTGGCCTCAA 2539

QY 3344 GCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGC 3403

Db 2540 GTGACCCCTCCACATCATCCTCTCAAAGCACTGGGATTACAGGTATGAGCCACCACCC 2599

QY 3404 GGC-----TACTTATTCTTTACATTCCA-----TCTTTCCAATAGAAT-- 3442

Db 2600 AGCCTTTTGAATTTATTCTAAGCATTTTAATGATTTTCATGTTCTTGTGAATAGAATTG 2659

QY 3443 -----GTAAGATCCACAGAACAGGGATTACTGCCTA 3473

Db 2660 TTTTTCACATTTCAATTTTCCAGTTGTGCATGCAATTATATAGAAATAGATTGATTTTC 2719

QY 3474 TTTTCTTCTTCTTTTGTAGACAGAGTCTCACTTTCATCACCTCAACCTCCGT----- 3527

Db 2720 TTTTCTTCTTCTTTTGTAGATGGATTCTTGCTTTGTGACCCAGGCTGGAGTGCAGTG 2779

QY 3528 -----TCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAG 3579

Db 2780 GCACATCTCGGCTCACTGCAACCTCCGCCACCTAGGTTCAAGCGATTCTCCTGCCTCAG 2839

QY 3580 CCTCCTGAGTAGCTGGAATTACAAAGCGTGCACCACCATGCTTGGCTAATTTTGTGATTT 3639

Db 2840 CCTCCTGAGTAGCTGGGATTACAGGCATGCGCCACCACCGCCTGGCTAA--TTTTTGTATT 2898

QY 3640 TTAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGT 3699

Db 2899 TTAGTAGACACAGGGTTTTCACCATATGGCTAGGCTGTTCTCAAACTCCTGACCTCAGGT 2958

QY 3700 GATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGAATCACTGTGCCTGG 3759

Db 2959 GATCCTCCCTCTTCAGCCTCCCATAGTGGTGGATTACAGGCATGAGCCACTGTGCCTGG 3018

QY 3760 CCGATTACTGTCTATTTTCTTTTATGCTATATCCCCAGA 3798

Db 3019 CCTAAAGTTGATTTTCTATATTAATTGATCCTGTGA 3057

RESULT 44

AU120942/c

LOCUS

DEFINITION AU120942 HEMBB1 Homo sapiens cDNA clone HEMBB1001749 5', mRNA

sequence.

ACCESSION AU120942

VERSION AU120942.1 GI:10936177

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 800)

AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

Location/Qualifiers

1. .800

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="HEMBB1001749"

/tissue_type="whole embryo, mainly body"

/dev_stage="embryo, 10 weeks"

/clone_lib="HEMBB1"

/note="Vector: pME18SFL3"

ORIGIN

Query Match 5.6%; Score 281.6; DB 1; Length 800;

Best Local Similarity 68.0%; Pred. No. 1.2e-14;

Matches 451; Conservative 1; Mismatches 201; Indels 10; Gaps 4;

QY 3107 TTTTGTGTTGTTGTAGACAGGGTCTTGCTCTGTCAACCAGGCATGAGCACAGTGGT 3166

Db 698 TGTATTCTTTTGTCTNAGATGGAGTCTCACACTGTCACTGGGCTAGAGTGGTGGC 639

QY 3167 GCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCC 3226

Db 638 TCGATCTTGGCTCACTGCAACCTCTGCCTCCGGGTTCAAGAGATTCTCTACCTCAGCC 579

QY 3227 TCCCAAGTAGCTGGGACTACGAGCGTGCACCACCAACGCCTGGCTAA--TTAAAAAAATTT 3284

Db 578 TCCTTAGTACGTGGGATTACAGGTGTGCACCACCGTACCTGGCTGATTTTAAAAAATTT 519

QY 3285 TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCAAG 3344

Db 518 TTTTGTAGAGATGGGTCTCACTTTGTGCCAGGTTGGTCTCTAACTCAATGACTCAAG 459

QY 3345 CAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCG 3404

Db 458 TGATCCTCCTGCCTTGGCCTCCACAGTGTGSGGATTATAGGTGTGAGCAACCACTGG 399

QY 3405 GCTACTTATTTCTTTACATTTCCATCTTTCCAAATAGAATGTAAGATCCACAGAACAGGGAT 3464

Db 398 CTTTCTATGTCTTCAATATATCTCTATCACTGTCTAATCCTGCAACCATCTCGATCCCG 339

QY 3465 TACTGCCTATTTTCTTCTTCTTTTCTTTTGTAGACAGAGTCTC---ACTTCATCACCTCAA 3520

Db 338 TTTTCTTTTTTTTTTCTGAGACAGAGTCTCACACTGTCACTGGGCTAGAGTGCCGTGG 279

QY 3521 CCTCCGTTCACTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGC 3580

Db 278 CTCGATCTTGGCTCACTGCAACCTCCGCCCTCCCGGGTTCAAGCTATTCTCTACCTCAGC 219

QY 3581 CTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTGTATTTT 3640

Db 218 CTCCTAGTAGTTGGGATTACTGGTGCGCCCCACCCGACCTGGCTAATTTTGTATTTT 159

QY 3641 TAGCAGA--GATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACCTCCTGACCTCAAG 3698

Db 158 TAGTAGAGTAGATGGGTTTCATCCTTTTGGCCAGTCTGGTCTCGAACTCCTGACCT--TG 101

QY 3699 TGATCTGCCTGCCTCAGTCTCCCAAAGTGTCTGGAATTATAGGCGTGAATGACTGTGCCTG 3758

Db 100 TGATCTGCCCGCCTCAGCCTCCCCCAAGTGTCTGGGATTACAGGTGTTAGCCACCAACGCCCA 41

QY 3759 GCC 3761

Db 40 GTC 38

RESULT 45

CR860168

LOCUS

DEFINITION Pongo pygmaeus mRNA; cDNA DKF2p459B2023 (from clone DKF2p459B2023).

linear

mRNA

3259 bp

HTC 12-NOV-2004

[illegible]

Qy 863 TCGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGTTACGCCATTCTCCCGCCTCAGC 922
|||||
Db 2936 TGCAACTTCAGCTCAATGCAACCTTACCTCCCGGTTCAAGCAATTCTCCTGCCTCGGC 2877

Qy 923 CTCCCACTAGCTGGGACTAAAGCGCCTGCCACCACGCCCGCTAATTTTGTGATTT 982
|||||
Db 2876 CTCCAAGTAGCTGGGACTATAGCGCGTGCCACCACGCCAGCTAATTTTGTCT-TTT 2818

Qy 983 TTAATAAGACGGGTTTCATCGTTAGCCAGGATGGTCTCGATCTCATGACCTTGTA 1042
|||||
Db 2817 TTAGTAGAGTTGGGTTTCATCATGTGTGGTCAGGATGGTCTCAATCTCCTGACCTCGTA 2758

Qy 1043 TCCGCCTGCCTCGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCGTGCCCGGCC 1102
|||||
Db 2757 TCTGCCGCTCGGCCTCCCGATATGCTGGGATTACAGGTGAGAGCCACCACCCAGCC 2698

RESULT 48
CA431692
LOCUS CA431692 672 bp mRNA linear EST 07-NOV-2002
DEFINITION UI-H-DF0-bet-b-22-0-UI.s1 NCI_CGAP_DF0 Homo sapiens cDNA clone
UI-H-DF0-bet-b-22-0-UI 3', mRNA sequence.
CA431692
CA431692.1 GI:24794418
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 672)
REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 11-299, >ALU (matched complement) 378-667, >ALU (matched
compliment)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..672
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-DF0-bet-b-22-0-UI"
/tissue_type="Subchondral Bone"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP DF0"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
NCI_CGAP_DF0 is a cDNA library containing the following
tissue(s): Subchondral Bone. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an Ecor I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GTTAAGCGTC.
TAG_TISSUE=subchondral bone

ORIGIN
TAG_LIB=UI-H-DF0
TAG_SEQ=GTTAAGCGTC

Query Match 5.6%; Score 280.4; DB 6; Length 672;
Best Local Similarity 67.7%; Pred. No. 1.7e-14;
Matches 457; Conservative 1; Mismatches 198; Indels 19; Gaps 4;

Qy 3106 TTTTGTGTTGTTAGAGACAGGGTCTTGCTGTACCCAGGCATGAGCACAGTGG 3165
|||||
Db 1 TTTTGTGTTTGTGAGATGGAGTCTCGCTGTGTGCCAGGCTGGAGTGCAGTGG 60

Qy 3166 TGCAACCATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGC 3225
|||||
Db 61 CACGATCTCGGCTCACTGCAAGCTCTGCCTCCGGGTTACGCCATTCTCCTCGCTCAGC 120

Qy 3226 CTCCCAAGTAGCTGGACTACGAGCGTGCACCACCGCTGGCTAATTAAAAAATTTT 3285
|||||
Db 121 CTCCTGAGTAGCTGGAACACTACAGGCGCCGCCACACGCCCGACTAATTTTGTGA-TTT 179

Qy 3286 TTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTGTCTTAAACTCCTGGCTTCAAGC 3345
|||||
Db 180 TTAGTAGAGACGGGTTTCACTGTGTAGCCAGGATGGTCGCGATCTCCTGACCTCATG- 238

Qy 3346 AATCCTCCTACCTTGGCATCCCAAAGTGTGGATTACAGGGGTGAGCCACCATGTGCGG 3405
|||||
Db 239 -ATCCGCGCGCCTCGGCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCACCATTTGG 297

Qy 3406 CTACTTATTTCTTTACATTCCATCTTTCCAAATAGAATGTAAGATCCACAGAACAGGATT 3465
|||||
Db 298 CCATAATATGCTCTTTTAAATTAACAATTACTTACTGTTATTTAATTTGATGCCAA 357

Qy 3466 ACTGCCTATTTTCTCCTTTCTTTTGTGAGACAGAGTCTCACTTCACTCACTCACTCC 3525
|||||
Db 358 GTTTTGTGTTTATTTGTGTGTTTTTTTGAGACAGGGTCTCACTATGTCACCCAGGATGGA 417

Qy 3526 GTTCA-----GCTCACTGCAACCTCTGCTCCTCCCGGTTCAAGYGAATTCTC 3570
|||||
Db 418 GTGCAGTGGCCATGATCTTGGCTCACTGGAACCTCTGCCTCCAGTGTTCAAAGTATCTT 477

Qy 3571 CTGCCTAAGCCTCCTGAGTAGCTGGAATTAAAGCGTGACCAACCATGCTTGGCTAATTT 3630
|||||
Db 478 ATGCCTCAGTCACCTGAGTAGCTGGGATTACAGGCGGTACCAACCATGCCAGCTAA-TT 536

Qy 3631 TTTGTATTTTAGCAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTG 3690
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Db 537 TTTGTATTTTCAGTAGACACAGGGCTTCGCCCATGTTGGCCAGGCTGGTCTCGAACTCCTC 596

Qy 3691 ACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAGTGTGGAATTATAGGCGTGAGTCAC 3750
|||||
Db 597 ACCTCAAGTGATCCACCTGCCTCAGCCTCNCAAAAGTGTAGGATTACAGGCATAAGCCAC 656

Qy 3751 TGTGCCTGGCCGATT 3765
|||||
Db 657 CAAGCTCAGCCTAAT 671

RESULT 49
HSM800886
LOCUS HSM800886 3474 bp mRNA linear HTC 22-SEP-2004
DEFINITION Homo sapiens mRNA; cDNA DKFZp434N174 (from clone DKFZp434N174).
ACCESSION AL110229
VERSION AL110229.1 GI:5817168
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 3474)
REFERENCE Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
AUTHORS Fobo,G., Han,M. and Wiemann,S.
CONSRTM The German cDNA Consortium

TITLE Direct Submission
JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Agowa (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKF2p434N174) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKF2p434N174
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES
source Location/Qualifiers
1..3474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RZPD:DKF2p434N174"
/db_xref="taxon:9606"
/clone="DKF2p434N174"
/tissue_type="testis"
/clone_lib="434 (synonym: htes3). Vector pSport1; host DH10B; sites NotI + SalI"
/dev_stage="adult"
/note="hypothetical protein, N-terminus truncated, not fully spliced"

ORIGIN
Query Match 5.6%; Score 280; DB 4; Length 3474;
Best Local Similarity 67.5%; Pred. No. 6.4e-15;
Matches 483; Conservative 1; Mismatches 221; Indels 11; Gaps 6;

QY 3103 GTTTTGTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCACAG 3162
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Db 2101 GTTTTGTGTTTTCCTTTTAGAGATGGCTTTTGCTCTTACCCAGGC-TGAGTGCAG 2159
|||||

QY 3163 TGGTGCAACCATAGGTCACATGCGCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC 3222
|||
Db 2160 TGGCAGAATCATAGCTCAGTGCAGCTCAAACTCCTGGGCTCAAGCCATCCTTCCACGTC 2219
|||

QY 3223 AGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCTGGCTAAATTAATAAAAT 3282
|||||
Db 2220 AGCCTCCAGGTAGCTGGGACTACAGGCACACACACACTGGCTAATTTTTTAAA- 2278
|||||

QY 3283 TTTTGTGAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAACTCCTGGCTTCA 3342
|||||
Db 2279 TTTTGTGAGAGATGAGGTCTCACTGTGTGGCCACGGTGATCTCGAACTCCTAGCCTCA 2338
|||||

QY 3343 AGCAATCCTCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTG 3402
|||
Db 2339 AGCGATCCTCCTGCTTCGGTCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCACTCC 2398
|||

QY 3403 CGGCTACTTATTTCTTTACATTCATCTTTCCAATA--GAATGTAAGATCCACAGAACA 3459
|||
Db 2399 TGGCCAGAGTTTATATGTATACTGTGGATACTAGATCCTCATGTGATTTGCAAAACTT 2458
|||

QY 3460 GGGATTACTGCCTATTTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCA 3519
Db 2459 TATTTATTATTATTATTTTGAATGGAATCTTGCTCTGTCTGCCAGGCTGGAGTGCA 2518
|||

QY 3520 A---CCTCCGTTACGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCCTCGCCT 3576
|
Db 2519 ATGGCGTGATCTCGGCTCACTGCAACTACCACTCTCGGTTCAAGCGATTTCGCTCGGT 2578
|||

QY 3577 AAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTGTGA 3636
|||
Db 2579 CAGCGTCTGAGTAGCTGGGACTACAGGGCGGCACCACCGCCAGCTAA-TTTTGTGA 2637
|||

QY 3637 TTTTACGAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCA 3696
|||||
Db 2638 TTTTGTAGAGACGGGATTTCACTATGTTGGTGGGATGGTCTTGATCTCTTGACCTC- 2696
|||

QY 3697 AGTGATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGGTGAGTCACTGTGCC 3756
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Db 2697 -GTGATCCACCACCTCGGCCTCCCATAGTCTGGGATTACAGGTGTGAGCCACCGCACT 2755
|||||

QY 3757 TGGCCGATTACTGTCTATTTTCTTTATTTGCTATATCCCCAGATCTAGAGCAGTGTC 3812
|||||

Db 2756 CAGCTGATTTGCAAAACTTTCTTCCATACTGTGTGTTTCACTTTCTGGATAGTGTC 2811
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RESULT 50
CN359768/c

LOCUS CN359768 718 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000418008134 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN359768
VERSION CN359768.1 GI:47359702
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 718 Std Error: 0.00.

FEATURES
source Location/Qualifiers
1..718
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_lib="GRN_ES"
/note="oligo dT-primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN
Query Match 5.6%; Score 279.2; DB 7; Length 718;
Best Local Similarity 68.1%; Pred. No. 2.1e-14;
Matches 403; Conservative 0; Mismatches 188; Indels 1; Gaps 1;

QY 514 TGTGCCCCAGGCTGGAGTGGGTGGCGTGATCTCAGATCACTACAACCTCCATCTCCTGG 573
|||
Db 690 TGTGCCCCAGGCTGGAGTGCAATGGCGGATCTCAGCTCATCACAACTCCGCTCCTGG 631
|||

QY 574 GTTCAAATAATTCTTGCCTCAGCCTCTCAAGTAGCTGGGACTTGTAGCTTCAAGTAG 633
|||||
Db 630 GTTCAAGTGATTCTGCTGCCTCAGCTTCCTGAGTAGTTGGGACTACAGGCATGTGCCACC 571
|||||

QY 634 CTGGCACACACCACCATGCCAGCTAATTTTGTGTGTTTTTTTGGTAGACAGGTT 693
|||

Db 570 ATGCCTGGCTAATTTGTATTTCGTAGAGATGGGTTTCTCCAATGTTGTCAGGCTGGTCT 511
|||

QY 694 TTCACCATGTTGGCCAGGCTGGGTGACCTCCCTTTTAGATTCTCCTCATCCTGCTTATT 753
|||

Db 510 TGAACCTCCCGACCTCAGTTGATCTGCCCCGCTCAGCCTCTCAAAGTCTGAGATTACAGG 451
|||

QY 754 CTTCCCTTTCTAATGCAGTATCCA-GTTTCCTTACTTATCACATTTATTATTATTCTTA 812
|||

Db 450 CATGAGCCATCATGCCCCGCCCAATACATTACTTCTTTTCTTTTCTTTTCTTTT 391
|||

JOURNAL COMMENT

Map Building
Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source

location/Qualifiers

1..658

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="2546H6"

/sex="male"

/cell_type="sperm"

/clone_lib="CITBI-E1"

/note="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"

ORIGIN

Query Match 5.6%; Score 278.8; DB 9; Length 658;
Best Local Similarity 68.5%; Pred. No. 2.4e-14;
Matches 462; Conservative 1; Mismatches 168; Indels 43; Gaps 4;

QY 3104 TTTT TTTT TTTT TTTT GTTGTGTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCACAGT 3163
|||||
DB 12 TTTT TTTT TTTT TTTT TTTTGAGACGGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGT 71
|||||

QY 3164 GGTGCAACCATAGGTCACCTGCAGCCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 3223
|||
DB 72 GGCATGATTCGGCTCACTGC AACCTCTGCCTCCCGGTTCAAGCGATTCTCCTGCCTCA 131
|||||

QY 3224 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACCGCTGGCTAATTA AAAAATT 3283
|||||
DB 132 GCCTCCCAAGTAGCTGGGACTAGAGGTGTGCGCCACCAACCGCGGAGTTTCTCGA--T 189
|||||

QY 3284 TTTTGTAGAGACTGGGTCTTACTAGCTTGGCCAGGCTTGCTTTAAACTCCTGGCTCAA 3343
|||||
DB 190 TTTTAGTAGAGATGGGTTTTCACCATGTTGGTCAGGCTGGTCTCGATCTGTGACCTC-- 247
|||||

QY 3344 GCAATCCTCCTACCTTGGCATCCCAAAGTGTCTGGGATTACAGGGTGAGCCACCATGTGC 3403
|||
DB 248 GTAATTCTCCTGCCTTGGCCTCCCAAGTGTCTGGGATTACAGGCGTGAGCCACTTGCGCC 307
|||||

QY 3404 GGCTACTTATTTCTTTACATTCCATCTTTC CAATAGATGTAAGATCCACAGAACAGGGA 3463
|||
DB 308 AGCCCCGGCCCTCTTTT TTTT TTTT TTTT TTTTCCGAGGGGAGTTTCGC----- 357
|||||

QY 3464 TTACTGCCATATTTCTTCTCTTTCTTTT TGAGACAGAGTCTCACTTCATCACCTCAACCT 3523
|||
DB 358 -----TC TTGTGCCCCAGGCTGAGTGCA GTGGTGC GATC- 392
|||||

QY 3524 CCGTTCACTCACTGCAACCTCTGCCTCCCGGTTCAAGYATTCTCCTGCCTAAGCCTC 3583
|||
DB 393 ----TCGGCTCACTGCAACCTCTGCCTCCCGGTTTCAAGTGATTTCTCCTGCCTCAGTCTC 448
|||||

QY 3584 CTGAGTAGCTGGAATTACAAGCGTGCACCAACCATGCTTGGCTAAATTTT TGTATTTTAG 3643
|||||
DB 449 ACGAGTAGCTGGGATTACAGGTGTCCGCCACCAACCCCGAGCTAAATTTT TGTATTTTAG 508
|||||

QY 3644 CAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC 3703
|||
DB 509 TAGAGTAGGGGTTTACCATTTTGGCCAGGTTGGTCTCGAACTCCTGACCTCAGGTGATC 568
|||||

QY 3704 TGCCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGCGTGAGTCACTGTGCCTGGCCGA 3763
|||
DB 3704 TGCCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGCGTGAGTCACTGTGCCTGGCCGA 3763
|||

Db 569 TACCTGCCTCGGCCTCCCAAAGTGCTAGGATTATAGGTGTGAGCCACCACACCGCGCCCC 628

QY 3764 TTACTGTCTATTTT 3777
|||
DB 629 CATTTTGTATTCT 642
|||||

RESULT 53
BM906989/c
LOCUS
DEFINITION
BM906989 1064 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6622443 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5735027
5', mRNA sequence.
ACCESSION
BM906989
VERSION
BM906989.1 GI:19357368
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 1064)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12741 row: e column: 12
High quality sequence stop: 697.

FEATURES
source

location/Qualifiers

1..1064

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5735027"

/tissue_type="hippocampus"

/lab_host="DH10B"

/clone_lib="NIH_MGC_124"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
(destroyed); Site_2: NotI; RNA source male hippocampus,
age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."

ORIGIN

Query Match 5.6%; Score 277.8; DB 3; Length 1064;
Best Local Similarity 72.0%; Pred. No. 2.1e-14;
Matches 427; Conservative 0; Mismatches 142; Indels 24; Gaps 4;

QY 514 TGTGCCCCAGGCTGGAGTGGGTGGCGTGATCTCAGATCACTAACCTCCTCCT-G 572
|||
DB 769 TGTGCCCCAGGCTGGAGTGCAGTGGTGTGATCTCGGCTCACCGCAACCTCCGCTCCCGG 710
|||||

QY 573 GGTTCAAATAATTCTCTTCCTCAGCCTCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTA 632
|||||
DB 709 GGTTCGAAGCGATTCTCTGCCTCAGCCTTCAGTAGCTGGGA-----TT 665
|||||

QY 633 GCTGGCACACACCACCATGCCAGCTAATTTTGTGTGTTTTTTTGGTAGACAGGT 692
|||
DB 664 ACAGGCATGGCCACCATGCCCGCTAATTTT-----TTATTTTAGTAGACAGGG 612
|||||

QY 693 TTTCACCATGTTGGCCAGGCTGGGTGACCTCCCTTTTAGATTCTCCTCATCTCTTAT 752
|||||
DB 611 TTCTCCACGTTGGTCAGGCTGGTCTCAAACCTCCGACCTCTGGTGATCCACCGCCTCA 552
|||||

Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match	5.6%	Score 277.6;	DB 9;	Length 877;
Best Local Similarity	66.7%;	Pred. No. 2.5e-14;		
Matches 467;	Conservative	1;	Mismatches 180;	Indels 52

QY	3070	AGATCACACAGCTTGTAAAGTGGTGACAGATTGGGTTTTTTTGTGTTGTTTAGAGACA	3129
Db	682	ATAACACTCCCAGTAATGAATGTCITTTTGTGTTTATTTTGTGTTTTTTTGTGAGACA	623
QY	3130	GGGTCTTGCTGTCAACCAGGCATGAGCAGTGGTGCAACCATAGGTCACTGCAGCCT	3189
Db	622	GAGTCTCACTTTGATGCCAGGCTGGAGTACAGTGGTGCAATCTCAGTCACTGCAACCT	563
QY	3190	CAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCCTCCCAAGTAGTGGGACTACGAG	3249
Db	562	TGCGCTCCAGGTTCAAGCAATTCCCTTGCCCTCAGCCTCCCAACTAGTGGGACTACAGG	503
QY	3250	CGTGCAACACCGCCTGGCTAATTAAAAAAAATTTTTTGTAGAGACTGGGTCTTACTAC	3309
Db	502	TGCCTGCCACACGCCCCAGCTAATTTTATA--TTTTTAGTAGAGACAGGGTTTCACCAT	445
QY	3310	GTGGCCAGGCTTGCTTTAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAA	3369
Db	444	GTTGGCCAGGCTTGCTTTGAACCTCCTGACCTCAGCGCATCCGCTAGCCTTGGCCTCCCAA	385
QY	3370	AGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTTACATTCCATC	3429
Db	384	AGTGTGGGATTATAAGCGTGAGCCACCGCACCCAACCAAGTAATTTTTTTTTTTTTT---	330
QY	3430	TTTCCAATAGAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTCTCTTCTTT	3489
Db	329	-----TTTTTGAGATGGAGTC	314
QY	3490	TTTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCC	3549
Db	313	TCACTCTGTACCCAGGCTGGAGTGCA GTGGCACGATCTTGGCTCACCGCAACCTCTGCC	254
QY	3550	TCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGC	3609
Db	253	TCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAATACGGGCACGT	194
QY	3610	ACCACCATGCTGGCTAATTTTTTTGTATTTTAGCAGAGATGGGGTTTACCATGTTGCC	3669
Db	193	GCCACCATGCCCGCTAA-TTTTTGTATTTTAGTAGAGACAGGGTTTCGCCATGTTGTC	135
QY	3670	CAGGCTGGTCTCAAACCTCCTGACCTCAAGTGATCTGCCCTGCCTCAGTCTCCCAAAGTGCT	3729
Db	134	CAGGGTTGTCTCGAACTCCTCACCTCAGGTGATCTGCCCTACCTCAGCCTCCCAAAGTGCT	75
QY	3730	GGAATTTATAGGCGTGAGTCACTGTGCTTGGCCGATTACTG	3769
Db	74	GGGATTATAGGCATGAGCCACCACATCTGGCCCCAGTAATG	35

RESULT 55	ACCESSION	REFERENCE
CR751077/c	VERSION	
LOCUS	KEYWORDS	
DEFINITION	SOURCE	
	ORGANISM	

AUTHORS Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

TITLE Pongo pygmaeus mRNA (Poustka,A., Albert,R., Moosmayer,P., et al.)

JOURNAL Unpublished (2004)

COMMENT Contact: MIPS

MIPS ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp459E1634

Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES Location/Qualifiers

source 1..711

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

/clone="DKFZp459E1634"

/tissue_type="cortex"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="459 (synonym: pcor1)"

/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

ORIGIN

Query Match 5.6%; Score 277.4; DB 7; Length 711;

Best Local Similarity 66.9%; Pred. No. 3e-14;

Matches 435; Conservative 0; Mismatches 211; Indels 4; Gaps 3;

QY 444 CATTTATTATTTTATTTTAAATTTTATTTTATTTTATTTTACTTTATTTTATTTTGAGACG 503

Db 650 CCTGAATTGATCTTGAGGTTTTTTTAAATTTTTTATTTATTTTATTTTATTTTATTTTATA 591

QY 504 GGGCTCACTGTGCGCCAGGCTGGAGTGGGTGGCGTGATCTCAGATCACTACAACTC 563

Db 590 TTTTTATTCTGTGCGCCAGGCTGGAGTGCAATGACACAATCTCGTCTCACTGCAACCTC 531

QY 564 CATCTCCGGTTCAAATAATTCTCTGCCTCAGCCTCTCAAGTAGCTGGGACTTGAGC 623

Db 530 CAGCTCCCGGTTCAAGCAATTCTCTGCCTCAGCCTCCTGAGTAGCTGGATTACAGGT 471

QY 624 TCTCAAGTAGCTGGCACACACCACCATGCCAGCTAAATTTTGTGTGTTTTTTTGGTA 683

Db 470 GACCGCCACCACACCCAGCTAAATTTTTTATTATTTTAGTAGAGATGGATTTTGCCATGT 411

QY 684 GAGACAGGTTTTCACCATGTTGGCCAGGCTGGTGACCTCCCTTTTAGATTCTCCTCATC 743

Db 410 TGGCCAGGCTGATCTCGAACTCCCGACCTCAGGTGATCCGCTGCCTTGGCCTCCCAAAG 351

QY 744 CTGCTCTATT-CTTCCCTTTCTAATGCAGTATCCAGTTTCTTACTTATCATATTATT 802

Db 350 TGTCTGGGATTACAGACATAGAGCCACCGCACCCGCGCGATTCTTGAGTTTT--TTTTGT 293

QY 803 ATTATTCTTATTATTATTGAGACAGATCTTGCTTTGTCGCAAGGCTGGAGTACAGTGG 862

Db 292 TTTGTTTTTGTTTTTTTGAGACAGATCTCGCTGTGATGCCAGGCTGGAGTGCAGTGG 233

QY 863 TGGGATCTCGGCTCACTGCAAGCTCCACCTGTGCGTTACGCCCATTTCTCCGCGCTCAGC 922

Db 232 TGTGATCTCGGCTCACTGCAAGCTCCACCTCCTGGGTTCAACCATTTCTCTGCATCAGC 173

QY 923 CTCCCCAGTAGCTGGGACTAAAGGCGCCTGCCACCACCGCCCGCTAATTTTTTTGTATT 982

Db 172 CTCCTGAGTAGCTGGGACTACAGGCGCCACACCATGCCAGCTAA-TTTTTTGTATT 114

QY 983 TTAATAAAGACGGGGTTTCATCTGTGTAGCCAGGATGGTCTCGATCTCATGACCTGTGA 1042

Db 113 TTAGTAGAGATGGGGTTTCACCGTGTAGCCAGGATGGTNTCAATCTCCTGACNTGGTGA 54

QY 1043 TCCGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACC 1092

Db 53 TCCGCNTGCCTCAGTCTCCCAAAGTGCTAGGATTACAGGCATGAGCCACC 4

RESULT 56

BQ898614/c

LOCUS BQ898614

DEFINITION AGENCOURT 8642570 NIH_MGC_113 Homo sapiens cdna clone IMAGE:6295801 5', mRNA sequence.

ACCESSION BQ898614

VERSION BQ898614.1 GI:22290628

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 893)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCM2502 row: k column: 02

High quality sequence stop: 612.

FEATURES Location/Qualifiers

source 1..893

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6295801"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_113"

/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 5.6%; Score 277.4; DB 5; Length 893;

Best Local Similarity 66.4%; Pred. No. 2.5e-14;

Matches 452; Conservative 0; Mismatches 208; Indels 21; Gaps 3;

QY 471 ATTTTATTTTACTTTATTTTATTTTGTGACGGGCTCACTCTGTGCGCCAGGCTGGAG 530

Db 832 ATATTTTATTTTAAATAATTTATGTGAGACAGGGTCTTGCTCTGGCACTCAGGCTGGAG 773

QY 531 TCGGGTGGCGTGATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAATAATTCTCT 590

Db 772 TGCAGTGGCGCAATCACAGCTCTCTGCAGTCTGGATCTCCTGGGCTCAAGGATCCTCCC 713

QY 591 GCCTCAGCCTCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACCAT 650

Db 712 ACNTCAGCCTTTGGAGAAAGCTGGGACT-----ATAGACATGTGCCACCAT 668

QY 651 GCCCAGCTAATTTTGTGTGTTTTTTTGGTAGAGACAGGTTTTTCACCATGTGGCCAG 710

Db 667 GCCCAGTTAATATAGT-TTTAAATAATTTTTGTAGAGACATGGTTTGCCATGTGCNCAG 609

QY 711 G-----CTGGGTGACCTCCCTTTTAGATTCTCCTCATCCTGCTCTATTCTCCCTTTCT 765

Db 608 GTTGATCTTGAACCTCTGGCTCAAATGTATCCACACAGCTCTTGGCCTCCCAAAGTGGGAGA 549

QY	766	AATGCAGTATCCAGTTTCCTTACTTATCACATTTATTTATTTCTTATTTATTTGAGAC	825
Db	548	TTATAGGGGTGAGCCACTGTGCTCAGCCTGAACATTTTATTTCTATTTTATTTTGGAGAC	489
QY	826	AGAGTCTTGCCTTTGTGCGCCAAAGGCTGGAGTACAGTGGTGGGATCTCGGGCTCACTGCAAGC	885
Db	488	GGAGTCTCGCTCTTCGCCCCAGGCTGGAGTGCAGTGGGGTGATCGCTGCTCACTGCAAGC	429
QY	886	TCCACCTGCTGGGTTCACGCCATTCTCCCGCCTCAGCCTCCCCAGTAGCTGGGACTAAAG	945
Db	428	TCCGCCCTCCAGGTTACGGCTATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAG	369
QY	946	GCGCCTGCCACACAGCCCCGCTAAATTTTTTTGTATTTTAAATAAGACGGGGTTTCATCG	1005
Db	368	GCGCCCGCCACACACCTTGGCTAAATTTTTTTTATTTTAGTAGACACGGGGTTTCACCA	309
QY	1006	TGTTAGCCAGGATGGTCTCGATCTCATGACCTTGTGATCCGCCCTCGCCTCCCAAA	1065
Db	308	TGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCTGCCCTCAGCCTCCCAAA	249
QY	1066	GTGCTGGGATTACAGGCATGAGCCACCGTGCCCGGCCCTTATCACATTTATTTATTATTGT	1125
Db	248	GTGCTGGGATTACAGGTGTGAGCCACCGCGCCCTTGCAACATTTTATTTTTTAAAAAATTA	189
QY	1126	TTTTTCTCTCCCACTAGGTTGT	1146
Db	188	AATTTAATAACTCATTTGTAGT	168

RESULT 57					
BX644719/c					
LOCUS	BX644719	782 bp	mRNA	linear	EST 04-SEP-2003
DEFINITION	DKFZp781N1434_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone DKFZp781N1434 5', mRNA sequence.				
ACCESSION	BX644719				
VERSION	BX644719.1 GI:34479052				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.				
REFERENCE	1 (bases 1 to 782)				
AUTHORS	Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S. EST (Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., et al.) Unpublished (2003)				
TITLE					
JOURNAL					
COMMENT	Contact: MIPS				
	MIPS				

ORIGIN

Query Match	5.5%;	Score 277.2;	DB 5;	Length 782;	
Best Local Similarity	69.8%;	Pred. No. 2.9e-14;			
Matches 444;	Conservative	0;	Mismatches 163;	Indels 29;	Gaps 4;
Qy	488	TTTTATTTTGTGAGACGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCGTGATCTC	547		
Db	745	TTTTTTTTTTGAGACAGAGTCTCGCTCTGTGTGCCAGGCTGGAGTGGGTGGCACAATCTC	686		
Qy	548	AGATCACTACAAACCTCCATCTCCTGGGTCAAATAATTCTCTTGCCCTCAGCCTCTCAAGT	607		
Db	685	GGTCACTGCAACCTCCGCCCTCCCGGTTCAAGTGATTCTCTCTGCTCAGCCTCCTGAGT	626		
Qy	608	AGCTGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACCATGCCAGCTAAATTTTGTG	667		
Db	625	AGCTGGACT-----ACAAAGGCCCGCCACCACGCCAGCTAAATTTTGTG	581		
Qy	668	TGTGTTTTTTTGGTAGAGACAGGTTTTTCACCATGTTGGCCAGGCTGGGTGACCTCCCTT	727		
Db	580	-----CATTTTAGTAGAGACAGGTTTCACCATGTTGGCCAGGATGGTCTCGATCTC--	528		
Qy	728	TTAGATTCTCTCATCTGCTCTATTCTTCCCTTTCTTAATGCAGTATCCAGTTTCCTTA	787		
Db	527	-----TTGACCTCGTGATCCACCTGCCTCGGCCCTCCCAAAGTCTGGAATTATAGGCGTG	473		
Qy	788	CTTATCACATTTATTATTATTCTTATTATTATGAGACAGAGTCTTGCTTTGTGCGCAAG	847		
Db	472	AGTCACCGTGCCGGCCTTTTTTTTTTTTTTTTGGAGATGGAGTCTTGCTCTGTCGCCCAG	413		
Qy	848	GCTGGAGTACAGTGGTGCATCTCGGCTCACTGCAAGCTCCACCTGCTGGGTTACGCCA	907		
Db	412	GCTGGAGTGGAGTGGCATGATCTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGTGA	353		
Qy	908	TTCTCCGCCCTCAGCCTCCCGAGTAGCTGGGACTAAAGGCGCCTGCCACACGCCCCCGCT	967		
Db	352	TTCTCCGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGCCCGCTACCACGCCTGGCT	293		
Qy	968	AATTTTTTTGTATTTTAAATAAGACGGGTTTCATCGTGTTAGCCAGSATGGTCTCGAT	1027		
Db	292	AATTTTTTTGTATTTTGTAGTAGACGGGTTACACCATGTTGGCCAGSGTGGTCTCAAA	233		
Qy	1028	CTCATGACCT--TGTGATCCGCCCTGCCTCGGCCCTCCCAAAGTGTCTGGGATTACAGGCATG	1085		
Db	232	CTCCTGACCTCAGGTGATCCATCCGCCCTCAACCTCTCTAAAGTGTCTGGGATTACAGGCTTG	173		
Qy	1086	AGCCACCGTGCCCGGCCTTATCACATTTATTATTTA	1121		
Db	172	AGCCACTGTGCCTGGCCCAAAGCCAGGATTTCTTTA	137		

RESULT 58	AQ743787/c
LOCUS	AQ743787 942 bp DNA linear GSS 16-JUL-1999
DEFINITION	HS_5501_A1_E07_T7A_RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1077 Col=13 Row=I, genomic survey sequence.
ACCESSION	AQ743787
VERSION	AQ743787.1 GI:5521309
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 942)
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED	10449764
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1077 row: I column: 13
Seq primer: T7
Class: BAC ends
High quality sequence stop: 942.
Location/Qualifiers
1. .942
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=1077 Col=13 Row=I"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

FEATURES

source
Query Match 5.5%; Score 277.2; DB 9; Length 942;
Best Local Similarity 70.4%; Pred. No. 2.6e-14;
Matches 452; Conservative 0; Mismatches 163; Indels 27; Gaps 5;

486 TATTTTATTTTGAGACGGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCGTGATC 545
|||||
824 TTTTTTTTGGAGACGGCGTCTCACTCTGTCACCCAGGCTGGAGTGCAATGGCGTGATC 765

546 TCAGATCACTACAACCTCCATCTCCTGGGTTCAAATAATTCTTGGCTCAGCCTCTCAA 605
|||||
764 TCGGCTCACTGCAACCTCTGTCTCCGGGTTCAAGTGATTCTCTCGCTCGGCCTCCCGA 705

606 GTAGTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACCATGCCAGCTAATTTT 665
|||||
704 GTAGCTGGGA-----TTACCCGCATGTGTATCATCAGCCTGGTTAATCT- 661

666 TGTGTGTTTTTTTGGTAGAGACAGGTTTTACCATGTTGGSCAGGCTGGGTGACCTCCC 725
|||||
660 -----ATATTTTATTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGCTTGAATC 607

726 TTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCTTTCTAATGCAGTATCCAGTTTCCT 785
|||
606 CCGACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAAAGTGTGGGATTACAGGTGTAGC 547

786 TACTTATCACATTTATTATTCTTATTATTATTATTAGACAGAGTCTTGCTTTGTCGCCA 845
|||
546 CACCACACCCTTTTTTTTTTTTTTTTTTTTTTA---AGATGGAGTCTTGCTCTGTCGCC 490

846 AGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGTTACGC 905
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RESULT 59
BC009270 1875 bp mRNA linear HTC 04-MAR-2003
LOCUS Homo sapiens, Similar to hypothetical protein PRO1722, clone
DEFINITION IMAGE:3342760, mRNA.
ACCESSION BC009270
VERSION BC009270.1 GI:14627272
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1875)
Strausberg,R.
Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letitia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 22 Row: j Column: 8
This clone has the following problem: retained intron.
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/tissue_type="Eye, retinoblastoma"
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Best Local Similarity 67.6%; Pred. No. 1.6e-14;
Matches 460; Conservative 1; Mismatches 189; Indels 30; Gaps 4;

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3175 AGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGCCTCCCAAGT 3234
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3235 AGCTGGGACTACGAGCGTGCACCACCACCGCCTGGCTAATTAATAAAATTTTTTGTAGAG 3294
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Qy 3295 ACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCT 3354

Db 1026 ATGGGGTTTCAACCATATTGGCCAGGCTGGTCTTTGAACCTCTGACCTCAAGTGATCGGCT 1085

Qy 3355 ACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATT 3414

Db 1086 GCCTTGGCCTCCCAAAGTCTGGGATTACAGGGGTGAGCCACCGTGCCCATCCAACCTAA 1145

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Db 1189 TTTTTTTTTTGTAGACAAATCTGTGTACCCCGGCGAGTGCGTGGTGG 1248

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Qy 3585 TGAGTACGCTGGAATTACAAGCGTGCACCACTGCTTGGCTAAATTTTGTATTTTAGC 3644

Db 1309 CGAGTAGCTGGGATTACAGGTGTGGGCCACCAACCCGGCTAA-TTTTGTATTTTAGT 1367

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RESULT 60

BI868328

LOCUS BI868328 744 bp mRNA linear EST 11-OCT-2001

DEFINITION 603392289F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402038 5', mRNA sequence.

ACCESSION BI868328

VERSION BI868328.1 GI:16042001

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 744)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM12025 row: b column: 23

High quality sequence stop: 741.

Location/Qualifiers

1. .744

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/mol_type="mRNA"

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/clone="IMAGE:5402038"

FEATURES

source

/tissue_type="adenocarcinoma, cell line"

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/clone_lib="NIH_MGC_90"

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ORIGIN

Query Match 5.5%; Score 276.8; DB 3; Length 744;

Best Local Similarity 71.5%; Pred. No. 3.2e-14;

Matches 455; Conservative 0; Mismatches 157; Indels 24; Gaps 6;

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Qy 537 GGCGTGATCTCAGATCACTACAACCTCCATCTCCTGGGTTCAAATAATCTCTTGCCTCA 596

Db 142 GGCGGATCTCGGCTCACTGCAAGCTCCGCCTCTCGGGTTACGCCATTCTCTGCCTCA 201

Qy 597 GCCTCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCATGCCCAG 656

Db 202 GCCTCCCAAGTAGCTGGGACT-----ACAGGCGTCTCTCCACCATGCCTGG 246

Qy 657 CTAATTTTGTGTGTTTGTGGTAGAGACAGGTTTTCACCATGTTGGCCAGGCTGGG 716

Db 247 CTAATATTT---GGTATTTTGTAGTAGACGGGGTTTCACCGTGTTAGCCAGGAT-GG 301

Qy 717 TGACCTCCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCCCTTTCTAATGCAGTATC 776

Db 302 TCTCGATCTCCTAACCTGGTGATCCGCCCGCTCGGCCCTCCCAAAGTATGGGGATTACCC 361

Qy 777 CAGTTTCCTTACTTATCACATTTATTATTATTTCTTATTATTAT-TGAGACAGAGTCTTGC 835

Db 362 GCGTAGCCACCGCGCCCGGCTGCAAATAATCTTTCTTTTCTTGAGACAGAGTCTCGC 421

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Db 542 CACCACGCCCCGTTAACTTTTGGGGTTTTCAGTAGAGACGGGGTTTCACCCGTGTAGCC 601

Qy 1014 AGGATGGTCTCGATCTCATGACCTTGTGATCCGCCTGCCTCGGCCCTCCCAAAGTGCCTGGG 1073

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Qy 1074 ATTACAGGCATGAGCCACCGTGCCCGGCCTTATCAC 1109

Db 661 ATTACAGGCGTGAGCCACCGCGCGGGGCGAAACAC 696

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Job time : 12171 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2006, 12:01:43 ; Search time 577 Seconds
(without alignments)
15406.561 Million cell updates/sec

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Perfect score: 4997.8
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
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4	434	8.7	304533 3 US-09-949-016-15372 Sequence 15372, A
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20	415	8.3	45299 3 US-09-949-016-12465 Sequence 12465, A
21	415	8.3	45300 3 US-09-949-016-13045 Sequence 13045, A
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C	86	369.6	7.4	47030	3	US-09-949-016-13038	Sequence 13038, A
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Qy 3713 CAGTCTCCCAAAGTGTGGAATATATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCT 3772
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
8450 CAGCTCCCAAAGTGTGGGATAACAGGCATAAGCTGCTGCGTGCAGCCTTTCTGTATTC 8509

Qy 3773 ATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCA 3832
Db      || | || | || | || | || | || | || | || | || | || | || | || | || |
8510 TTTATTCTGTTTCATTGATCTGTTCTCTTTTGGTTTTCAGTATCATACTATTTTGTGTTGT 8569

Qy 3833 ATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTAAACAA 3892
Db      || | || | || | || | || | || | || | || | || | || | || | || | || |
8570 TTCTATAGCTTAAAAATATGTATTT--TTTGTAGATAGGTTCTCACTGTGTACCCAG 8626

Qy 3893 TCTTGACAACTTTGCAGAAATAATACAAATCTTGCAATCTGCTTTTTCATTAATCAGCTG 3952
Db      || | || | || | || | || | ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
8627 GCTGGAGTGTAAGTGTGATCATGGCTCAGTGCATCCTCAACCTCCTATACTCA-ATG 8685

Qy 3953 TTAATGACTTTTTCATAATTGCCCTCAAACTTTATTTGTTACTGTTTTCATTTGTTACTATT 4012
Db      || | || | || | || | || | || | || | || | || | || | || | || | || |
8686 ATCCTCCACCTCAGCCTCCCAAGTAGCTGCACCACCATGTTTGGCTAAATTTTAAATTT 8745

Qy 4013 TTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAGG 4072
Db      || | || | || | || | || | || | || | || | || | || | || | || | || |
8746 TTTGTAGAAACAGAGTCTTGGCATGTACCCAGGCTGGTCTTGAACCTCCTGGGCTGAAG- 8804

Qy 4073 CCAATTTACAAATCTGATGAAGCTATGAACCTCTCCCCAGAGAAATACACACACACA 4132
Db      || | || | || | || | || | || | || | || | || | || | || | || | || |
8805 --AGATCCGCTGACCTCATCTCCCAAAGTGTGGAATTACAGGTGTGCACCACTTGCC 8862

Qy 4133 CACACACTCACACACAGTTTTTTTTTAATGTTTGTCAACTAAGACAAGAA-----ACC 4184
Db      || | || | || | || | || | || | || | || | || | || | || | || | || |
8863 CAGCCAAAAATATGTTTTTGGCAGATCACCTGAGGTCCGGAGTTCAAGACCAGCCTTGCC 8922

Qy 4185 TGCAATAGAGGATGTTTGTTCATATTAATTAATAATAACTCAGTTGGGCACAGTGACTCA 4244
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
8923 AACATGGCAAAACCTTGCTCTACTAAAGAAATACAAAAATATATCTGGCGCAGTGGCTCA 8982
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Qy 4245 AGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCATTGAGGTGAGAAGTT 4304
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
8983 TGTCTGTAAATCCAGTACTCTGGAAGGCCAAGGCAGGTGGATCACCTGAGTCAAGGAGTT 9042

Qy 4305 CGAGACCAGCCTGTTCAATATGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCT 4364
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
9043 TAAGACCAGCCTGGCAAACCTGGTGAACCCCTGTCTCTACTAAAAATACAAAAATTAGCT 9102

Qy 4365 GGGTGTAGTATGATGATGCTGCTGTAGTCCCAGTACTCGGGAGGCTGAGGCAAGAGAAATTGC 4424
Db      || | || | || | || | || | || | || | || | || | || | || | || | || |
9103 GGGCGTGGTGACCGGTGCTGTAAATCCCAGCTACTCAGGAGGCTGAGGCAGAGAAATCAC 9162

Qy 4425 TTGAACCTGGGAGCAGAGGTTGCAGTGAAGCCGAGATCCCACCACCTGCACCTCCAGCCTGG 4484
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
9163 TTGAACCTGGGAGTAGAGGTTGCAGTGAAGCCGAGATCATGCCATTGCCACTGTAGCCTGG 9222

Qy 4485 GCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAATAA 4530
Db      || | || | || | || | || | || | || | || | || | || | || | || | || |
9223 GTGACAGAGCGAGATTCTGTCTCAAAAAAGAAAAAAGAAAAA 9268

RESULT 2
US-09-949-016-16064
; Sequence 16064, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16064
; LENGTH: 70131
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16064
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Query Match      8.9%;      Score 444.4;      DB 3;      Length 70131;
Best Local Similarity 54.1%;      Pred. No. 3.1e-91;
Matches 1225;      Conservative 3;      Mismatches 987;      Indels 51;      Gaps 14;
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Qy 2291 AGCCAGGCGGTGGCTCATGCCTGTAATCCAGCAGCTTTTGGAGGCCGAGGCGGCGG 2350
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
12682 AGCCAGGCGGTGATGGCTCATGCCTGTGATCCAGCAGCTTTGGGAGGCCAAGTGGTGG 12741

Qy 2351 ATCACTTGAGTCAAGGATTCGAGACCAGCCTGGCCAAACATGGTGAAACCCCTGTCTCTAC 2410
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
12742 ATCAGTGAAGTCAGGATTTGAGAACAGCCTGGCCAAACATGATGAAACCTTTGTGCCAC 12801

Qy 2411 TAAAAAATACAAAAATTAGCCGACATGGTGGGAGCGCC-----TGTAACCCAGCTAC 2465
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
12802 T-AAAAAATACAAAAATTAGTGGCCGTGGTGGCAGACACCTATAGTCTAGTCTAGCTAC 12860

Qy 2466 TTGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCAAAGGTGCTGTCACTGTGTCCAGCCTGG 2525
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
12861 TTGGGAGGCTGAGGCGGGAATCGTTTGAACCCGGAGGTAGAGGCTGAAGTGAGCTGAG 12920

Qy 2526 GTAACAGAGCAACTCTGTCTCAAA---AAAAAATAATGCTTTCAATAAATATATATATAA 2581
Db      || | || | || | || | || | || | || | || | || | || | || | || | || |
12921 ATCACACCACCTGCCTCCAGCCTAGGTGACAGAGCAAGCCTCATCTCAAAAAACAATG 12980

Qy 2582 AAGGACTTATATTTTTCAGGCCATAGGATCATTTCTCCTGAAGCATCTTGGCGAAGTCA 2641
Db      || | || | || | || | || | || | || | || | || | || | || | || | || |
12981 GTGGCCAGGCACGGTGGCTCAGTCAAGTATCCAGCAGCTTTTGGGAGGCCAAGCGGGC 13040
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15371
; LENGTH: 304533
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(304533)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15371

Query Match      8.7%; Score 434; DB 3; Length 304533;
Best Local Similarity 54.3%; Pred. No. 1.4e-88;
Matches 1269; Conservative 3; Mismatches 968; Indels 96; Gaps 16;

Qy 2279 AAAATCGCTTTTCAGGCCAGGCGCGGTGGCTCATGCTGTAAATCCAGCACCTTTGGGAGGC 2338
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2339 CGAGGCGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGTGRAA 2398
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 257379 CAAGGCAGGAGGATCGCTTGAAGCTAGGAGTTCTCAACCAGCCTGGGCAGCAAAAGCAAGC 257438
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2399 CCCTGTCTCTACTAAAAAATACAAA-----AATTAGCCGGACATGGTGGCGAGCG 2448
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2449 CCTGTAAOCCAGCTACTTGGGAGACT-----GAGTTGG 2482
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2483 AGTTTTCAGTGAGCCAAGGTCGTGTCACCTGTGTCCAGCCTGGGTAACAGAGCAACTCTG 2542
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 257559 AGTTTGCAGTGAGCTATGATCATGCCACTGCACCCAGCCTGGGCAGCAAGACTCCA 257618
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2543 TCTCAAAAAA-----ATGCTTTCAATAAATATATGATAAAAGGACTT 2589
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 257619 TCTTTAAAAAACAACACAGAGGTCAGGCACAGTGACTCACACCTGTAATCCCAGCACTT 257678
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2590 ATATTTTTCAGGCCATAGGATCATTTCTCCTGAAGCATCTTGGCGAAGTCATCCCCACC 2649
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 257679 TGGGAGGCAGGCAGGCAAATCACTTGAGCCTAGGAGTTTCGAGACCACCCTGGCCACA 257738
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2650 TGTTCTTGAGAGTGGCAGGTGAGGGTGACCTATTGCTGTGCACTTACTCCTATCTCAG 2709
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2710 CTGTCCTCCCACTTTCCAGGTGTGCCAGACACATGACAACTGTAYGACCAGGCCAAG 2769
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2770 AAGCTGGACAGCTG--TAAATTTCTGTGGACAMMCCGTACACCCACACCTATTTCATAC 2826
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 27859 GTTACAGTGAGCTGAGATCACACCACTGCACCTCCAGCCTGAGCAACAGAGCAAGTCTCAA 257918
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2827 TCGTGTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCCTTGACCTATGAA 2886
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 257919 AAAATAATAATAATAAAAAATAAATATGTCTTTATTTTTCACGAGCCACTAACTAAATTT 257978
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2887 TTCTAGTTGGTTCTCAGTAGGCCGGGGGAAATAATAGTAACAACAGCCATGATTTAGTG 2946
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 257979 TAACATTTCTCTCCATCTTAAAGGGAGATAACAAACCCCTTAGTATTAGTATTATCAACC 258038
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2947 TTAATTTTCTTGGTTCTGGGCAGTGTCTCCTTTAATCCTCAGA-----ACAACACT 2997
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 258039 TTAATATTATCAACA-TGACCTGTGTGCTTATATAAACATCAGATATTTTCATACTGCATT 258097
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2998 ATGGGATAGGPACAATATTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGGCTGA 3057
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 258098 ATAAGAGCTGCAGATACCTTAACATTTAATTTGCAATTCATCATGCTTTAAAAATGTTGCT 258157
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 3058 GCTATTTGCCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTGT 3117
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3118 TGTGATTAAACCTACAGCTAGAAATTTGTTACTCAGTGTTTTTTTTGTGTGTTCTGT-T 258216
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3178 TCACTGCAGCCCTCAACCTCCTGAGCTCAAGGGATCTGTGACCTCAGCCTCCCAAGTAGC 3237
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3238 TGGGACTACGAGCGTGCACCAACCAACGCGCTGGCTAATAAAAAAATTTTGTGTAGAGACT 3297
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3298 GGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACC 3357
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3358 TTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTCT 3417
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3418 TTACATTCCATCTTTCCAATAGAAATGTAAGATCCACAGAAACAGGGATTACTGCCTATTT 3477
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3478 CTTCCCTTCTTTTGTGACAGAGTCTCA-CTTCATCACCTCAACCTCCGTTCAGCTCAC 3536
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3537 TCGAACCTCTGCCTCCCGGTTCAAGYGATTCCTCCTGCCTAAGCCTCCTGAGTAGCTGGA 3596
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3597 ATTACAAGCGTGCAACCATGCTTGGCTAATTTTTTGTATTTTTTAGCAGAGATGGGGTT 3656
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3657 TTACCATGTTGCCAGGCTGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTGCCTCAGT 3716
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3717 CTCCCAAAGTCTGGAATTATAGGCGTGAGTCACTGTGCTGCGCTGGCCGATTACTGTCTATTT 3776
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3777 TCTTTATTGCTATATCCCCAGAT----CTAGAGCAGTGTCTGACATATAGTAGGTGCTCA 3832
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3833 ATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCTTTTTTTTAAACAA 3892
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3893 TCTTGACAACTTTGCAGAAATAAAATCAATCTTGCAATTCTGCTTTTTCACTTATCACCTT- 3951
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3952 -----GTTATGACTTTTTCATATTGCTCAAACTTTTATTGTTACTGTTTTT 3997
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3998 TTCATTGTTACTATTTTACTCACTGAATAATATGCTTAATTTGCTTATACATCCTCCTG 4057
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4058 CT-----CCACTTTAGAGGCCAAATTTACAATCTGATGAAAGCTATGAACCTCTCCCC 4112
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4113 CAGAGAAATAACACACACACACACTCACACAGATTTTTTTTTTAAATGTTTGCAACTA 4172
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Db 259231 CAGTGAGCCGAGATCTTGCCCACTGCACCTCCAGCCTGGGTGACAGAGTGAGACTCCATCTC 259290
Qy 4173 AGACAAGAA--ACCTGCATTAGAGGATGTTTGTTCATATTAAATTAAAAATAA ACTCAGTTG 4230
Db 259291 AATAAATAAATAAAATTAAATTAAATTAAATTAATAATTATTTTAAAAAAATTGGGGGCTG 259350
Qy 4231 GGCACAGTGA CTCAAGCCTGTAACCAACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACT 4290
Db 259351 AGTGTGATGGCTCACACCTGTAATCCCGCAGTTTGGGAGCTTGAGGAGGCGAGATCCCT 259410
Qy 4291 TGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAA 4350
Db 259411 TGAGGTGAGAGTTCAGACCAGCCTGGACAACATGGTGAACCCCGTCTCTACTAAAAA 259470
Qy 4351 TACAAAAATTAGCTGGGTGATGATGCATGCCTGTAGTCCCACTACTCGGGAGGCTGA 4410
Db 259471 TACAAAAATTAGCCAGGCATGGTGGCGTGTGCCTGTAATCCCACTACTCTCGTGAGGCTGA 259530
Qy 4411 GGCAAGAGAAATGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACT 4470
Db 259531 GGCCCAAGCATCGCTTGAACCTGTGAGCGGAGGTTGCAGTGAGCCAAAGATGGCACCACT 259590
Qy 4471 GCACTCCAGCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAAA 4526
Db 259591 GCACTCCAGCTGGGTGACAGAGTGAGACTTGTCTCAAAAAATAAATAAA 259646

RESULT 4
US-09-949-016-15372
; Sequence 15372, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15372
; LENGTH: 304533
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(304533)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15372

Query Match 8.7%; Score 434; DB 3; Length 304533;
Best Local Similarity 54.3%; Pred. No. 1.4e-88;
Matches 1269; Conservative 3; Mismatches 968; Indels 96; Gaps 16;
Qy 2279 AAAATCGCTTTCAGGCCAGCGCGGTGCATGCCCTGTAATCCAGCACTTTGGGAGGC 2338
Db 257319 AAAACTGAATCAGGCTGAGCACAGTGGCTCATGCCCTGTAATCCTAGCACTTCAGGAGGC 257378
Qy 2339 CGAGCGGGCGGATCACTTGAGGTCAGAGTTCGAGACCAGCCTGGCCAAACATGGTGAAA 2398
Db 257379 CAAGGCAGGAGATCGCTTGAAGCTAGAGTTCTCAACCAGCCTGGGAGCAAGCAAGC 257438
Qy 2399 CCCTGTCTCTACTAAAAATACAAA-----AATTAGCCGACATGGTGGCGAGCG 2448
Db 257439 CCCTGTCCCTACAAAAAATAAATTTTTTTTAAATTAGCCAGGCATGGTAACTCGTG 257498

Qy 2449 CCTGTAACCCAGCTACTTGGGAGACT-----GAGTTGG 2482
Db 257499 CCTGTAGTGCCAGTTACTCAGGAGGCTGAGGTGGGAAGATATTTTGAGCCCGAGGAGTGG 257558
Qy 2483 AGGTTTCAGTGAGCCAAAGGTCGTGTCACTGCTGCCAGCCTGGGTAACAGAGCAACTCTG 2542
Db 257559 AGTTGCACTGAGCTATGATCATGCCACTGCACCCAGCCTGGGCAACAGCAAGACTCCA 257618
Qy 2543 TCTCAAAAAAATAA-----ATGCTTTCAATAAATATATATGATAAAAGGACTT 2589
Db 257619 TCTTTAAAAAACAACACAGAGGTCAGGCACAGTCACTCACACCTGTAATCCCAGCACTT 257678
Qy 2590 ATATTTTTCAGGCATAGGATCATTTCTCTGAAGCATCTTGGCGAAGTCAATCCCACC 2649
Db 257679 TGGGAGGCAGAGGCGAGCAAAATCACTTGAGCCTAGGAGTTCGAGACCACTTGGGCAACA 257738
Qy 2650 TGTTCTCTGAGAGTGGCAGGCTGAGGCTGACCTPATTTGCTCTGCACCTTACTCCTATCTCAG 2709
Db 257739 TGGCAAAACCCCATCTCTACTATAAACTACAAAAAATTAGCCTGGCGTGTGTGGGTGCC 257798
Qy 2710 CTGTCCCTCCCACCTTCCAGGTGCTGCCAGACACATGACAACTGCTAYGACCAGGCCAAG 2769
Db 257799 CATGATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCCCAAAAGTGGAG 257858
Qy 2770 AAGCTGGACAGCTG--TAAATTTCTGCTGGACAMMCCGTACACCCACACCTATTTCATAC 2826
Db 257859 GTTACAGTGAGCTGAGATCACACCACTGCACCTCCAGCCTGAGCAACAGAGCAAGTCTCAA 257918
Qy 2827 TCGTGTCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCTTGACCTATGAA 2886
Db 257919 AAAAAATAATAATAAAAAATAATATGTCTTTATTTTTCACCAGCCACTAATAAATTT 257978
Qy 2887 TTCTAGTTGGTTCTCAGTAGGCGCGGGGGAATAATAAGTAACAACAGCCATGATTTAGTG 2946
Db 257979 TAACATTTCTTCCATCTTAAAGGGAGAGATAACAAACCCCTTAGTATTATATCAACCC 258038
Qy 2947 TTAATTTTCTTGGTCTGGGCAGTGTCTCCTTTTAATCCTCAGA-----ACAACACT 2997
Db 258039 TTAATATTATCAACA-TGACCTGTGTCACTTATAAACATCAGATATTTTCATACTGCATT 258097
Qy 2998 ATGGGATAGGTACAATATATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGGCTGA 3057
Db 258098 ATAAGAGCTGCAGATACCTTAACATTTAATTTGCAATTCATCATTTGCTTTAAAAATGTTCT 258157
Qy 3058 GCTATTTGCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTTGTTGT 3117
Db 258158 TGTGATTAAACCTACAGCTAGAATTTGTTACTCAGTGTTTTTTTTGTGTTGTTCTGTT-T 258216
Qy 3118 TGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCACAGTGGTGCAACCATAGG 3177
Db 258217 TGTTTTGTTTGAGACAGTCTCGCTGTTGCCCAAGGCTGGAGTGCAGTGGCGCAATCTCGGC 258276
Qy 3178 TCACTGCAGCCTCAACCTCCTGAGCTCAAGGGA TCTGCTGACCTCAGCCTCCCAAGTAGC 3237
Db 258277 TCACTGAAAGCTCCACCCCTGGTTTCAGCCATTTCTCCTGCCTCAGCCTCCCGAGTAGC 258336
Qy 3238 TGGGACTACGAGCGTGCACCAACCGCCTGGCTAAATTAATAAATAAATTTTTTTGTAGAGACT 3297
Db 258337 TGGGACTACAGTGCCTGCCACCAACACCTGGCTAAATGTTTGTA-TTTTGTAGTAGAGATG 258395
Qy 3298 GGGTCTTACTACGTTGGCCAGGCTTGTCTTAACTCCTGGCTTCAAGCAATCCTCCTACC 3357
Db 258396 GGGTTTCACCATGTTGGCCAGGATGGTCTTTGATTTCCTGACCTCATG--ATCCGCGCGCC 258453
Qy 3358 TTGGCATCCCAAGTCTGGGATTACAGGGGTGAGCCACCATTGTGCGGCTACTTATTCT 3417
Db 258454 TCGGCCTCCCAAGTGTGGGATTACAGGGGGAGCCACCGCACCCGGCCTACTCAGTGT 258513
Qy 3418 TTACATTTCCATCTTTTCCAATAGAAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTT 3477
Db 258514 GTTAATGGAGAAGTAT--ATTCA'TTGTTAGATCGCCATTTTAAAAACTTTTTTTTTTTT 258571
Qy 3478 CTTCCCTTTCTTTTTTGAGACAGAGTCTCA-CTTCAATCACTCAACCTCCGTTCAAGTCAC 3536

Db 258572 TTGAGACACAGTCTTGCTCTGTTGCCCAAGCTGGAGTACCGTGGCACAATCTTGGCTCAC 258631

Qy 3537 TGCACCTCTGCCCTCCCGGTTCAAGYGATTCTCCTGCCCTAAGCCTCCTGAGTAGCTGGA 3596

Db 258632 TGAACCTCCACCTCCTGGGTTCAAGCGATTCTCCCATCTCAGCCTTCTGAGTAGCTGGG 258691

Qy 3597 ATTACAAGCGTGCAACCACCATGCTTGGCTAAATTTTTTGTAATTTTTTAGCAGAGATGGGTT 3656

Db 258692 ACTACAGATGCACACCAGCATGCCAGGCTAA-TTTTTATATTTTAGTAGAGACGGGTT 258750

Qy 3657 TTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGT 3716

Db 258751 TCACCATGTTGCCCAGGCTGGTCTCGAACTCCTGGCATCAAGCAATCTGCCTGCTTCAGC 258810

Qy 3717 CTCCCAAAGTGCTGGAATTATAGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTT 3776

Db 258811 CTCCCAAATGCTGGATTACAGGCATGAGACACTGTGCCTAGCCTTAAAAAATATTTG 258870

Qy 3777 TCTTTATTGCTATATCCCCAGAT----CTAGAGCAGTGTCTGACATATAGTAGGTGCTCA 3832

Db 258871 ATAGCTATTTTATTACAAAAGGTAACCTTGCAGCCCTTGCTATTTTGTATGCATTACA 258930

Qy 3833 ATAAATAATTGATGAATGCACAGCCTAGATATAAACTTCTCTTTTCTTTTAAAAACAA 3892

Db 258931 AGCCTTTATGCATAAAATAAAATAGCCAGCACTATTCTACATGGCCAAGGTTTCATAGCA 258990

Qy 3893 TCTTGACAACTTTGCAGAATAAATACAACTTTGCATCTCGTTTTTCACTTATCACCTT- 3951

Db 258991 CACACAAAAAGTATAGTTGGCTGAGTGGTGCTCAGCTGAGTCAACCTGTAATCCCAACACTTG 259050

Qy 3952 -----GTTATGACTTTTTCATATTTGCCTCAAACTTTTATTGTTACTGTTTT 3997

Db 259051 GGAGACAGAGGTGGGTGGATCATGAGGTCAAGAGATCCAGACCACCTTGCCAAACATGGT 259110

Qy 3998 TTCAATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCTG 4057

Db 259111 GAAACCCCATCTCTACTAAAAAGTACAAAAATTAGCTGGGTGTTGGCGCATGCCTGTA 259170

Qy 4058 CT-----CCACTTTAGAGGCCAAAATTTACAAATCTGATGAAGCTATGAACCTCTCCC 4112

Db 259171 GTCTCAGCTACTCGGGAGGCTGAGCGAGGAGAAATCATTTGAAAGTGGGAGCGGAGTTG 259230

Qy 4113 CAGAGAAATACACACACACACACTCACACAGTTTTTTTTTTTAAATGTTTGGCAACTA 4172

Db 259231 CAGTGAGCCGAGATCTTGCCACTGCACTCCAGCCTGGGTGACAGAGTGAGACTCCATCTC 259290

Qy 4173 AGACAAGAA--ACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATAACTCAGTTG 4230

Db 259291 AATAAATAAATAAATAAATAAATTAAATTAAATTAATTTTAAAAAATTGGGGGCTG 259350

Qy 4231 GGCACAGTGACTCAAGCCTGTAAACACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACT 4290

Db 259351 AGTGTGATGGCTCACACCTGTATCCCGGAGTTTGGGAGCTTGAGGAGGCGAGATCCCT 259410

Qy 4291 TGAGTGAGAAGTTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAA 4350

Db 259411 TGAGGTCAGGAGTTCAAGACCAGCCTGGACAACATGGTGAACCCCGTCTCTACTAAAAA 259470

Qy 4351 TACAAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCAGCTACTCGGAGGCTGA 4410

Db 259471 TACAAAAATTAGCCAGGCATGGTGGCGTGTGCCTGTAATCCAGCTACTCGTGAGGCTGA 259530

Qy 4411 GGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACT 4470

Db 259531 GGCCCAAGCATCGCTTGAACCTGTGAGGCGGAGGTTGCAGTGAGCCAAAGATGGCACCAGT 259590

Qy 4471 GCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAAA 4526

Db 259591 GCACTCCAGCCTGGGTGACAGAGTGAGACTTTGTCTCAAAAAATAAATAA 259646

US-09-949-016-15786

; Sequence 15786, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 15786

; LENGTH: 35629

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(35629)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15786

Query Match 8.5%; Score 424.6; DB 3; Length 35629;

Best Local Similarity 54.1%; Pred. No. 7.9e-87;

Matches 1272; Conservative 3; Mismatches 922; Indels 156; Gaps 14;

Qy 2283 TCGCTTTTCAGGCCAGCGCGGTGGCTCATGCCCTGTAAATCCCAGCACTTTGGGAGGCCGAG 2342

Db 26911 TCTACTTTTGGCTGGGTGGGTGGCTCACGCCCTGTAATCCCAGCACTTTGGGAGGCTGAG 26970

Qy 2343 GCGGGCGGATCACTTGAGGTCAGGATTCGAGACCAGCCTGGCCAACATGGTGAACCCCT 2402

Db 26971 GCAGGTGGATCAC--AAGGTCAAGAGATCGAGACCATCCTGGCTAACAGGGTGAACCCCT 27028

Qy 2403 GTCTCTACTAAAAATACAAAAATTAGCCGACATGGTGGCGAGCGCTGTAAACCCAGC 2462

Db 27029 GTCTCTACTAAAAATACAAAAATTAGCCGGCGTGGTGACGAGCCTGTATTCCAGC 27088

Qy 2463 TACTTGGGAGACT-----GAGTTGGAGGTTTTCAGTGAGC 2496

Db 27089 TACTAGGAGGCTGAGCAGGAGAAATCGCTTGAACCTGGGAGGCTGAGGTTGCAGTGAGC 27148

Qy 2497 CAAGGTCGTGTCACCTGTCTCCAGCCTGGGTAACAGAGC--AACTCTGTCTCAAAAAAAA 2554

Db 27149 CGAGATCGCACCGCTGCACCTCCAGCCTGGGAGACAGAGCGAGACTCCGTTTCAGAAAAA 27208

Qy 2555 AAAATGCTTTCAATAAATATATGATAAAAGGACTTATATTTTTCAAAGCCATAGGATCAT 2614

Db 27209 AAAAAAATAACCCCTACTTTAGCTAAACAACCCCCCTTTACCTCTTCCAGCACCAC 27268

Qy 2615 TTCTCCTGAAGCATCTTGGCGAAGTCAATCCCCACC-----TGTTTCCT 2656

Db 27269 TAACTCCTGAGCATTTTGAGGATTTTAAATGTAAGTAACTTAGATTTGTTCTGGATTCTCTCA 27328

Qy 2657 GAGAGTGGCAGGTGAGGCTGACCTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCC 2716

Db 27329 TATAGGTTTAGGATTTGCTTTCTCCAGTCCACTACATAACCGCTACTCTTCCATGTCT 27388

Qy 2717 TCCCACTTTCCAG-----GTGCTGCCAGACACATGACAACTGCT 2755

Db 27389 TTCTAACTTGCAGAATTATTATTATTATTTTTTTGTGAGACGGTTTTTTCGCTCTG 27448

Qy 2756 AYGACCAGGCCAAGAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCACA 2815

Db 27449 TCGCCCAAGGCTGGAGTGCAGTGGCACAAATCTCGGCTCACTGCAACCTCCACCTCTTGGGT 27508

Qy 2816 CCTATTCTACTCTGCTCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCT 2875

Db	27509	TCATGCCAATCTCTCGCCTCAGCCTCCGAGTAGCTGGAGCTACAGGTGCCCGCCAACAT	27568
Qy	2876	TGACCTATGAATTCTAGTTGGTTCTCAGTAGGCCGGGGGGAATAATAAGTAAACAACAGCC	2935
Db	27569	GCCCAGCTAATTTTGTATTTTCAGTAGATACGGGGTTTCACTGTGTAGCCAGGATGG	27628
Qy	2936	ATGATTTAGTGAATTTTCTTGGTTCTGGGCAGTGTCTCCTTTAATCCTCAGAACACA	2995
Db	27629	TCTCAATCTCCTGACCTCGTGATCTGCTTGCCCTTGGTCTCCCAAAGTCTGGGATTACAG	27688
Qy	2996	CTATGGGATAGGTACAATTATCCTCACTTAACAGATAAGAAAACCTGAGGCTCAGAAGGCT	3055
Db	27689	CGGTGAGCCACCGCGCCTGGCACTAACTTGCAAAATTATATTTTAA-----	27735
Qy	3056	GAGCTATTTGCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTGTCT	3115
Db	27736	-----ATCTTCTCTGATGCTTCCCTTCCCTTTTAGAGTCTTGGGGTGGTGTGTGTGTC	27790
Qy	3116	GTTGTTTAGACAGGGTCTTGGTCTGTCAACCCAGGCATGAGCACAGTGGTGCAACCAT	3175
Db	27791	ATTGTTTTTGGACACAGTCTTGTCTGTGACCCAGGCTGGAGTGCAGCAGCAATCTTG	27850
Qy	3176	GGTCACTGCAGGCTCAACCTCCTGAGCTCAAGGGATCTGTGACCTCAGCCTCCCAAGTA	3235
Db	27851	GCTCACTGCAACCTCCGCTCCAGGTTCAAGCAATTTCTCTGCTCAGCCTCCTGTAGTA	27910
Qy	3236	GCTGGGACTACGAGCGTGCACCACCGCTGGCTAATTAA--AAAAATTTTTTTGTPAGA	3293
Db	27911	GCTGGGACTACAGGAGGCACCCGCCACCATGCCAGCTAAGTTTGTATTTTTTAGTAGA	27970
Qy	3294	GACTGGGCTTTACTACGTTGGCCAGGCTGTCTTAAACTCCTGGCTTCAAGCAATCCTCC	3353
Db	27971	GGCGGAGTTTTACCATGTTGTCCAGGCTGGTCTTGAACCTCTGACCTCAAGTGATCTGCC	28030
Qy	3354	TACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTAT	3413
Db	28031	TGCCTTGGCCCTCCCAAAGTTAAAGGATTACAGGTGTGAGCCACTGCACCTGGCCAGAGTT	28090
Qy	3414	TTCTTTACATTCATCTTTTCCAATAGAAATGTAAAGATCCACAGAACAGGGATTACTGCCTA	3473
Db	28091	TTGGTGTTTTGTGTGTTTTTTTTTTTGGAGAGGGA-----	28125
Qy	3474	TTTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTCATCACTCAACCTCCCGTTCAAGT	3533
Db	28126	--GTCTCACTCTGTGTGCCAGGCTGGAGTGCAGTGGCACGATC-----TCAGCT	28172
Qy	3534	CAC TGCAACCTCTGCTCCTCCGGGTTCAAGYGATTTCTCCTGCCTAAGCCTCCTGAGTAGCT	3593
Db	28173	CAC TGCAACCTCTGCTCCTCGTGGGTTCAAGCAATTTCTCCTGCCTCAGTCTCCTGAGTAGCA	28232
Qy	3594	GGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTGATTTTGTAGCAGAGATGGG	3653
Db	28233	GG-ACTACAGGCATGTGCCACCACCGCCAGCTAATTTTTTTGTATTTTGTAGAGACGGG	28291
Qy	3654	GTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTC	3713
Db	28292	GTTTCACCATGTTAGCCAGGATGGTCTCTATCTCCTGACCTC--GTGATCTGCCTGCTGC	28349
Qy	3714	AGTCTCCCAAAGTCTGGAATTTATAGCGCTGAGTCACTGTGCTGGCCGATTACTGTCTA	3773
Db	28350	AGCCTCCTAAAGTCTGGGATTACAGGCGTGAGCCACCGCGCCCGCCCGCCCGGTTT	28409
Qy	3774	TTTTCTTTA-----TTGCTATATCCCCAGATCTAGAGCAGTGTCT	3813
Db	28410	TTTTAACAAAGATTCAAGACATCCAAATTGGATGTGCTCTTCTCCTCAAATCTCTTGCC	28469
Qy	3814	GACATATAGTAGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCT	3873
Db	28470	CATAGTTTCAAAGCCCTCTCTATTTCTTTACATATGACGAAGCGAATCTGTTTTATATTC	28529
Qy	3874	TTTTTCTTTTTTAAAAACAATCTTGGACAACTTT---GCAGATAAATAACAATCTTGCATT	3929

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RESULT 6
US-09-949-016-12970/c
; Sequence 12970, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12970
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12970

```


Best Local Similarity 60.7%; Pred. No. 6.9e-86; Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;									
Qy	3104	TTTTTTTTTGTGTTTGTAGACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAG	3162						
Db	27493	TTTTTCTCCTTTTTTTTGTAGACGGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTGCAA	27434						
Qy	3163	TGGTGAACCATAGGTCACCTGAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC	3222						
Db	27433	TGGTGCAATCTTGGCTCACCGCAACCTCCGCCTTCTCGGTTCAAGCAATCTCTCGCTC	27374						
Qy	3223	AGCTCCCAAGTAGCTGGGACTAGCAGCGTGCACCACCGCTGGCTAAATTAACAAAAT	3282						
Db	27373	AGCTCCCAAGTAGCTGGGATTACAGGCAATGCGCCACCATGCGCCGGCTAGTTTTGTGA---	27317						
Qy	3283	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCA	3342						
Db	27316	TTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGATCTGGAACCTCCCGACTCA	27257						
Qy	3343	AGCAATCCTCTACCTTGGCATCCCAAGTCTGGGATTACAGGGTGAGCCACCATGTG	3402						
Db	27256	GGTATTCGCTGCCTTGGCCTCCCAAGTGTGGGATTACGGCTGAGCCACTCGGCC	27197						
Qy	3403	CGGCTACTTATTTCTTTACATTCATCTTTCCAAATAGAAATGTAAGATCCACAGAACGGG	3462						
Db	27196	CAG---CTGATTTTCTTCTTTCAGTATGTCCAATGATGTTCTTGAGCCCGCTTATACCT	27140						
Qy	3463	ATTACTGCCTATTTTCTTCTTCTTTTGTGACACAGAGTCTCACTTCACTCAACCTCAACC	3522						
Db	27139	TATTTTTTTTTTTGTAGATGGAGTTTGTCTTCTTGTGCCCAGGCTGGAGTGCAATGAGG	27080						
Qy	3523	TCCGTTCAGCTCACTGCAACCTCTGCTCCTCCGGGTTCAAGYATTTCTCCTGCCTAAGCCT	3582						
Db	27079	TGATCTGGCTCACCGCAACCTCCACCTCCAGGTTCAAGCAATTTCTCCTGCCTCAGCCT	27020						
Qy	3583	CCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTT-TTGTATTTT	3641						
Db	27019	CCTGAGTAGCTGGATTACAGGCATGCACCACCACCGCCCGCTAAATTTGTATTTTTT	26960						
Qy	3642	AGCAGAGATGGGTTTTTACCATGTTGCCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGA	3701						
Db	26959	AGTAGACGGGGTTTCTCCATGTTG--AGGCTAGTCTCTAACTCCGACCTCAGGTGA	26903						
Qy	3702	TCTGCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGCGTGAGTCACTGTGCTGGCC	3761						
Db	26902	TCCGCTGCCTCGCCTCCCAAAGTCTGGGATTACAGGTGTGAGCCACCTGCCCCGCC	26843						
Qy	3762	GATTACTGTCTATTTTCTTTTATGCTATATCCCAGATCTFAGAGCAGTGTCTGACATATA	3821						
Db	26842	TATACCT--TATTTTTCATAATAAATAATATATGACCTTAAACTACCTGTGTCTACTTTA	26786						
Qy	3822	GTAGGTCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTT	3881						
Db	26785	TTAAATGAGACCATTAACACACCGATTTCACTAAATAAAAAAAATTTAAAGTCAAAA	26726						
Qy	3882	TTTTA---AAACAATCTTGACRACTTTGCAGAAATAAATACAATCTTGCTTTT	3937						
Db	26725	ATTAATACTAAACATTTGTTTTTCTGTGCAGATCTAGCCCAAAATGCTCTGTCTCT	26666						
Qy	3938	TCACTTATCACCTTGTATGACTTTTTCATATTGCTCAACCTTTATTGTTACTGTTTT	3997						
Db	26665	TCTGGCTTCAATGCTTTCTATCTTCCCTACATGTATACTAGCTTGCACTGGCTTCCCAC	26606						
Qy	3998	TTCAATGTTACTATTTTAGTCACTGA--ATAATATGGCTTAATTTGCTTATACATCCTCC	4055						
Db	26605	TTCAATACTAAATCTACACCTTAACAGACCGTAAGATGTATTGAAGATTTGTTACTAATGA	26546						
Qy	4056	TGCTCCACTTTTAGAAG-----GCCAAATTTACAAATCTGATGAAAGC	4097						
Db	26545	GTATCAAGTTATAACCTATTTTATGTTATTTCACAACAATATTTCTTAGTCAATTGCA	26486						
Qy	4098	TATGAACCTCTCCTCCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTT	4157						

Db	26485	TCTGCTTAGATTTCTAAGACAAAAAGATAGAGGTTAAAAAGCTAGACTCAGAGCCTATCTC	26426						
Qy	4158	TAATGTTTGCAACTAAGACAAGAAACCTGCATTAAGAGGATGTTTGTTCATATTAATTAAA	4217						
Db	26425	AACCACGTGGCTTCAGTAGAACAAAGGTTAAGAAATTTAGCTTAAGGCAATGACGTATT	26366						
Qy	4218	AATAACTCAGTTGGCA---CAGTGACTCAAGCCTGTAACCACACAGTACTTTTGGAGTCC	4273						
Db	26365	AAAAACACTTAAGGCCAGGTGCAGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCC	26306						
Qy	4274	AAGGTGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGTTGAAAC	4333						
Db	26305	TAGGCAGGCAGATCAC--GAGGTCAAGAGATCGAGACCATCTCTGGCTAACACCGTGAAAC	26248						
Qy	4334	CCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCC	4392						
Db	26247	CCCATCTCTACTAAAAATACAAAAAATTAGCCGTGCATGGTGGCACACGCCTGTAGTCCC	26188						
Qy	4393	AGTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGTTGCAGTG	4452						
Db	26187	AGCTACTTGTGGGCTGAGGCAGGAGAAATGGTGTGAACCCGGGAGGCAGAGCTTGAGTA	26128						
Qy	4453	AGCCGAGATCCCACCACTGCACCTCCAGCCTGGGCACACACAGCGAGACTCTATCTCAAAA	4512						
Db	26127	AGCCAAGATCATGCCACTGCACCTCCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAAAA	26068						
Qy	4513	AATAAATAAATAAATAAAGGATCGGAGAGAAACAAAACTAATAAGATTTCCTGAAGST	4570						
Db	26067	AAAACAAAACAAAAAACCCAAAAACCAAAAAACAAAAAGAACACAAAAACGAATGT	26010						

RESULT 7

US-09-949-016-12971/c
; Sequence 12971, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12971
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12971

Query Match 8.4%; Score 420.4; DB 3; Length 32068; Best Local Similarity 60.7%; Pred. No. 6.9e-86; Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;									
Qy	3104	TTTTTTTTTGTGTTTGTAGACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAG	3162						
Db	27493	TTTTTCTCCTTTTTTTTGTAGACGGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTGCAA	27434						
Qy	3163	TGGTGAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC	3222						
Db	27433	TGGTGCAATCTTGGCTCACCGCAACCTCCGCCCTTCTCGGTTCAAGCAATTTCTCTGCCCTC	27374						
Qy	3223	AGCTTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGGCTAATTAACAAAAT	3282						
Db	27373	AGCTTCCCAAGTAGCTGGGATTACAGGCATGCGCCACCATGCCCGGCTAGTTTTGTGA---	27317						
Qy	3283	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCA	3342						

Db	27079	TGATCTCGGCTCACCGCAACCTCCACCTCCAGGTTCAAGCAATTCCTCGCTCAGCCT	27020
QY	3583	CCTGAGTAGCTGGAATTACAAGCGTGCAACCATGCTTGGCTAAATTTT-TTGTATTTTT	3641
Db	27019	CCTGAGTAGCTGGGATTACAGGCATGCAACCAACCGCCCGCCTAAATTTTGTATTTTTTT	26960
QY	3642	AGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGA	3701
Db	26959	AGTAGAGACGGGGTTTCTCCATGTTG--AGGCTAGTCTCTAACTCCCAGACCTCAGGTGA	26903
QY	3702	TCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGCGGTGAGTCACTGTGCCTGGCC	3761
Db	26902	TCCGCCTGCCTCGGCCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGTGCCCGGCC	26843
QY	3762	GATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGCACATATA	3821
Db	26842	TATACCT---TATTTTCATCAAAATAAAATATATGACCTTFAAACTACCTGTGTCACTTA	26786
QY	3822	GTAGGTGCTCAATAAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTT	3881
Db	26785	TTAAATAGACCATTTAAACACCAAGTATTCACTAAATAAAAAAAAATTTAAAGTCAAAA	26726
QY	3882	TTTTA----AAACAATCTTGACAACTTTGCAGAATAAAATACAATCTTGCAATCTCGCTTT	3937
Db	26725	ATTAATACTAAAAACATTTGTTTTTCTGTGCAGATCTAGCCAAAATGTCTCTGTCTCTCT	26666
QY	3938	TCACTTATCACCTTGTTATGACTTTTTCATATTTGCCTCAAAACCTTATTGTTACTGTTTT	3997
Db	26665	TCGGCTTCAATGCTTTCTATCTTTCCCTACATGTATCTAGCTTGCACTGGCTTCCAC	26606
QY	3998	TTCAATTGTTACTATTTTAGTCACTGA--ATAATATGGCTTAATTTGCTTATACATCCTCC	4055
Db	26605	TTCAATTACTAATCTACACCTAACAGACCGTAAGATGTATTGAAAGATTTGTTACTAATGA	26546
QY	4056	TGCTCCACTTTAGAAG-----GCCAAATTTACAAATCTGATGAAAGC	4097
Db	26545	GTATCAAAGTTATAACCTATTTTATGTTATTTCAACAACATATCTTAGTCATTGTCAT	26486
QY	4098	TATGAACCTCTCTCCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTT	4157
Db	26485	TCTGCTTAGATTTCTAAGACAAAAAGATAGAGGTTAAAGCTAGACTCAGAGCCTATCTC	26426
QY	4158	TAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTGTTCATATTAATATAA	4217
Db	26425	AACCACGTGCTTCAGTAGAACAAAGGTTAAGAAATTGTTAGTTAAGGCAATGACGTATT	26366
QY	4218	AATAACTCAGTTGGGCA---CAGTGACTCAAGCCTGTAAACCACAGTACTTTGGAACTCC	4273
Db	26365	AAAAACACTTAAGGCCAGGTGCAGTGGCTCAGCCTGTATCCAGCACTTTTGGGAGGCC	26306
QY	4274	AAGTGGGTGGATCACCTTGAGGTGAGAAATTCCAGACCGCCTGGTCAATATGGTGAAC	4333
Db	26305	TAGGCAGGCAGATCAC--GAGGTCAGGAGATCGAGACCATCCTGGCTTAACACGGTGAAC	26248
QY	4334	CCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCC	4392
Db	26247	CCCATCTCTACTAAAAATACAAAAAATTAGCCGTGCATGTTGGCACACGCCCTGTAGTCCC	26188
QY	4393	AGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGTTTGCAGTG	4452
Db	26187	AGCTACTTTCGGGCTGAGGCAGGAGAAATGGTGTGAACCCGGGAGGCAGAGCTTGAGTA	26128
QY	4453	AGCCGAGATCCCACCACTGCACCTCCAGCCTGGCGACACAGCGAGACTCTATCTCAAAA	4512
Db	26127	AGCCAAGATCATGCCACTGCACCTCCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAAACA	26068
QY	4513	AATAAATAAATAAAATAAAGGATCGGAGAGAAAAACAAACTAATAAGATTCTTGAAGT	4570
Db	26067	AAAACAAAACAAAAAAACCCAAAAACCAAAAAACCAAAAGAAACAAAAACGAATGT	26010

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US-09-949-016-12973/c
; Sequence 12973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12973
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12973

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Query Match 8.4%; Score 420.4; DB 3; Length 32068;
Best Local Similarity 60.7%; Pred. No. 6.9e-86;
Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;

QY	3104	TTTTTTTGTGTTGTTGTAGAGACAGGGTCTTGCTC-TGTCACCCAGGCGATGAGCACAG	3162
Db	27493	TTTTTCTTCCTTTTTTTTTTGAGACGGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTGCAA	27434
QY	3163	TGGTGCAAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC	3222
Db	27433	TGGTGCAAATCTTGGCTCACGCAACCTCCGCTTCTCGGTTCAAGCAATTCCTCGCCTC	27374
QY	3223	AGCCTCCCAAGTAGCTGGGACTACGAGCGTGCAACCACACGCTTGGCTAAATTAATAAATAAT	3282
Db	27373	AGCCTCCCAAGTAGCTGGGATTACAGGCATCGGCCACCATGCCGGCTAGTTTGTGA---	27317
QY	3283	TTTTTTGTAGAGACTGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCA	3342
Db	27316	TTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGATCTGGAACTCCCGACTTCA	27257
QY	3343	AGCAATCCTCCTACCTTTGGCATCCCAAAGTGCTGGGATTACAGGGTGAGCCACCATGTG	3402
Db	27256	GGTGATTCGCCTGCCTTGGCCTCCCAAAGTGTGGGATTACGGCGTGAGCCACTGCGCC	27197
QY	3403	CGGCTACTTATTCTTTACATTCCATCTTTCCAAATAGAAATGTAAGATCCACAGAACAGGG	3462
Db	27196	CAG---CTGATTTTCTCTTTCAGTATGTCCAATGATGTTCTTGAGCCCCGCTTATACCT	27140
QY	3463	ATTACTGCCTATTCTTCTCCTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACC	3522
Db	27139	TATTTTTTTTTTTGAGATGGAGTTTTTGCTCTTTGTTGCCAGGCTGGAGTGCAATGAGG	27080
QY	3523	TCCGTTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCT	3582
Db	27079	TGATCTCGGCTCACCGCAACCTCCACCTCCAGGTTCAAGCAATTCTCCTGCCTCAGCCT	27020
QY	3583	CCTGAGTAGCTGGAATTACAAGCGTGCAACCACCATGCTTGGCTAATTTT-TTGTTATTTT	3641
Db	27019	CCTGAGTAGCTGGGATTACAGGCATGCACCACCCGCGCCCTAATTTTGTATTTTTTTT	26960
QY	3642	AGCAGAGATGGGGTTTTACCATTGTTGCCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGA	3701
Db	26959	AGTAGAGACGGGGTTTCTCCATGTTG---AGGCTAGTCTTAACCTCCCGACCTCAGGTGA	26903
QY	3702	TCGTCCTGCCTCAGTCTCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCC	3761
Db	26902	TCCGCCTGCCCTCGGCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGTCCCGGCC	26843
QY	3762	GATTACTGTCTATTTTCTTTATTGCTATATCCCAAGATCTAGAGCAGTGTCTGACATATA	3821


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Db 26842 TATACCT---TATTTTCATCAAAATAAAATATATATGACCTTAAACTACCTGTGTCACTACTTA 26786
Qy 3822 GTAGGTGCTCAATAAAATAATTGATGAATGCACAGCCTAGATATAAAACTTTTCTTTTCTTT 3881
Db 26785 TTAAAAATGAGACCATTAAACACACCAGTATTACATAAATAAAAAAAAATTTAAAGTCAAAA 26726
Qy 3882 TTTTA----AAACAATCTTGACAACTTTGCAGAATAAATACAACTTGCATTCTGCTTTT 3937
Db 26725 ATTAATACTAAACATTTGTTTTTCTTGTTCAGATCTAGCCCCAATGTCTCTCTCTCT 26666
Qy 3938 TCACCTTATCACCTTGTTATGACTTTTTCATATTGCCCTCAAAACCTTTATTGTTACTGTTT 3997
Db 26665 TCTGGCTTCAATGCTTTCTATCTTTCCCTACATGTATACGTAGCTTGCAGTGGCTTCCAC 26606
Qy 3998 TTCATTGTTACTATTTTAGTCACTGA--ATAATATGGCTTAATTGCTTTATACATCCICC 4055
Db 26605 TTCATTACTAATCTACACCTAACAGACCGTAAGATGTATTGAAAGATTTGTTACTAATGA 26546
Qy 4056 TGCTCCACTTTAGAG-----GCCAAATTTACAAATCTGATGAAAGC 4097
Db 26545 GTATCAAAGTTATAACCTATTTTATGTTATTTCAACAACATTATTCTTAGTCAATTTGCA 26486
Qy 4098 TATGAACCTCTCCCCCAGAGAAATACACACACACACACTCACACACAGATTTTTTTT 4157
Db 26485 TCTGCTTAGATTTCTAAGACAAAAAGATAGAGGTTAAAGCTAGACTCAGAGCCTATCTC 26426
Qy 4158 TAATGTTTGCACTAAGACAAGAAACCTTGCATTAGAGGATGTTTGTTCATATTAAATTA 4217
Db 26425 AACCACGTGGCTCAGTAGAACAAAGGTTAAGAATTGTTAGCTTAAGGCAATGACGTATT 26366
Qy 4218 AATAACTCAGTTGGGCA----CAGTGACTCAAGCCTGTAACCACAGTACTTTTGGAAAGTCC 4273
Db 26365 AAAACACCTTAAGGCCAGGTGCAGTGGCTCAGCCTGTAATCCCAGCAGCTTTGGGAGGCC 26306
Qy 4274 AAGTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAAC 4333
Db 26305 TAGGCAGGCAGATCAC--GAGGTCAGGAGATCGAGACCATCCTGGCTAACACACGGTGAAC 26248
Qy 4334 CCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCC 4392
Db 26247 CCCATCTCTACTAAAAATACAAAAAATTAGCCGTGCATGGTGGCACACGCCTGTAGTCCC 26188
Qy 4393 AGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGCAGAGGTTGCAGTG 4452
Db 26187 AGCTACTTGTGGGCTGAGGCAGGAGAAATGGTGTGAACCCGGGAGCAGAGCTTGCAGTA 26128
Qy 4453 AGCCGAGATCCCAACCACTGCACCTCCAGCCTGGCGGACACAGCGGAGACTCTATCTCAAAA 4512
Db 26127 AGCCAAGATCATGCCACTGCACCTCCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAAACA 26068
Qy 4513 AATAAATAAATAAATAAAGGATCGGAGAGAAAAACAAACTAATAAGATTCTCTGAAGGT 4570
Db 26067 AAACAAAAACAAAAAAACCCAAAAACCAAAAAACAAAAAGAACACACAAACGAATGT 26010
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RESULT 10
US-09-949-016-12974/c
; Sequence 12974, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12974
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12974

Query Match      8.4%; Score 420.4; DB 3; Length 32068;
Best Local Similarity 60.7%; Pred. No. 6.9e-86;
Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;

Qy 3104 TTTT TTTT TTTT TTTT TTTT TAGAGACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAG 3162
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 27493 TTTT TCTT CCTT TTTT TTTT TGAGACGGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTGCAA 27434
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3163 TGGTGAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC 3222
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 27433 TGGTGCAATCTTGGCTCACCGCAACCTCCGCCCTTCTCGGTTCAAGCAATTCCTCTGCCTC 27374
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3223 AGCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACACGCTGGCTAATTTAAAAAAAT 3282
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 27373 AGCTCCCAAGTAGCTGGGATTACAGGCATGCGGCCACCATGCCCGCTAGTTTGTGA-- 27317
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3283 TTTT TTTT GTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCA 3342
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 27316 TTTT TAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGATCTGGAACCTCCCGACTTCA 27257
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3343 AGCAATCCTCCTACCTTGGCATCCCAAAGTGTCTGGGATTACAGGGGTGAGCCACCATGTG 3402
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 27256 GGTGATTGCGCTTGGCCTCCCAAAGTGTGGGATTACCGCGTGAGCCACTTGGGCC 27197
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3403 CGGCTACTTATTTCTTTACATTCATCTTTTCCAAATAGAAATGTAAGATCCACAGAAACAGGG 3462
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 27196 CAG---CTGATTTTCTTCTTTTTCAGTATGTCCAATGATGTTCTGAGCCCGCTTATACCT 27140
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3463 ATTACTGCCTATTTCTTCTCTTTCTTTTGTAGACAGAGTCTCACCTTATCACCTCAACC 3522
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 27139 TATTTT TTTT TTTT TGAGATGGAGTTTGTCTCTTGTGCCCAGGCTGGAGTGCAATGAGG 27080
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3523 TCCGTT CAGCTC ACTGCAACCTCTGCTCTCCCGGTTCAAGYGATTCTCCTGCTCAAGCCT 3582
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 27079 TGATCTCGGCTCACCCGCAACCTCCACCTCCCAAGGTTCAAGCAATTCCTCTGCTCAGCCT 27020
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3583 CCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTT-TTGTATTTT 3641
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 27019 CCTGAGTAGCTGGGATTACAGGCATGCACCACCGCCGCCCTAATTTTGTATTTT 26960
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3642 AGCAGAGATGGGGTTTACCATGTTGCCCAAGGCTGTCTCAAACTCCTGACCTCAAGTGA 3701
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26959 AGTAGAGACGGGGTTTCTCCATGTTG--AGGCTAGTCTCTAACTCCCGACCTCAGGTGA 26903
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3702 TCTGCCCTGCCCTCAGTCTCCCAAAGTCTGGAATTATAGGCGTGAGTCACTGTGCCCTGGCC 3761
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26902 TCCGCCCTGCCCTCCCAAAGTCTGGGATTACAGGTGTGAGCCACCGTGCCCGGCC 26843
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3762 GATTACTGTCTATTTTCTTATTTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATA 3821
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26842 TATACCT--TATTTTCATCAAAATAAAATATATGACCTTAAACTACCTGTGTCACTACTTA 26786
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3822 GTAGGTGCTCAATAAATAATTGATGAATGCACAGCCCTAGATATAAACTTTCTTTTCTTT 3881
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26785 TTAAATGAGACCAATTAAACACCAAGTATTTCACATAAATAAAAAAAAATTTAAAGTCAAAA 26726
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3882 TTTTA----AAACAATCTTGACAACTTTGCAGAATAAATAACAATCTTGCATTTCTGCTTT 3937
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26725 ATTAATACTAAACATTTGTTTCTTGTCTGAGATCTAGCCCCAAATGTCTCTCTCTCT 26666
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3938 TCACCTTATCACCTTGTTATGACTTTTTCATATTGGCTTCAATTTGCTTAAACCTTTTATTGTTACTGTTT 3997
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26665 TCTGGCTTCAATGCTTTTCTATCTTTCCCTACATGTATACGTAGCTTGCAGTGGCTTCCAC 26606
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 3998 TTCATTGTTACTATTTTAGTCACTGA--ATAATATGGCTTAATTTGCTTATACATCCCTC 4055
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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[illegible]

RESULT 11
 US-09-949-016-12975/c
 ; Sequence 12975, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 12975
 ; LENGTH: 32068
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-12975

QY	3163	TGGTGCAACCATAGGTCACTGCGAGCCTCAACCTCTCTGAGCTCAAGGGATCTGCTGACCTC	3222
Db	27433	TGGTGCAATCTTGGCTCACGCAACCTCCGCCTTCTCGGTTCAAGCAATCTCTCTGACCTC	27374
QY	3223	AGCCTCCCAAGTAGCTGGGACTACGAGCGTGACACCAACACGCTTAAATAAATAAATAA	3282
Db	27373	AGCCTCCCAAGTAGCTGGGATTACAGGCATCGGCCACCATGCGCGCTAGTTTGTA---	27317
QY	3283	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCTGGCTTCA	3342
Db	27316	TTTTTTGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGATCTGGAACTCCGACTTCA	27257
QY	3343	AGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGTGAGCCACCATGTG	3402
Db	27256	GGTGATTCGCCCTGCCCTTGGCCCTCCCAAAGTGTTGGGATTACCGGCGTGAGCCACTGCGCC	27197
QY	3403	CGGCTACTTATTCTTTACATTCATCTTCCAAATAGAATGTAAGATCCACAGAACAGGG	3462
Db	27196	CAG--CTGATTTTCTCTTTTCAGTATGTCCAATGATGTTCTTGAGCCCGCTTATACCT	27140
QY	3463	ATTACTGCCCTATTCTCTCTTTTGTAGACAGAGTCTCACCTTCATCACCTCAACC	3522
Db	27139	TATTTTTTTTTTTGAGATGGAGTTTGTCTTGTGCCCAGGCTGGAGTGAATGAGG	27080
QY	3523	TCCGTTCAAGTCTACGTCAACCTCTGCCCTCCCGGTTCAAGYGATTTCTCTGCTAAGCCT	3582
Db	27079	TGATCTCGGCTCACCGCAACCTCCACCTCCAGGTTCAAGCAATTTCTCTGCTCAGCCT	27020
QY	3583	CCTGAGTAGCTGGAATTAACAAGCGTGCAACCACTGCTGGCTAAATTT-TTGTATTTT	3641
Db	27019	CCTGAGTAGCTGGATTACAGGCATGCACCACCGCCGCTTAATTTTGTATTTTTTTT	26960
QY	3642	AGCAGAGATGGGTTTTTACCATGTTGCCCGAGGCTGGTCTCAAACTCCTGACCTCAAGTGA	3701
Db	26959	AGTAGAGACGGGGTTTCTCCATGTTG--AGGCTAGTCTCTAACTCCCGACCTCAGGTGA	26903
QY	3702	TCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTAAGGCGTGAGTCACTGTGCCTGGCC	3761
Db	26902	TCCGCTGCCTCGGCCCTCCCAAAGTGCTGGATTACAGGTGTGAGCCACCGTGCCCGGCC	26843
QY	3762	GATTACTGTCTATTTCTTTATTTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATA	3821
Db	26842	TATACCT--TATTTTCATCAAATAAAATATATGACCTTAAACTACCTGTGTCTACTTAA	26786
QY	3822	GTAGTGTCTCAATAAATAAATGATGAATGCACAGCCTAGATATAAACTTTTCTTTCTTT	3881
Db	26785	TTAAATGAGACCATTTAAACACCAGTATTCACTAAATAAATAAATAAATAAAGTCAAAA	26726
QY	3882	TTTTA---AAACAATCTTGACAACTTTGCAGATAAATAACAATCTTGCAATCTGCTTTT	3937
Db	26725	ATTAATACTAAACACATTTGTGTTTCTGTGAGATCTAGCCCAAATGTCTCTGTCTCT	26666
QY	3938	TCACTTATCACCTTGTATGACTTTTTCATATTTGCCTCAAACTTTTATTTGTTACTGTTT	3997
Db	26665	TCTGCTTCAATGCTTTCTATCTTCCCTACATGTATCTAGCTTGACGTGGCTTCCAC	26606
QY	3998	TTCAATTTGTTACTATTTTAGTCACTGA--ATAATATGCTTAAATTTGCTTATACATCCTCC	4055
Db	26605	TTCAATTAATACTACACCTTAACAGACCGTAAGATGTATTGAAAGATTTGTTACTAATGA	26546
QY	4056	TGCTCCACTTTAGAAG-----GCCAAATTTACAAATCTGATGAAAGC	4097
Db	26545	GTATCAAAGTTATAACCTATTTTATGTTATTTCACAACAACATATTCTTAGTCAATTTGCAT	26486
QY	4098	TATGAACCTCTCTCCCGAGAGAAATACACACACACACACTCACACACAGTTTTTTTTT	4157
Db	26485	TCTGCTTAGATTTCTTAAGACAAAAGATAGAGGTTTAAAGCTAGACTCAGAGCCTATCTC	26426
QY	4158	TAATGTTGCAACTAAGACAAGAAACCTGCATTTAGAGGATGTTTGTTCATATTAATTA	4217
Db	26425	AACCAGTGGCTTCAGTAGAACAAAGGTTAAGAAATGTTAGCTTAAGGCAATGACGTATT	26366
QY	4218	AATAACTCAGTTGGGCA---CAGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAGTCC	4273

Db 26365 AAAAACTAAAGCCAGGTGCAGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCC 26306
Qy 4274 AAGGTGGTGGATCACTTGAGGTGAGAAAGTTTCGAGACCAGCCTGGTCAATATGGTGAAAC 4333
Db 26305 TAGGCAGGCAGATCAC--GAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC 26248
Qy 4334 CCTATCTCTACTAAAAATAC-AAAAATTAGTGGGTGATGATGCATGCCTGTAGTCCC 4392
Db 26247 CCCATCTCTACTAAAAATACAAAAATTAGCCGTGCATGGTGGCACACGCCTGTAGTCCC 26188
Qy 4393 AGCTACTCGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGAGGCAGAGTTGCAGTG 4452
Db 26187 AGCTACTTGTGGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCAGAGCTTGCAGTA 26128
Qy 4453 AGCCGAGATCCCACCACTGCACCTCCAGCCTGGCGGACACAGCGAGACTCTATCTCAAAA 4512
Db 26127 AGCCAAGATCATGCCACTGCACCTCCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAAA 26068
Qy 4513 AATAAATAAATAAAATAAAGGATCGGAGAGAAAAACAAACTAATAAGATTCTCTGAAGGT 4570
Db 26067 AAAACAAAAACAAAAAAACCCAAAAACCAAAAAACAAAAAGAACACAAACGAATGT 26010

RESULT 12
US-09-949-016-14436/c
; Sequence 14436, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14436
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14436

Query Match 8.4%; Score 420.4; DB 3; Length 32068;
Best Local Similarity 60.7%; Pred. No. 6.9e-86;
Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;

Qy 3104 TTTTTTTTTTGTGTTTGTAGAGACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAG 3162
Db 27493 TTTTCTTCCTTTTTTTGTAGACGGAGTTTCGCTCTTGTGTCAGGCTGGAGTGCAA 27434
Qy 3163 TGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGTGACCTC 3222
Db 27433 TGGTGCAATCTTGGCTCACCGCAACCTCCGCCTTCTCGGTTCAAGCAATCTCTCGCTC 27374
Qy 3223 AGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGGCTAATTAATAAAT 3282
Db 27373 AGCCTCCCAAGTAGCTGGGATTACAGGCATCGCCACCATGCGCGGCTAGTTTGTGA--- 27317
Qy 3283 TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCA 3342
Db 27316 TTTTGTAGTACAGACAGGGTTTCTCCATGTTGGTTCAGGCTGATCTGGAACCTCCGACTTCA 27257
Qy 3343 AGCAATCCTCTACCTTGGCATCCCAAAAGTCTGGGATTACAGSGGTGAGCCACCATGTG 3402
Db 27256 GGTGATTCGCCTTGGCCTTGGCCTCCCAAAAGTGTGGGATTACCGGCGTGAGCCACTGCGCC 27197

Qy 3403 CGGCTACTTATTTCTTTACATTCCATCTTTCCAAATAGAAATGTAAGATCCACAGAACAGGG 3462
Db 27196 CAG--CTGATTTTCTTCTTTTCAGTATGTCCAATGATGTTCTCTGAGCCCGCTTATACCT 27140
Qy 3463 ATTACTGCCTATTTTCTTCTTTCTTTTGAGACAGAGTCTCATTTCATCACCTCAACC 3522
Db 27139 TATTTTTTTTTTTTGAGATGGAGTTTGTCTCTTGTGCCAGGCTGGAGTGCAATGAGG 27080
Qy 3523 TCCGTTTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCT 3582
Db 27079 TGATCTGGCTCACCGCAACCTCCACCTCCCAAGTTCAAGCAATTCTCCTGCCTCAGCCT 27020
Qy 3583 CCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTT-TTGTATTTT 3641
Db 27019 CCTGAGTAGCTGGGATTACAGGCATGCCACCACCGCCCGCTTAATTTTGTATTTT 26960
Qy 3642 AGCAGAGATGGGTTTACCATGTTGCCAGGTGGTCTCAAACTCCTGACCTCAAGTGA 3701
Db 26959 AGTAGAGACGGGTTTCTCCATGTTG--AGGCTAGTCTCTAACTCCCGACCTCAGGTGA 26903
Qy 3702 TCTGCCTGCCCTCAGTCTCCCAAAGTCTGGAAATTATAGGCGTGAGTCACTGTGCTGGCC 3761
Db 26902 TCCGCCTGCCCTCGGCTCCCAAAGTCTGGGAATTACAGGTGTGAGCCACCGTGCCCGGCC 26843
Qy 3762 GATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATA 3821
Db 26842 TATACCT--TATTTTCATCAATAAAATATATAGACCTTAAACTACCTGTGTCTACTTA 26786
Qy 3822 GTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTTAGATATAAACTTTCTTTTCT 3881
Db 26785 TTAAATGAGACCATTAACACCAGTATTTCACATAAATAAATAAATAAAGTCAAAA 26726
Qy 3882 TTTTA---AAACAATCTTGACAACTTTGCAGAAATAAATACAATCTTGCAATCTGCTTT 3937
Db 26725 ATTAATACTAAAAACATTTGTTTTTCTTGTAGATCTAGCCCAATGTCTCTGTCTCT 26666
Qy 3938 TCATTATCACCTTGTATGACTTTTTCATATTGCTCAAACTTAAATGTTACTGTTTT 3997
Db 26665 TCTGGCTTCAATGCTTCTATCTTTCCCTACATGTATAGTCTGCAGTGGCTTCCCAC 26606
Qy 3998 TTCATTGTTACTATTTTAGTCACTGA--ATAATATGGCTTAATTTGCTTATACATCCTCC 4055
Db 26605 TTCATTACTAATCTACACCTAACAGACCGTAAGATGTATTGAAAGATTTGTTACTAATGA 26546
Qy 4056 TGCTCCACTTTTAGAG-----GCCAAATTTACAAATCTGATGAAAGC 4097
Db 26545 GTATCAAGTTATAACCTATTTTATGTTATTTTCAACAACATTTATCTTAGTCAATTTGCAT 26486
Qy 4098 TATGAACCTCTCCCCAGAGAAATACACACACACACACACTCACACACAGTTTTTTT 4157
Db 26485 TCTGCTTAGATTTCTAAGACAAAAAGATAGAGGTTAAAGCTAGACTCAGAGCCTATCTC 26426
Qy 4158 TAATGTTTGCAACTAAGACAAGAAACCTGCAATTAGAGGATGTTTGTTCATATTAATAAA 4217
Db 26425 AACACGTGGCTTCAGTAGAACAAAGGTTAAGAAATTGTTAGCTTAAGGCAATGACGTATT 26366
Qy 4218 AATAACTCAGTTGGCA---CAGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAGTCC 4273
Db 26365 AAAAACTTAAGGCCAGGTGCAGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCC 26306
Qy 4274 AAGGTGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAAAC 4333
Db 26305 TAGGCAGGCAGATCAC--GAGGTCAGGAGATCGAGACCATCCTGGCTAACACCGTGAAAC 26248
Qy 4334 CCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCC 4392
Db 26247 CCCATCTCTACTAAAAATACAAAAAATTAGCCGTGATGGTGGCACACGCCTGTAGTCCC 26188
Qy 4393 AGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGTTGCAAGTG 4452
Db 26187 AGCTACTTGTGGGCTGAGGCAGGAGAAATGGTGTGAACCCGGGAGGCAGAGCTTGCAAGTA 26128
Qy 4453 AGCCGAGATCCCACTGCACTCCAGCCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAA 4512

Db 26127 AGCCAAGATCATGCCACTGCACCTCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAAACA 26068

Qy 4513 AATAAATAAAATAAAGGATCGGAGAGAAACAAAACCTAAATAAGATTCTCTGAAGGT 4570

Db 26067 AAACAAAACAAAACAAACCCCAAAAACCAAAAACCAAAAAGAACACAAACGAATGT 26010

RESULT 13

US-09-949-016-14437/c

; Sequence 14437, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 14437

; LENGTH: 32068

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14437

Query Match 8.4%; Score 420.4; DB 3; Length 32068;

Best Local Similarity 60.7%; Pred. No. 6.9e-86;

Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;

Qy 3104 TTTTCTTCTTGTGTTAGAGACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAG 3162

Db 27493 TTTTCTTCTTCTTTTGTGAGACGGAGTTTCGCTCTTGTGCCCCAGGCTGGAGTGCAA 27434

Qy 3163 TGGTCAACCATAGGTCACCTGACGCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC 3222

Db 27433 TGGTCAATCTTGGCTCACCGCAACCTCCGCCCTTCTCGGTTCAAGCAATCTCCTGCTC 27374

Qy 3223 AGCTCCCAAGTAGCTGGGACTACGAGCGTGCAACCAACGCTGGCTTAATTAATAAAT 3282

Db 27373 AGCTCCCAAGTAGCTGGGATTACAGGCATCGCCACCATGCTCCCGGCTAGTTTGTGA--- 27317

Qy 3283 TTTTGTAGAGACTGGGCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCA 3342

Db 27316 TTTTGTAGAGACAGGGTTTCTCCATGTTGTCAGGCTGATCTGGAACCTCCCGACTTCA 27257

Qy 3343 AGCAATCCTCCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGGTGAGCCACCATGTG 3402

Db 27256 GGTGATCGCCTGCCTTGGCTCCCAAGTGTTGGGATTACCGCGTGAGCCACTCGGCC 27197

Qy 3403 CGGCTACTTATTCTTTACATTCCATCTTTCCAATAGATGTAAAGATCCACAGAACAGGG 3462

Db 27196 CAG---CTGATTTTCTTCTTTCAATATGTCCAATGATGTTCTCTGAGCCCCGTTTACCT 27140

Qy 3463 ATTACTGCCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCATCTCATCACCTCAACC 3522

Db 27139 TATTTTCTTTTGTGATGGAGTTTGTCTTGTGTTGCCAGGCTGGAGTGCAATGAGG 27080

Qy 3523 TCCGTTAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYCATTTCTCCTGCCTAAGCCT 3582

Db 27079 TGATCTCGGCTCACCGCAACCTCCACCTCCAGGTTCAAGCAATTTCTCCTGCCTCAGCCT 27020

Qy 3583 CCTGAGTAGCTGGAATTACAAGCGTGCAACCATGCTTGGCTGAATTTT-TTGTATTTT 3641

Db 27019 CCTGAGTAGCTGGATTACAGGCGATGACCAACCACCGCCCGCTAATTTTGTATTTT 26960

Qy 3642 AGCAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGA 3701

Db 26959 AGTAGAGACGGGGTTTCTCCATGTTG---AGGCTAGTCTCTAACTCCCGACCTCAGGTGA 26903

Qy 3702 TCTGCCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGCGGTGAGTCACTGTCCTGGCC 3761

Db 26902 TCCGCCTGCCTCGGCTCCCAAAGTCTGGGATTACAGGTGTAGGCCACCGTGCCCGGCC 26843

Qy 3762 GATTACTGTCTATTTTCTTTATTTGCTATATCCCCAGATCTAGAGCAGTGTGACATATA 3821

Db 26842 TATACCT--TATTTTCATCAATAAAATATATGACCTTAAACTACCTGTGTACTACTTA 26786

Qy 3822 GTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTT 3881

Db 26785 TTAAATGAGACCATTAAACACCAAGTATTTCATCAATAAAATAAAATAAAATTTAAAGTCAAAA 26726

Qy 3882 TTTTA---AAACAATCTTGACAACTTTGCAGATAAATAACAATCTTGCAATTTGCTTTT 3937

Db 26725 ATTAATACTAAACAATTTGTTTTTCTTGTCTAGATCTAGCCCCAAATGTCTCTCTCT 26666

Qy 3938 TCACCTTATCACCTTGTATGACCTTTTTCATATATGCTCAAACTTTTATTGTTACTGTTTT 3997

Db 26665 TCTGGCTTCAATGCTTCTATCTTCCCTACATGTATATACTAGCTTGCACTGCTCCAC 26606

Qy 3998 TTCATTGTTACTATTTTAGTCACTGA--ATAATATGGCTTAATTTGCTTATACATCCTCC 4055

Db 26605 TTCATTACTAATCTACACCTAAACAGACCGTAAGATGTATTGAAAGATTTGTTACTAATGA 26546

Qy 4056 TGCTCCACTTTTAGAAG-----GCCAAATTTACAAATCTGATGAAAAGC 4097

Db 26545 GTATCAAAGTTATAACCTATTTTATGTTATTTCAACAACATTATTCTTAGTCAATTTGCAT 26486

Qy 4098 TATGAACCCCTCTCCCCAGAGAAATACACACACACACACACTCACACACAGTTTTTTT 4157

Db 26485 TCTGCTTAGATTTCTAAGACAAAAAGATAGAGGTTAAAGCTAGACTCAGAGCCTATCTC 26426

Qy 4158 TAATGTTTGCAACTAAGACAAAGAACCTGCATTAGAGGATGTTTGTTCATATTAATAA 4217

Db 26425 AACCAGTGGCTTCAGTAGAACAAAGGTTAAGAAATTGTTAGCTTAAGGCAATGACGTATT 26366

Qy 4218 AATAACTCAGTTGGCA---CAGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAAAGTCC 4273

Db 26365 AAAAACACTTAAGGCCAGGTGAGTGGCTCACGCCCTGTAATCCAGCACTTTTGGAGGCC 26306

Qy 4274 AAGGTGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAAAC 4333

Db 26305 TAGGCAGGCAGATCAC--GAGGTCAGGAGATCGAGACCATCCTGGCTAACACCGGTGAAC 26248

Qy 4334 CCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCC 4392

Db 26247 CCCATCTCTACTAAAAATACAAAAAATTAGCCGTGCATGGTGCCACACGCCCTGTAGTCCC 26188

Qy 4393 AGTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGTTGCAGTG 4452

Db 26187 AGTACTTGTGGGCTTGAGGCAGGAGAAATGGTGTGAAACCCGGGAGGCAGAGCTTGCA 26128

Qy 4453 AGCCGAGATCCCACCTGCACCTCCAGCCTGGCGGACACAGCGAGACTCTATCTCAAAAA 4512

Db 26127 AGCCAAGATCATGCCACTGCACTCCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAAAACA 26068

Qy 4513 AATAAATAAATAAATAAAGGATCGGAGAGAAACAAAACTAATAAGATTCTCTGAAGGT 4570

Db 26067 AAAACAAAACAAAAAAACCCAAAAACCAAAAAACAAAAAGAAACACAAACGAATGT 26010

RESULT 14

US-09-949-016-14438/c

; Sequence 14438, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

Query Match		8.4%;	Score 420.4;	DB 3;	Length 32068;
Best Local Similarity		60.7%;	Pred. No. 6.9e-86;		
Matches 910;		Conservative 1;	Mismatches 542;	Indels 45;	Gaps 12;
Qy	3104	TTTTTTTTTGTGTTTGTAGACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAG	3162		
Db	27493	TTTTTCTCCTTTTTTTTTTGAGACGGAGTTTCGCTCTTGTTGCCAGGCTGGAGTGCAA	27434		
Qy	3163	TGGTGCAACCATAGGTCACCTGAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC	3222		
Db	27433	TGGTGCAATCTTGGCTCACCGCAACCTCCGCCTTCTCGGTTCAAGCAATTCTCCTGCCTC	27374		
Qy	3223	AGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCTGGCTAATTAATAAAAT	3282		
Db	27373	AGCCTCCCAAGTAGCTGGGATTACAGGCATGCGCCACCATGCCCGGCTAGTTTTGTGA---	27317		
Qy	3283	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCA	3342		
Db	27316	TTTTTTAGTAGACAGGGTTTCTCCATGTTGGTCAGGCTGATCTGGAACTCCCGACTTCA	27257		
Qy	3343	AGCAATCCTCCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGGTGAGCCACCATGTG	3402		
Db	27256	GGTGATTCGCCTGCCTTGGCCCTCCCAAGTGTGGGATTACGGCGTGAGCCACTCGGCC	27197		
Qy	3403	CGGCTACTTATTTCTTTACATTCATCTTTTCCAATAGAAATGTAAGATCCACAGAACAGGG	3462		
Db	27196	CAG---CTGATTTTCTTCTTTTCAGTATGTCCAATGATGTTCTCTGAGCCCCGCTTATACCT	27140		
Qy	3463	ATTACTGCCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTTCATCACCTCAACC	3522		
Db	27139	TATTTTCTTTTGTGATGGAGTTTGTCTCTTGTGCCCCAGGCTGGAGTGCAATGAGG	27080		
Qy	3523	TCCGTTCAGCTCACTGCAACCTCTGCTCCTCCGGGTTCAAGYGATTTCTCCTGCCTAAGCCT	3582		
Db	27079	TGATCTCGGCTCACCGCAACCTCCACCTCCAGGTTCAAGCAATTTCTCCTGCCTCAGCCT	27020		
Qy	3583	CCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTT-TTGTATTTT	3641		
Db	27019	CCTGAGTAGCTGGGATTACAGGCATGCACCACCACCGCCCGCTAATTTTGTATTTTTT	26960		
Qy	3642	AGCAGAGATGGGGTTTTACCATGTTGCCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGA	3701		
Db	26959	AGTAGAGACGGGGTTTCTCCATGTTG---AGGCTAGTCTCTAACTCCCGACCTCAGGTGA	26903		
Qy	3702	TCTGCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGCGGTGAGTCACCTGTGCTGGCC	3761		
Db	26902	TCCGCTGCCTCGGCTCCCAAAGTGTGGGATTACAGGTGTGAGCCACCGTGCCTCGGCC	26843		
Qy	3762	GATTACTGTCTATTTTCTTTTATGCTATATCCCAGATCTCAGAGCAGTGTCTGACATATA	3821		
Db	26842	TATACCT---TATTTTCATAAATAAAATATATGACCTTAAACTACCTGTGTCACTACTTA	26786		
Qy	3822	GTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTTAGATATAAACTTTTCTTTTCTTT	3881		
Db	26785	TTAAAAATGAGACCATTAACACACCACTATTCACTAAATAAAAAAAATTTAAAGTCAAAA	26726		
Qy	3882	TTTTTA---AAACAATCTTGACAACTTTGCAGAAATAAATACAATCTTGCAATTTCTGCTTTT	3937		
Db	26725	ATTAATACTAAACATTTGTTTTTCTGTGCAGATCTAGCCCAAAATGTCCTCTGTCTCTCT	26666		
Qy	3938	TCACTTATCACCTTGTATGACTTTTTCATATTGCTCCTCAACCTTTTATTGTTACTGTTTT	3997		
Db	26665	TCTGGCTTCAATGCTTCTATCTTTCCCTACATGTATACTAGCTTGCAGTGGCTTCCCAC	26606		
Qy	3998	TTCAATGTTACTATTTTAGTCACTGA--ATAATATGGCTTAATTTGCTTATACATCCTCC	4055		
Db	26605	TTCAATTAATAATCTACACCTTAACAGACCGTAAGATGTATTGAAAGATTTGTTACTAATGA	26546		
Qy	4056	TGCTCCACTTTAGAAG-----GCCAAATTTACAAATCTGATGAAGC	4097		
Db	26545	GTATCAAGTTATAACCTATTTTATGTTATTTCAACAACATATATTCTTAGTCAATTGTCAT	26486		

Qy	4098	TATGAACCCCTCTCCACAGAGAAATACACACACACACACACACTCACACACAGTTTTTTTT	4157		
Db	26485	TCTGCTTAGATTTCTAAGACAAAAAGATAGAGGTTAAAAAGCTAGACTCAGAGCCTATCTC	26426		
Qy	4158	TAATGTTTGCAACTAAGACAAGAAACCTGCAATTAGAGGATGTTTGTTCATATTAATTAAA	4217		
Db	26425	AACCACGTGGCTTCAGTAGAAACAAAGGTTAAGAAATTGTAGCTTAAGGCAATGACGTATT	26366		
Qy	4218	AATAACTCAGTTGGGCA---CAGTGACTCAAGCCTGTAAACCACACAGTACTTTTGGAGTCC	4273		
Db	26365	AAAAACACTTAAGGCCAGGTGCAGTGGCTCACGCCTGTAAATCCAGCACCTTTGGGAGGCC	26306		
Qy	4274	AAGTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGSGTAAAC	4333		
Db	26305	TAGGCAGGCAGATCAC--GAGGTCAGGAGATCGAGACCATCCTGGCTAACACCGGTGAAAC	26248		
Qy	4334	CCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCC	4392		
Db	26247	CCCATCTCTACTAAAAATACAAAAAATTAGCCGTGCATGGTGGCACACGCCCTGTAGTCCC	26188		
Qy	4393	AGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTG	4452		
Db	26187	AGCTACTTGTGCGGCTGAGGCAGGAGAAATGGTGTGAACCCCGGAGGCAGAGCTTGCACTA	26128		
Qy	4453	AGCCGAGATCCCACCCTGCACTCCAGCCTCGGCGACACACAGCAGACTCTATCTCAAAAA	4512		
Db	26127	AGCCAAGATCATGCCACTGCACTCCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAAAACA	26068		
Qy	4513	AATAAATAAATAAATAAAGGATCGGAGAGAAACAAAACTAATAAGATTCTCTGAAGGT	4570		
Db	26067	AAACAAAAACAAAAAACCCAAAAAACCAAAAAACAAAAAGAACACAAAAACGAATGT	26010		
RESULT 16					
US-09-949-016-14440/c					
; Sequence 14440, Application US/09949016					
; Patent No. 6812339					
; GENERAL INFORMATION:					
; APPLICANT: VENTER, J. Craig et al.					
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED					
; FILE REFERENCE: CL001307					
; CURRENT APPLICATION NUMBER: US/09/949,016					
; PRIOR FILING DATE: 2000-04-14					
; PRIOR APPLICATION NUMBER: 60/241,755					
; PRIOR FILING DATE: 2000-10-20					
; PRIOR APPLICATION NUMBER: 60/237,768					
; PRIOR FILING DATE: 2000-10-03					
; PRIOR APPLICATION NUMBER: 60/231,498					
; PRIOR FILING DATE: 2000-09-08					
; NUMBER OF SEQ ID NOS: 207012					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 14440					
; LENGTH: 32068					
; TYPE: DNA					
; ORGANISM: Human					
US-09-949-016-14440					
Query Match		8.4%;	Score 420.4;	DB 3;	Length 32068;
Best Local Similarity		60.7%;	Pred. No. 6.9e-86;		
Matches 910;		Conservative 1;	Mismatches 542;	Indels 45;	Gaps 12;
Qy	3104	TTTTTTTTTGTGTTTGTAGACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAG	3162		
Db	27493	TTTTTCTTCCCTTTTTTTTTTGAGACGGAGTTTCGCTCTTGTTGCCAGGCTGGAGTGCAA	27434		
Qy	3163	TGGTGCAACCATAGGTCACCTGAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC	3222		
Db	27433	TGGTGCAATCTTGGCTCACCGCAACCTCCGCCTTCTCGGTTCAAGCAATTCTCCTGCCTC	27374		
Qy	3223	AGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCTGGCTAATTAATAAAAT	3282		
Db	27373	AGCCTCCCAAGTAGCTGGGATTACAGGCATGCGCCACCATGCCCGGCTAGTTTTGTGA---	27317		

Qy	3283	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCA	3342
Db	27316	TTTTTAGTAGACAGGGTTTCTCCATGTTGGTCAGGCTGATCGGAACCTCCGACTTCA	27257
Qy	3343	AGCAATCCTCCTACTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTG	3402
Db	27256	GGTGATTCGCCTTGGCCTCCCAAGTGTGGGATTACCGCGGTGAGCCACTCGCC	27197
Qy	3403	CGGCTACTTAATTTCTTTACATTCATCTTTCCAATAGAAATGTAAGATCCACAGAACAGGG	3462
Db	27196	CAG---CTGATTTTCTTCTTTTCAGTATGTCCAATGATGTTCTCTGAGCCCGCTTATACCT	27140
Qy	3463	ATTACTGCCTAATTTCTCTTCTTTTGGACAGAGTCTCAGTTCATCACCCTCAACC	3522
Db	27139	TATTTTTTTTTTTTGAGATGGAGTTTTGCTCTTGTGGCCAGGCTGGAGTGCAATGAGG	27080
Qy	3523	TCCGTTCAGCTCACTGCAACCTCTGCGCTCCCGGGTTCAAGYGATTTCTCCTGCCTAAGCCT	3582
Db	27079	TGATCTCGGCTCACCGCAACCTCCACCTCCAGGTTCAAGCAATTTCTCCTGCCTCAGCCT	27020
Qy	3583	CCTGAGTAGCTGGAATTACAAGCGTGCACCAACCATGCTTGGCTAAATTTT-TTGTATTTT	3641
Db	27019	CCTGAGTAGCTGGGATTACAGGCATGCACCAACCGCCCGCCTAAATTTTGATTTTTTT	26960
Qy	3642	AGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGA	3701
Db	26959	AGTAGAGACGGGTTTCTCCATGTTG--AGGCTAGTCTCTAACTCCCGACCTCAGGTGA	26903
Qy	3702	TCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCC	3761
Db	26902	TCCGCTGCCTCGGCCTCCCAAAGTCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCC	26843
Qy	3762	GATTACTGTCTATTTTCTTTTATTTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATA	3821
Db	26842	TATACCT---TATTTTCATCAAATAAAATATATGACCTTAAACTACCTGTGTATACITTA	26786
Qy	3822	GTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTT	3881
Db	26785	TTAAATGAGACCAATTAAACACCAAGTATTCACTAAATAAAAAAAATTTAAAGTCAAA	26726
Qy	3882	TTTTA----AAACAATCTTGACAACCTTTGCAGAAATAAATACAACTCTTGCTTTT	3937
Db	26725	ATTAATACTAAACATTTGTTTTTCTGTGCAGATCTAGCCCAAATGTCCTGTCTCTCT	26666
Qy	3938	TCACTTATCAGCTTGTTATGACTTTTTTCATATTTGCCTCAAACTTTATTTGTTACTGTTT	3997
Db	26665	TCTGGCTTCAATGCTTTCTATCTTTCCCTACATGTATACTAGTTCAGTGGCTTCCAC	26606
Qy	3998	TTCATTGTTACTAFTTTTAGTCACTGA--ATAATATGGCTTAATTTGCTTATACATCCTCC	4055
Db	26605	TTCATTACTAATACACCTTAACAGACCGTAAGATGTATTGAAAGATTTGTTACTAATGA	26546
Qy	4056	TGCTCCACTTTAGAAG-----GCCAAATTTACAAATCTGATGAAAGC	4097
Db	26545	GTATCAAAGTTATAACCTATTTTATGTTATTTCACAACATTTATTCTTAGTCATTTGCA	26486
Qy	4098	TATGAACCTCTCCCCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTT	4157
Db	26485	TCTGCTTAGATTTCTAAGACAAAAAGATAGAGGTTAAAGCTAGACTCAGAGCCTATCTC	26426
Qy	4158	TAATGTTTGCACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTA	4217
Db	26425	AACCACGTGGCTTCAGTAGAACAAGGTTAAGAAATTGTTAGCTTAAGGCAATGACGTATT	26366
Qy	4218	AATAACTCAGTTGGGCA----CAGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAA	4273
Db	26365	AAAAACACTTAAGGCCAGGTGCAGTGGCTCAGCCTGTAATCCCAGCACTTTGGGAGGCC	26306
Qy	4274	AAGGTGGGTGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGA	4333
Db	26305	TAGGCAGGCAGATCAC--GAGGTACGGAGATCGAGACCATCCTGGCTAAACACCGTGA	26248

Qy	4334	CTATCTCTACTAAAAATAC-AAAAATTAGCTGGTGTAGTGATGCATGCCTGTAGTCCC	4392
Db	26247	CCCATCTCTACTAAAAATACAAAAAATTAGCCGTGCATGGTGCCACACGCCTGTAGTCCC	26188
Qy	4393	AGTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTG	4452
Db	26187	AGTACTTGTGGGCTGAGGCAGGAGAAATGGTGTGAACCCGGGAGGCAGAGCTTGCAGTA	26128
Qy	4453	AGCCGAGATCCCACCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAA	4512
Db	26127	AGCCAAGATCATGCCACTGCACCTCCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAAA	26068
Qy	4513	AATAAATAAATAAAATAAAGGATCGGAGAGAAACAAAACTAATAAGATTCTCTGAAGGT	4570
Db	26067	AAAACAAAACAAAAAAACCCCAAAACCAAAAAACAAAAAAGAACACAAACGAATGT	26010
RESULT 17			
US-09-949-016-14441/c			
; Sequence 14441, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001307			
; CURRENT APPLICATION NUMBER: US/09/949,016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 14441			
; LENGTH: 32068			
; TYPE: DNA			
; ORGANISM: Human			
US-09-949-016-14441			

Query Match			
Best Local Similarity 8.4%; Score 420.4; DB 3; Length 32068;			
Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;			
Qy	3104	TTTTTTTTTGTGTTGTAGAGACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAG	3162
Db	27493	TTTTTCTTCTTTTTTTTTTGAGACGGAGTTTCGCTTGTGTCAGGCTGGAGTGCAA	27434
Qy	3163	TGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC	3222
Db	27433	TGGTGCAATCTTGGCTCACCGCAACCTCGCCCTTCTCGGTTCAAGCAATTCTCCTGCTC	27374
Qy	3223	AGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACACCAACGCTGGCTAATTAAAAAAT	3282
Db	27373	AGCCTCCCAAGTAGCTGGGATTACAGGCATGCGCCACCATGCCCCGGCTAGTTTGTGA---	27317
Qy	3283	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGTTGTCTTAAACTCCTGGCTTCA	3342
Db	27316	TTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGATCTGGAACCTCCGACTTCA	27257
Qy	3343	AGCAATCCTCCTACCTTGGCATCCCAAAGTGTCTGGGATTACAGGGGTGAGCCACCATGTG	3402
Db	27256	GGTGATTCGCCCTGCCCTTGCCCTCCCAAAGTGTGGGATTACCGCGGTGAGCCACTGCGCC	27197
Qy	3403	CGGCTACTTATTTCTTTTACATTCATCTTTTCCAATAGAAATGTAAGATCCACAGAACAGGG	3462
Db	27196	CAG---CTGATTTTTTCTTTTCAGTATGTCCAATGATGTTCTCTGAGCCCGCTTATACCT	27140
Qy	3463	ATTACTGCCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCATTTCACCTCAACC	3522
Db	27139	TATTTTTTTTTTTTGAGATGGAGTTTTTGCTCTTTGCTTGTGCCCAGGCTGGAGTGCATGAGG	27080

QY	3523	TCCGTTACGCTCACTGCAACCTCTGCTCCCGGTTCAAGYGATTTCTCCTGCCTAAGCCT	3582
Db	27079	TGATCTCGGCTCACCGCAACCTCCACCTCCAGGTTCAAGCAATTTCTCCTGCCTCAGCCT	27020
QY	3583	CCTGAGTAGCTGGAATTAACAAGCGTGCACCAACCATGCTTGGCTAAATTTT-TTGTATTTTT	3641
Db	27019	CCTGAGTAGCTGGATTACAGGCATGCACCAACCGCCCGCTAAATTTTGTATTTTTTTT	26960
QY	3642	AGCAGAGATGGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGA	3701
Db	26959	AGTAGAGACGGGGTTTCTCCATGTTG--AGGCTAGTCTCTAACTCCGACCTCAGGTGA	26903
QY	3702	TCTGCCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGAGTCACTGTGCCTGGCC	3761
Db	26902	TCCGCCCTGCCTCGGCCCTCCCAAAGTGTGGGATTACAGGTGTAGCCACCGTGCCTGGCC	26843
QY	3762	GATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATA	3821
Db	26842	TATACCT--TATTTTCATCAAAATAAATATATGACCTTAAACTACCTGTGTCACTTA	26786
QY	3822	GTAGGTGCTCAATAAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTT	3881
Db	26785	TTAAATAGAGACCATTAAACACCAAGTATCTACTAAATAAAAAAATAATTAAGTCAAAA	26726
QY	3882	TTTTA----AAACAATCTTGACAACTTTGCAGAATAAATACAACTTTGCAATCTGCTTTT	3937
Db	26725	ATTAATACATAAAACATTTGTTTTCTTGTTCAGATCTAGCCCAATGTCCTCTGTCTCTCT	26666
QY	3938	TCACTTATCACCTTGTATGACTTTTTCATATTGCCCTCAAACCTTTATTTGTTACTGTTTT	3997
Db	26665	TCTGGCTTCAATGCTTTCTATCTTTCCCTACATGTATCTAGTGTGAGTGGCTCCAC	26606
QY	3998	TTCAATTGTTACTATTTTAGTCACTGA--ATAATATGGCTTAATTTGCTTATACATCCTCC	4055
Db	26605	TTCAATTACTAATCTACACCTAACAGACCGTAAGATGTATTGAAAGATTGTTACTAATGA	26546
QY	4056	TGCTCCACTTTAGAAG-----GCCAAATTTACAAATCTGATGAAGC	4097
Db	26545	GTATCAAGTTATAACCTATTTTATGTTATTTCACAACATATTCTTAGTCATTTGCAT	26486
QY	4098	TATGAACCTCTCCCCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTT	4157
Db	26485	TCTGCTTAGATTCTAAGACAAAGATAGAGGTTAAAGCTAGACTCAGAGCCTATCTC	26426
QY	4158	TAATGTTTGCAACTAAGACAAGAACCTGTCATTAGAGGATGTTGTTTCAATTAATATAA	4217
Db	26425	AACCACGTGCTTCAGTAGAACAAAGGTTAAGAAATTGTTAGCTTAAGGCAATGACGTATT	26366
QY	4218	AATAACTCAGTTGGGCA---CAGTGACTCAAGCCTGTAACCAACAGTACTTTGGAGTCC	4273
Db	26365	AAAAACACTTAAGCCAGGTGCAGTGGCTACGCCTGTAATCCAGCACTTTGGGAGGCC	26306
QY	4274	AAGTGGGTGGATCACCTTGAGGTGAGAAATTTCGAGACCAGCTGGTCAATATGGTGAAC	4333
Db	26305	TAGGCAGGCAGATCAC--GAGGTGAGAGATCGAGACCATCCTGGCTAACACGGTGAAC	26248
QY	4334	CCTATCTCTACTAAAAATAC-AAAAATTAGTGGGTGTAGTGAATGCCTGTAGTCCC	4392
Db	26247	CCCATCTCTACTAAAAATACAAAAAATTAGCCGTGTCATGGTGCAACGCCTGTAGTCCC	26188
QY	4393	AGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGTTGCACTG	4452
Db	26187	AGCTACTTGTGGGCTGAGGCAGGAGAAATGGTGTGAACCCGGGAGGCAGAGCTTGCAGTA	26128
QY	4453	AGCCGAGATCCCACCACTGCCTCCAGCTGGCGCACACAGCGAGACTCTATCTCAAAAA	4512
Db	26127	AGCCAAGATCATGCCACTGCCTCCAGTCTAGGAGACAGAGCAAGACTGTCTCAAAAAACA	26068
QY	4513	AATAAATAAATAAAGGATCGGAGAGAAAAACAAATAAAGATTCTCTGAAGGT	4570
Db	26067	AAAACAAAACAAAAAAACCCAAAAAACCAAAAAACAACAAAGAACACAAACGAATGT	26010

RESULT 18
US-09-949-016-15628/c
; Sequence 15628, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15628
; LENGTH: 31111
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(31111)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15628

Query Match	8.4%;	Score	419.2;	DB	3;	Length	31111;
Best Local Similarity	57.8%;	Pred.	No. 1.3e-85;				
Matches	913;	Conservative	1;	Mismatches	629;	Indels	37;
							Gaps
							8;
QY	2987	AGAACAACTATGGATAGGTACAATTATCCTC	ACCTTAACAGATAAGAAAAC	CTGAGGCT	3046		
DB	13996	AGATGGCCTTATCGGGTAAAGAACATTTCTTT	TATTCCTAGATCCTAAGACTTTTTTA	13937			
QY	3047	CAGAAGGCTGAGCTATTTGCCCAAGATCACAC	AGCTTGTAAAGTGGTGACAGTTTGGGTTT	3106			
DB	13936	AAAAAGGATGTTGAATTTATTGAC	TTTTTTTACATCAATTGAAACCATTTTTTAGCT	13877			
QY	3107	TTTTTTGTTGTTTAGAGACAGGGTCTTGCTCT	GTGCACCCAGGCATGAGCACAGTGGT	3166			
DB	13876	TTAATTAATTAATTTTGAGACAAGGTCTCGCT	CTGCCACCCAGGCTGAAGTGCAGTAGG	13817			
QY	3167	GCAACCATAGGTCAC	TGCAGCCCTCAACCTCCTGAGCTCAAGG	ATCTGCTGACCTCAGCC	3226		
DB	13816	GCAATCTTGGTTCACTGCAACCTCTGCCTT	CCAGGCTCCAGC	CAATCTCTCCACGTCAGCC	13757		
QY	3227	TCCCAAGTAGCTGGGACTACGAGCGTGCA	CCACCACCGCTGGCTA-----ATTAAAAA	3280			
DB	13756	TCCCCAGTACTTGGGGCTACAGGTATGCG	CTCCAAAGCCTGGCTACTTTTTTTTCTTTG	13697			
QY	3281	ATTTTTTTGTAGAGACTGGGTCTTACTAC	GTGGCCAGGCTTGCTTTAAACTCCTGGCTT	3340			
DB	13696	TATTTTGTAGAGACGGGGTTTGGCATATT	GGCCAGGCTGGTCTCGAACTCCTGGGCT	13637			
QY	3341	CAAGCAATCCTCCTACCTTGGCATCCCA	AAGTGTCTGGGATTACAGGGGTGAGCCACATG	3400			
DB	13636	CAAGCAATCCTCCTGCTTTGGCCTCCCA	TATGTGGAATTACAGGGCTGAGCCACCGCA	13577			
QY	3401	TGCGGCTACTTATTTCTTTTACATTC	CAATCTTTTCCAAATAGAAATGTAAGATCCACAGAACAG	3460			
DB	13576	CACAGCCCATTTTTTAGCTTTAATAC	ATTAATGTATGAATTTACGTTAAATTTGATTTCTT	13517			
QY	3461	GGATTACTGCCATTTTCTTCTTTTCT	TTTTTTTGAGACAGAGTCTCACTTCATCACCTCAA	3520			
DB	13516	TTTTTTTGC	GGGAGGGGACGGAGTTTCGCTCTTGTGGCCAGGCTGGAGTGCAATGG	13457			
QY	3521	CCTCCGTTACAGCTCACTGCAACCTCT	GCCTCCCGGGTTTCAAGYGATTTCTCTGCCCTAAGC	3580			
DB	13456	CGGATCTTGGCTCCGCCCAAACTCCG	CTCTCAGGTTTCAAGGATTTCTCTCGCTTAGC	13397			

QY	3581	CTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCACCATGCTTGGCTAAATTTTTTGTATTTT	3640
Db	13396		
QY	3641	TAGCAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTG	3700
Db	13338		
QY	3701	ATCTGCCTGCCTCAGTCTCCCAAAGTGTGGGAATTATAGGCGTGAGTCACTGTGCCTGGC	3760
Db	13278	ATCCACCCGCTCAGCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCCGAGC	13219
QY	3761	CGATTACTGTCTATTTTCTTTATTGCTATATATCCCCAGATCTAGAGCAGTGTCTGACATAT	3820
Db	13218	CGTTAATTGATTTTCTAATATTTAAATCAATCTTGATGGGATAAACCAAACTTGGTCTATGC	13159
QY	3821	AGTAGG-----TGCTCAATAAATAATTGATGAATGCACAGCCCTAGATATAAACTTTTCTTT	3875
Db	13158	ATATTGCAGTTTGTGTTTATATACATGCTTGATTTAATTGCTGAAATTTTGTGGTGGTTT	13099
QY	3876	TTCTTTTTTTTAAACAATCTT-----GACAACTTTTGCAGATAAATAACAATCTTGCAAT	3929
Db	13098	AGCATTTTTTTACATATATGTTGAGGAGGACATGCTGTTTATTAAATTCACACAAAGACT	13039
QY	3930	CTGCTTTTTCACTTATCACCTTGTTA---TGACTTTTTTCAATGTCCTCAAACTTTTATT	3986
Db	13038	CTAAATGGTAGAAGTTGGCTGGGTACAGTGACTTACGCTGFAAATCCAGCACTTTGGG	12979
QY	3987	GTTACTGTTTTTTCATGTTACTATTTT---AGTCACTGAATAATATGGCTTAATTTGC	4042
Db	12978	AGGCCAAGGTGACGGATTGCTTGAGCTCAAGAGCTCGAGACCAGCCTGGGCAACATGSC	12919
QY	4043	TTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAATTTA-----CAAATCTGATGAAG	4096
Db	12918	GAAACCCCTGCTCTACTATAAAATTTTAAAAACTAGCTGAATGTGATGTTGTGTCCTGTAG	12859
QY	4097	CTATGAACCCCTCTCCCCAGAGAAATACACACACACACACTCACACACAGTTTTTTT	4156
Db	12858	CAAAGATACTTGGGAGGCTGAGGTGGGAAGATCACCTGAGGTGGGAGGTCAAGGATGCA	12799
QY	4157	TTAATGTTTGCAACTAAGACAAGAAACCTGTCATTAGAGGATGTTTGTTCATATTAATTA	4216
Db	12798	GTAACCCATAATCACACCACCTGCCTCCTGCTGGCGCACCGAGTGAGACCCCTGCTCAA	12739
QY	4217	AAATAAATC-----AGTTGGGCACAGTGACTCAAGCCTGTAACCAACAGTACTTTGGAA	4271
Db	12738	AAATAAATAAATAAAGCTGGGGCAGTGGCTCAAGCCTGTAATCCAGCAGTTTGGGAGG	12679
QY	4272	CCAAGTGGGTGGATCACTTGAGGTGAGAAGTTTCGAGACCAGCCTGGTCAATATGGTGAA	4331
Db	12678	CTGAGGCGAGGAGTCACTGGAGGTGAGGAGTTCAAGACTAGCCTGGCCAATATGGTGAA	12619
QY	4332	ACCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCC	4391
Db	12618	ACCCCGCCTCTACTAAAAATACCACAATTAGCCAGGTGTGGTGGCACACGCTGTAATCC	12559
QY	4392	CAGCTACTCGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGT	4451
Db	12558	CAGCTACTCGGAGGCTGAGGCAAGAAATTGCTTGAACCCGGGAAGTGGAGGCTGCAGT	12499
QY	4452	GAGCCGAGATCCCACCACTGCATCCAGCCTGGCGACACAGCGAGAGCTCTATCTCAAAA	4511
Db	12498	GAGCTGAGTCGTGCCATTGCACTCCAGGCTGGGTGACAGGCGAGACCCCATCTCAAAA	12439
QY	4512	AAATAAATAAATAAATAAAA 4531	
Db	12438	TAATAGTAATAAATAAATA 12419	

RESULT 19
US-09-920-671-11
; Sequence 11, Application US/09920671

; Patent No. 6900306
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF COREST EXPRESSION
; FILE REFERENCE: RTS-0297
; CURRENT APPLICATION NUMBER: US/09/920,671
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 11
; LENGTH: 139257
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 10445
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 23754
; OTHER INFORMATION: unknown
; US-09-920-671-11

Query Match 8.3%; Score 416; DB 3; Length 139257;
Best Local Similarity 54.0%; Pred. No. 1.4e-84;
Matches 1222; Conservative 3; Mismatches 948; Indels 89; Gaps 15;

QY	2291	AGCCAGGCGGTGGCTCATGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGGCGG	2350
Db	63398	AGGCTGAGCATAGTGGCTCATACCTGTAATCCTAGCACCTTTGGGAGGCTGAGCGAGCGA	63457
QY	2351	ATCATTGAGGTCAGGATTCGAGACCAGCCCTGGCCAAACATGGTGAAACCCCTGTCTCTAC	2410
Db	63458	ATTGCCTGAGGTCAGGATTAAGACCAGCCCTGGCCAAACATGGTGAAACCCCGTCTCTAC	63517
QY	2411	TAAAAAATACAAAAATTAGCCGGACATGGTGGCAGCGCCTGTAAACCCAGCTACTTGGG	2470
Db	63518	T-AAAAAATACAAAAATTAGCCGGGTGTGGTCACAGGCGTCTGTAAATCCCAGCTACTCAGG	63576
QY	2471	AGACTGA-GTTGGAGGTTTCAGTGAGCCAAAGTCGTGTCACTGCTGTCCAGCCTGGGTAA	2529
Db	63577	AGGCTGAGGCAAGAGAATTCTTGAACCTGGGAGGTGGAGGTTGCGGTCACTCGAGATCG	63636
QY	2530	CAGAGCAACTCTGTCTCAAAAAAATAAATGCTTTCATAATAATATATGATAAAAGGACTT	2589
Db	63637	CGCCACTGCACCTCAGCCTGGGCAACAGAGTGAGACTTTTGTCAACACACACACACAC	63696
QY	2590	ATATTTTTTCAAGCCATAGGATCATTTCTCTCTGAAGCATCTTGGCGGAAGTCATCCCCACC	2649
Db	63697	ACACACACACACACACACGCTGAAATAAACCTATGAACC--AACTAATGCAGTGGATTTC	63754
QY	2650	TGTTCTCTGAGAGTGGCAGGTGAGGGCTGACCTATTGCTCTGCACCTTACTCTATCTCAG	2709
Db	63755	CAAAATTAAGATTAAAGTTGTGTAAATGTTTCTTGATGTACCCATTATTATTGAG	63814
QY	2710	CTGTCCCTCCCACCTTCCAGGTGCTGCCA-GACACATGACAACTGCTAYGACCAGGCCAA	2768
Db	63815	TGGAACACAGATTCCTTTTCATTCCTTGAAATCACTTTGCTGAGATTTTTTTATTTTTTA	63874
QY	2769	GAAGCTGGACAGCTGTAATAATTTCTGTGGACAMMCGGTACACCCACACACCTATTCTACTC	2828
Db	63875	TTTTTTTTTTGGAGACAGAGTCTCGCTGTGTGCGCCAGACTGGAGTGCAGTGGTGTGATC	63934
QY	2829	GTGCTCTGGCTCGCAATCACCTGTAGCAGT-AGGTTTATCCCTTCCCTTGACCTATGAAT	2887
Db	63935	TAGGCTCACTGCAACCTCCACCTCCCGGGTTCGAAGCGATTCTCTCGCTCAGCCTCCTGA	63994
QY	2888	TCTAGTTGGTTCTCAGTAGGCCGGGGGGAATAATAGTAACAACAGCCATGATTAGTGT	2947
Db	63995	GTAGCTAGGATTATAGGCATGTGCCACCACACTCAGCTAAATTTTTGTATTTTCAGTAGAGG	64054
QY	2948	TAATTTTCTTGGTTCTGGGCAGTGTCTCTCTTTAACTCCTCAGAAACAACACTATGGGATAGG	3007
Db	64055	TAGGGTTTTCACCATGTAGGCCAGGCTGGTCTCAAAACTCCTGACCTCAAGCGATCCGCCTG	64114

Qy	3223	AGCCTCCCAAGTAGCTGGGACTACGAGCGGTGCACCACCGCTGGCTAAATTAAAAAAAT	3282
Db	38833	AGTCTCCCAAGTAGCTGGGACTATAGGAGCCTGCCACCACCGCTGGCTAAATTTTTTTGTA	38774
Qy	3283	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCA	3342
Db	38773	ATTTTAGTAGACGCGGGTTTCACCATATTTGGCCAGGCTGGTCTCGAACTCCTGAC--CT	38716
Qy	3343	AGCAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGSGGTGAGCCACCATGTG	3402
Db	38715	TGTGATCCGCCCCACCTCAGCCTCCCAAAGTCTGCGATTCCAGSGGTGAGTCACCGTGCC	38656
Qy	3403	CGGCTACTTATTCTTTACATTCCATCTTTCCAATAGAAATGTAAGATCCACAGAACAGGG	3462
Db	38655	TGGCCAGTTAAATGTTTTTTTAGATGTGCTGTGAAGGTTGTTTTTTC-----	38607
Qy	3463	ATTACTGCCTATTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACC	3522
Db	38606	-TTGTTTCTTTTTTTTTTTTTTTTTTTTGTGAGATAGAGTCTCGCTCTGTTCCCCAGGCT	38548
Qy	3523	TCCGT-----TCAGCTCACTGCAACCTCTGCCTCCGGGTTCAAGYGATTC	3568
Db	38547	GGAGTGCAATGTRCGGATCTCGGCTCACTGCAACCTCCACCTCCAGGTTCAAGTGAATC	38488
Qy	3569	TCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAA-	3627
Db	38487	TCCTGCCTCAGCCTCCCAAATAGCTGGGATTACAGGCATGCACCACCATACCCGGGTAAT	38428
Qy	3628	---TTTTTTGTATTTTTAGCAGAGATGSGGTTTTTACCATGTTGGCCAGGCTGGTCTCAA	3684
Db	38427	CTTTTTTTTTGTATTTTAGGAGAGACGGGTTTTCACCATGTTGGCCAGGCTGGTCTCGAA	38368
Qy	3685	CTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTG	3744
Db	38367	CCCCTGACCTCAGGTGATCTGCCACCTCAGCTTCCCAAAGTGTGGAATTATAAGTGIG	38308
Qy	3745	AGTCACTGTGCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATATCCCCAGATCTAGA	3804
Db	38307	AGTCACCGCGCTCAGCCTGTTT-TTTTATTTGTAGAGATGGGCTTGCTATGTTGTTC	38249
Qy	3805	GCAGTGTCTGACATATAGTAGGTGCTCAATAAAATAATTGATGAATGCACAGCCTAGATAT	3864
Db	38248	CCAGGCTGGAATTGAACGCCTGACCTCAAGTGATCCTCCTGCCTCGGCCCTCCCAATGTGC	38189
Qy	3865	AAACTTTCTTTTCTTTTTTTAAACAATCTTGACAACCTTTGCAGAATAAATACAATCTT	3924
Db	38188	TGGGATT-----ACAGCTGTGAGCCACTGTGCCTCACATGCAAAATTTT	38145
Qy	3925	GCATTCTGCTTTTCACTTATCACCTTGTATGACTTTTTTCATATTTGCCTCAAAACCTTTA	3984
Db	38144	TTTTTTTTTTTTTGATGTGATTCACATT----TAAATCCGTAGACTTCAAGCACAGCAGGT	38089
Qy	3985	TTGTTACTGTTTTTTCATTGTTACTATTTTTAGTCACTGAATAATATGGCTTAATTTGCYT	4044
Db	38088	GACCGTCTGTAATGCAGATGGGCCTCATCTAATCAGTTGAAGGCTTAAGAGAAAAAGCC	38029
Qy	4045	ATACATCCTCTGCTCCACTTTTAGAAGGCCAAAATTTACAAATCTGATGAAAGCTATGAAC	4104
Db	38028	TGGGTCCCTTCCAGGAGGAGGAACTCTGCCTCCAGGTGGCCTTGGGGTTCCAGCTGCAG	37969
Qy	4105	CCTCTCCCCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTTAATGTT	4164
Db	37968	CACCAACTCTTCCTGGGTCTCCAGCCTGTGGCCTACACTGCAGATTTTCAGAGCTTGCC	37909
Qy	4165	TGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAACT	4224
Db	37908	TTAAATAAATCTGACAA-GGCGCAGCCTCAAGTGTGATCCTTGTAAAAAACTTCAAAC	37850
Qy	4225	CAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAGTCCAAGGTGGGTGG	4284
Db	37849	GGGCCAGGCATGTTGGCTCACGCTGGAATCCAGGACTTTTGGAGGCCGAGGCAGGCGG	37790

Qy	4285	ATCACTTGAGGTGAGAAGTTTCGAGACCAGCCTGCTCAATATGGTGAAACCCCTATCTCTAC	4344
Db	37789	ATCACCTGAAGTTAGGAGTTCAAGACCAGCCTGGCAACATGGCGAAACGCCGTCTCTAC	37730
Qy	4345	TAAAAATAC-AAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGG	4403
Db	37729	TAAAAATACAAAAAATTAGCCAGGCATGGTGGTGATGCCTGTAAATCCCAGCTATTGGG	37670
Qy	4404	AGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCC	4463
Db	37669	AGTTTGAGACAGAAGAAATTGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGATCG	37610
Qy	4464	CACCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAATAAAT	4523
Db	37609	CACCACTGCACCTCCAGCCTGGGTGACAGAGCAAGACTCCGTCTCAAAACAACAAACAAA	37550
Qy	4524	AAAAAT 4528	
Db	37549	CAAAAT 37545	
RESULT 21			
US-09-949-016-13045/c			
; Sequence 13045, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001307			
; CURRENT APPLICATION NUMBER: US/09/949,016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 13045			
; LENGTH: 45300			
; TYPE: DNA			
; ORGANISM: Human			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (1)...(45300)			
; OTHER INFORMATION: n = A,T,C or G			
US-09-949-016-13045			
Query Match 8.3%; Score 415; DB 3; Length 45300;			
Best Local Similarity 60.7%; Pred. No. 1.4e-84;			
Matches 877; Conservative 1; Mismatches 511; Indels 56; Gaps 10;			
Qy	3104	TTTTTTTTTGTGTTTAGAGACAGGGTCTTGTCTGTGTACCCAGGCAT-GAGCACAG	3162
Db	38953	TTTGTTTTGTGTTTTTCTGAGATGGAGTCTCACCTGTGCTTGGGTTGGAGGGCAG	38894
Qy	3163	TGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGTGACCTC	3222
Db	38893	TGGCGCAATCTCAGCTCACTGCAACCTCTGCCTCTCGGGTTCAAGCTATTCTCCTGACTC	38834
Qy	3223	AGCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGGCTAATTTAAAAAAAT	3282
Db	38833	AGTCTCCCAAGTAGCTGGGACTATAGGAGCCTGCCACACCGCCTGGCTAATTTTTTGTGA	38774
Qy	3283	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCA	3342
Db	38773	ATTTTAGTAGAGACGGGTTTTCACCATATTGGCCAGGCTGGTCTCGAACTCCTGAC--CT	38716
Qy	3343	AGCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTAAGGGGTGAGCCACCATGTG	3402
Db	38715	TGTGATCCGCCCCACCTCAGCCTCCCAAAGTGTGCGATTCCAGGCGTGGATTCACCGTGCC	38656

QY 3645 AGAGATGGGGTTTTACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCT 3704
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68811 AGAGACGGGGTTTTACCATATATTGGCCAGGCTGGTCTCAAACTCCTGACCTGAGGTGATCC 68752

QY 3705 GCCTGCCCTCAGTCTCCCAAAGTGTCTGGAATATAGGCGTGAGTCACTGTGCCCTGGCCGAT 3764
|| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68751 ACCACCTCAGCCTCCCAAAGTGTCTGGGATTACAGGCGTGAACCAACCGCGCTGGCGA- 68693

QY 3765 TACTGTCTATTTTCTTTATTTGCTATATCCCGAGATCTAGAGCAGTGTCTGACATATAGTA 3824
|| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68692 ---CTTTTATTTCTTAGGCCACTCTGATTACAAAATGACTTGGGTGTGAAATGTTGAA 68637

QY 3825 GGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTT 3884
| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68636 GCACATTTCATCCATAGCTTGATCTGTTCCCTTGGAGCAAGGAAGGGAACCTGA----- 68584

QY 3885 TAAACAACATCTTGACAACTTTGCAGAAATAAATACAACTCTTGCAATTCTGCTTTTTCACTTA 3944
||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68583 -GGAACGAACTGGGAAAATGTGCAG-----GGCCACCTTACCTACCGTTGTGTGACATC 68531

QY 3945 TCACCTTGTATTGACTTTTTCATATTTGCCCTCAAACTTTATTGTTACTGTTTTTTCATTG 4004
|| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68530 CCGAC-AGAAAGGCACTTGTGAAATCGACAATACTAGGCAATTTGTTCTGTTCTTTTCTG 68472

QY 4005 TTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCTGCTCCACT 4064
|| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68471 ----GATCTTGCAGCTGCGGTGCGCACTTGTGCATACACAGCTTGAAGTGAATCGTTTCGCC 68416

QY 4065 TTAGAAGGCCAAATTTTACAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAAATACA 4124
|| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68415 GAAAGAAGCCCTGTGAGGGTAATACACAGTGGATTAAAGACCTGGGCCACTGAGAAACC 68356

QY 4125 CACACACACACACACTCACACACAGTTTTTTAAATGTTTGCRACTAAGACAAGAAACC 4184
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Db 68355 AGCGCACTTGCTTACTCACCTTTTGTGCTCATTTATTGTTCTTTTAAATGAACA 68296

QY 4185 TGCATTAGAGGATGTTTGTTCATATTAATTAATAAATAAATCACTGTTGGGCACAGTACTCA 4244
||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68295 AAATTTAGAGAAAAGTTATTC-----CAGGCAGGCATGGTGATCA 68255

QY 4245 AGCCTGTAAACCACAGTACTTTTGAAGTCCAAAGGTGGGTGGATCACTTGAGGTGAGAAAGTT 4304
||||||| ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68254 TGCCTGTAAATCCAGCACTTTAGGAGGCTGAGGCGGTGGATCACTGAGGTCAAGGAT 68195

QY 4305 CGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCT 4364
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Db 68194 CGAGACCAGCCTAGCCAACATGGTGCAACCCCTGTCTCTACTAAAAATACAAAAATTAGCC 68135

QY 4365 GGGTGTAGTGATGCATGCCTGTAGTCCCAGTACTCGGGAGGCTGAGGCAAGAGAAATGC 4424
||| | ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68134 GGGCATGGTGATGTAAGTCTGTAGTCCCAGTACTCAGGAGGCTGAGGTAGGACAATCAC 68075

QY 4425 TTGAACCTGGGAGCAGAGGTTGCAGTGAGCCGAGATCCCACCCTGCACCTCCAGCCTGG 4484
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 68074 TTGAACCCAGGAGGCGGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACCTCCAGCCTGC 68015

QY 4485 GCGACACAGCGGAGACTCTATCTCAAAAAATAAATAAATAAAGGATCGGAGAGAA 4544
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Db 68014 GCGACAGAGTGAGACTCCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 67955

RESULT 23
US-09-949-016-11840
; Sequence 11840, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11840
; LENGTH: 44377
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-11840

Query Match 8.2%; Score 412.2; DB 3; Length 44377;
Best Local Similarity 59.4%; Pred. No. 6.1e-84;
Matches 843; Conservative 1; Mismatches 509; Indels 66; Gaps 6;

QY 3105 TTTTNTTTTGTGTGTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCACAGTG 3164
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Db 13181 TTAATTTTTTTTTTAATGAGACGGAGTCTTGCTGTGCCAGGCTGGAGTGCAGTG 13240

QY 3165 GTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAG 3224
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Db 13241 GTGCAATATTGGCTCACCGCAACCTCCACCTCCCGGTTCAAGCGATTCTCCCGTTTAG 13300

QY 3225 CCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCAACCGCTGGCTAATTAATAAAAAATTT 3284
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Db 13301 CGTCCGAGTAGCTGGGATTACAGGCATGCGCCACCAACCGCTGGCTAACTTTTGTGTA---TT 13357

QY 3285 TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCAAG 3344
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Db 13358 TTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGG 13417

QY 3345 CAATCCTCCTACCTTGGCATCCCAAAGTGTCTGGGATTACAGGGGTGAGCCACCATTGCG 3404
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Db 13418 TGATCTGCCCTGCCCTCAGCCTCCGAAGTGATGAGATTACAGGCGTGAGCCACCACGCTG 13477

QY 3405 GCTACTTATTTCTTTACATTCCATCTTTTCCAATAGAAATGAAGATCCACAGAACAGGGAT 3464
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 13478 ACCTCTTTTATTTTATTTTATTTTATTTTGTAGACAGAGTTTACTCTGTGCCCCAGG--- 13534

QY 3465 TACTGCCATTTTCTCTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCTC 3524
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Db 13535 -----CTGGAGTTCAGTGGCATG 13552

QY 3525 CGTTCAGCTCACTGCAACCTCTGCTCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCC 3584
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Db 13553 ATCTGGCTCACTGCAACCTCTACCTCCTGGGTTCAACGATTCTCCTGCTTCTGCCACC 13612

QY 3585 TGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTTTTGTATTTTAGC 3644
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Db 13613 CTAGTAGTTGGAATTACAGGCACCTACCACCAACGCTGGCTAA-TGTTTGTATTTTAGT 13671

QY 3645 AGAGATGGGGTTTTA-CCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC 3703
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 13672 AGAGACGGGGTTTCACCCATGTTGGCCAGGCTGSTATTGAATTTCTGACCTCAGGTGATC 13731

QY 3704 TGCTTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGAGTCACTGTGCTGGCCGA 3763
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Db 13732 CGCCCACTTCAGCCTCCCAAAGTGGTGGGATTAGAGACGTGAGCCACCGCCTCCGGCCCC 13791

QY 3764 TTACTGTCTATTTTCTTTATTTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGT 3823
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Db 13792 AAGTTTTTATTTCTGTAGGCACCTGTAAT-----GAAACATGTAGTTTGTGACT 13838

QY 3824 AGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTT 3883
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Db 13839 AAAAGCTTTGTTGAAAAGGCTGGAGACTGGAATCTAGAATTT---GTTTTCTTTCTTGAA 13895

QY 3884 TTAATAACAATCTTGACAACTTTGCAGAAATAAATAACAATCTTGCAATTTCTGCACTT 3943
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Db 13896 ATAATTCACTTCTGAGATTTCAGATAGAAGACGAAACTTTTGTATTTGAACGGCTCTGT 13955

QY	2164	GGCA---	GAATGTAGCAACAGTAAACATACAGCAACTATCCACGTGTCAATTTTCTAGCA	2220
Db	33460	GAAAATCAATTGTTACAAATGTAGGGTTATTTCTGGACTCTCACTTCTATTCAATTG	33401	
QY	2221	GTGGTTGTCACGCACTTCTGAATACAGGATTTTACTGTATTCTTGCACCATGTTAAA	2280	
Db	33400	GTCATATGTTCTCTTGTGCCAGTAAACAAATTACTATTGCTTTATAGTAAGTTTAAAA	33341	
QY	2281	AATCGCTTTTCAGGCCAGCGCGGTGCTCATGCCTGTAAATCCACGACACTTTGGGAGGCCG	2340	
Db	33340	TTGAGAAAGTAAAGCCAGGTACAGCTGCTCACACCTGTAATCTCAGCACTTTGGGAGTCCA	33281	
QY	2341	AGCGGGCGGATCACTTTGAGGTCAGGATTCAGAGTTCGAGACCCAGCCTGGCCAAACATGGTGAAACC	2400	
Db	33280	AGGAGAGCAGATTGTTTCGAGCCCAGAAGCTCGAGACCCAGCCTGGATAACTCGATGAAAAAC	33221	
QY	2401	CTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGGAGCGCCTGTAAACCCA	2460	
Db	33220	CCATCTCTAC-AAAAACTACAAAAATTAGCTGGACATGTTGTTGTCACGCCCTGTAGTCCCA	33162	
QY	2461	GCTACTTTGGGAG-----	ACTGAGTTGGAGGTTTTCAGTGAGC	2496
Db	33161	GCTACTTTGGGAGGTGAGGTGAGAGGATCGCTTAGCCCCAGGAGGGCGGAGGACGACGTGAAC	33102	
QY	2497	CAAGTCTGTCACTGCTGTCCAGCCTGGGTAAACAG--AGCAACTCTGTCTCAAAAAAAA	2554	
Db	33101	TGAGATCATGCCACTGCACCTCCAGCCTGGGTGACTGCAGCGAGGCCCTGTCTCAAAAAAAT	33042	
QY	2555	AAAATGCTTTCAATAAATATATGTATAAAGGACTTATATTTTTCAGGCCATAGGA---	2610	
Db	33041	TAATAAAATAAAATTGAGAAACATGAAGCCAGGCGCAGTGGCTCATGCCTGTAAACCCA	32982	
QY	2611	---TCATTTCTCTGAAGCATCTTGGCGAAGTCAATCCCACTGTTCCTGAGAGTGGGC	2666	
Db	32981	GCACTTTGTGAGGCAGAGGTGGTGGATCACCTGAGGTGAGAGTTTGAGACCAGCCTGA	32922	
QY	2667	AGGTGAGGGCTGACCTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCCTCCCACCTTC	2726	
Db	32921	CCAACATAGTGAACCCCGGCTCTACTAAAAATACAAAAATTAGCTGGGTATGGTGGTGCA	32862	
QY	2727	CAGGTGCTGCAGACACATGACAACTGCTAYGACCAGG-----CCAAGAAGCTGGACAGC	2781	
Db	32861	TGCCTGCAATCCCAGCTATGTGGGAGGCTAACGCCGGAGATCCCTTGAACCCAGGAGGC	32802	
QY	2782	TGTAAATTTCTGCTGGACAMMCCGTACACCCACACCTATTCT-----ATACTCGTG	2831	
Db	32801	AGAGGCTGCAGTGAGCTGAGATCGTGCCATTACACTCCAGCCTGGGCGACAACAGTGAAA	32742	
QY	2832	CTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCTTGACCTATGAATTCTA	2891	
Db	32741	CTCCGTCTCAAAAAAAAAAAAAAAGAGAGAGAGCCTGAGGGTCTCCCAACTTGTT	32682	
QY	2892	GTTGGTTCTCAGTAGGCCGG-----GGGGAATAATAGTAACAACAGCCATGATTTAG	2944	
Db	32681	GTTTTTCAAGATTGTTTGGCTATTCCGGGTCTCTTCTATTCTTCTTTCAGTGTTTTTA	32622	
QY	2945	TGTTAATTTTCTGGTTCTGGGCAGTGTCTCCTTTAATCCTCAGAAACAACACTATGGGAT	3004	
Db	32621	TCATGAAAAAGTGTCAAAATGTTTTTCTGTATTACAAAGGTGATCATGTGGTTTCTGT	32562	
QY	3005	AGGTACAATTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGGCTGAGCTA---	3061	
Db	32561	TGTTTAAATTATATTACCACAGTGTATTACAATGATTAAATGATCATATGTTGAACCAACC	32502	
QY	3062	TTTGCCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTGTT	3121	
Db	32501	TTCCTCGGATAAATCCCACCTTAGTTCATGGATTATGATCCCTTTTGTGTTGTTGTT	32442	
QY	3122	TAGAGACAGGTTCTGCTCTGTCAACCAGGCATGAGCACAGTGGTGCAACCATAGGTCAC	3181	
Db	32441	TTGAGACAGAGTCCCGCTCTGTCACTTAGGCTGGAGTGCAGTGGCAAAAATCTCGGCTCAC	32382	

QY	3182	TGAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGG	3241
DB	32381	CGCAACTTCTGCCTCCTGGGTTAAGCAATTCTCCTGCCTCAGCCTCCTGGTAGCTTGG	32322
QY	3242	ACTACGAGCGTGCACCAACGAGCTGGCTAAATTAATAAAAAATTTTTTTGTAGAGACTGGGT	3301
DB	32321	ATTA - GTCACCCGCCACCCAGGCCAGCTAAATTTTGTGTA - TTTTGTGAGACACGGGT	32266
QY	3302	CTTACTACGTTGGCCAGGCTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGG	3361
DB	32265	TTACACCATGTTTGGCCAGGCTGGTCTCGAACTCCTGACCTCATG - ATCCGCCACCTCAG	32208
QY	3362	CATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATTGTGCGGCTACTTATTTCTTTAC	3421
DB	32207	CCTCCCAAAGTCTGGGATTACAGGCAGGAGCCAGCATGCCCGCTGATCCTTTTCATAT	32148
QY	3422	ATTCCATCTTTCCAATAGAAATGTAAGATCCACAGAACAGGGATTACTGCGCTATTTTCTTC	3481
DB	32147	GTTACTGAAATCAGTCATCTAGTATTTTGAAGACATGGCGGTACAAGCATACTTTTTTT	32088
QY	3482	CTTTCTTTTTTGAGACAGAGTCTCACTTTCATCACTCAACCTCCCGT-----	3527
DB	32087	TTATTTTTTTGGGATGAAGTCTCTCTTCGTCGCCCAAGGTTGGAGTGCCATGGAGCAATC	32028
QY	3528	TCAGCTCACTGCAACCTCTGCCTCCC---GGGTTCAAGYGATTCTCCTGCTAAGCCTC	3583
DB	32027	TCAGCTCACTGCAACCTCTGTCTCCCCCTCGGGTCAAGGCTATTCTTGTGCTCAGCCTC	31968
QY	3584	CTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTTTTGTATTTTAG	3643
DB	31967	CCAAGTAGTCAGGATTACAGGCCAACCAACCACTGTGCTGGCTAA-GTTTTGTATTTTAG	31909
QY	3644	CAGAGATGGGGTTTTTACATGTTGGCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTGATC	3703
DB	31908	CAGAGACGGGGTTTTCACCATGTTGGCCAGGCTAGTCTCAAACCTCCTGATCTCA-----	31856
QY	3704	TGCCTGCCTCAGTCTCCCAAAGTGTCTGGAATTATAGGCGTGAGTCACTGTGCTGGCCGA	3763
DB	31855	----CACCTTGGCCTCCCAAAGTGTGGGATTACAGGCATAAGCTACTGTGCCACGCCCA	31800
QY	3764	TTACTGTCTATT-----TTCTTTATTGCTATATCCCAGATCTAGAGCAGTGTCTGACAT	3818
DB	31799	TACTTGTTTTTAATCAGTAAAGATATCTCTAAATTTTAAGACGAGGTAATTTCCAAGTCC	31740
QY	3819	ATAGTAGGTGCTCAATAAATAAATTGATGAATGCACAGCCTAGATATAAACCTTTCTTTTC	3878
DB	31739	TGATCAATTACTCATACATCACTTCTCTCTTTAATTTCATACTTCCCTAAAAAATGTCCC	31680
QY	3879	TTTTTTTAAACAATCTTGACAACTTTGCAGAAATAAATACAATCTTGCATCTTGTCTTTT	3938
DB	31679	TAGAAATAAACTAGTAATGACCATTGAGGACCTTTTCTTTGGACACAGTATGGCTCTAAGT	31620
QY	3939	CACCTATCACCTTGTATGACT-----TTTTTCATATTGCTCAAAACCTTTTA	3984
DB	31619	CGTAGGTCTCCCTTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	31560
QY	3985	TTGTTACTGTTTTTTCATTTGTTACTATTTTAGTCA-----CTGAATAATATGGCTTAATT	4039
DB	31559	CTAGGTGAACGTTCCCTTAGTCTCTGTTGTTGGCTATATTCTGAAATATAGTCAGTAATG	31500
QY	4040	TGCTTATACATCCTCTGCTCCACTTTTAGAAGGCCAAAATTTACAAATCTGATGAAAGCTA	4099
DB	31499	AATAAGTATTTTCTCCTATACCTATAGAATGGTGTAGTCAATTTTCCAAAGGTATAGCT	31440
QY	4100	TGAA-----CCCTCTCCCCAGAGAAATACACACA	4130
DB	31439	TTAAGAGGGCCAAGTCCAGCCCCACTAAGTAGTTCCTACTTAGTAATGAGAAAAATACTTT	31380
QY	4131	CACACACACTCACACAGATTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATT	4190
DB	31379	CAGAAAGGATAAGTGATCGCCTCAATAGCATCTCAACAAGTAAAGATAGAGCCCCAGGCT	31320
QY	4191	AGAGGATGTTGTTTCATTAATAATAAAAAAT---AACTCAGTTGGGCACAGTGACTCAAGCC	4248

Db 31319 AGAATCTAGGCTTAATATTCTTAAGACTTTGTTCTCGGCCGGGCACGGTGGCTCATGCC 31260
Qy 4249 TGTAAACCACAGTACTTTGGAAGTCCAAGTGGGTGGATCACTTGAGGTGAGAAGTTTCGAG 4308
Db 31259 TATAATCCCAGCACTTTGGAGGCCGAGGTGGCGGATCAC--GAGGTGAGGATCGAG 31202
Qy 4309 ACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATAC-AAAAATTAGCTGGG 4367
Db 31201 ACCATCCTGGCAAAACACAGCTGAACCCCATCTGTACTAAAAACACAAAAAATTAGCTGGA 31142
Qy 4368 TGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGAGGCTGAGSCAAGAGAATTGCTTG 4427
Db 31141 CATGGTGGTGACACCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGAATGGCATG 31082
Qy 4428 AACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCAGCTGCAGCTCCAGCCTGGCG 4487
Db 31081 AACCTGGGAGGCGGAGCTTGCAGTGAGCTGAGACTGGGCCACTGGCACTACAGCCTGGTG 31022
Qy 4488 ACACAGCGAGACTCTATCTCAAAAAAATAAATAAATA 4524
Db 31021 ACAGAGCGAGACTCCATCTCAAAAAAATAAATAAATA 30985

RESULT 26
US-09-949-002-693/c
; Sequence 693, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 63467
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-693

Query Match 8.1%; Score 406.8; DB 3; Length 63467;
Best Local Similarity 59.8%; Pred. No. 1.2e-82;
Matches 874; Conservative 1; Mismatches 548; Indels 39; Gaps 10;
Qy 3081 CTTGTAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTTGTTAGACAGGGTCTTGCTC 3140
Db 26935 CCTAAAGGTACAAAACCTTGCCTTTTTTTTTTTTTTTGTGATGAAGTCTCACTC 26876
Qy 3141 -TGTCACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTG 3199
Db 26875 TTGTTGCCCAGGCTGCAGTGCAATGGTGCAATCTCGGCTCATTTGCAACCTCCACCTCCCG 26816
Qy 3200 AGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAC 3259
Db 26815 GGTTCAGCGATTCTCTGCCTCAGCCTCCCGAGTAGCTGGGTTTACAGCGCCTGCCAC 26756
Qy 3260 CACGCTGGCTAATTAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGG 3319
Db 26755 CACACCCAGCTAATTTTGTGTA--GTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGG 26698
Qy 3320 CTTGTCTTAACTCTGGCTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGTGGGA 3379
Db 26697 CTGGTCTCGAACTTTTGACCTCAGCGGATCTGCCCCACCTCAGCCTCCCAAAAGTGCTAGGA 26638
Qy 3380 TTACAGGGGTGACCCACCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAG 3439
Db 26637 TTACAGGCATGAGCCACCGTGCCCCAGCCAAACCTTGCCTATTCTTTAGGCTT----- 26586

Qy 3440 AATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCTCTCTTTTGTGAGACAG 3499
Db 26585 ATTCTTGGA CTTACAAAACAGCACAAACCTGGCCTTTGTGTTTTTTTGTGATGG 26526
Qy 3500 AGTCTCACTTTCATCACCTCAACCTCCGT-----TCAGCTCACTGCAACCTCTGCCT 3550
Db 26525 AGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGA TCTCGGCTCACTGCAACCTCCATCT 26466
Qy 3551 CCCGGGTTCAAGYGA TTTCTCTCTGCCTAAAGCCTCTCTGAGTAGCTGGAATTACAAAGCTGCA 3610
Db 26465 TCCGGGTTCAAGCGA TTTCTCTGTCTCAGCCTCCAAAGTAGCTGGGACTACAGGCACAG 26406
Qy 3611 CCACCATGCTTGGCTAA TTTTGTATTTTGTAGCAGAGATGGGTTTACCATGTTGCC 3670
Db 26405 CCACCATGCC T-----AATTTTGTATTTTGTAGTAGAGACGAGGTTTTCACCTTATTGCTC 26351
Qy 3671 AGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCTGCCTGCCTCAGTCTCCCAAAGTCTG 3730
Db 26350 AGGCTGCTCTCGAACTAT TGACCTCAGGTGATCCACCACCTAGGCCTCCCAAAGTCTG 26291
Qy 3731 GAATTATAGGCGTGAGTCACTGTGCCTGGCCGATTA CTGTCTATTTTCTTTATTGCTATA 3790
Db 26290 GGATTACAGGCGTGAGCCACCATGCCCGCC---AACCTAGCCTGTCTTTATCTTATG 26234
Qy 3791 TCCCCAGATCTAGAGCAGTGTCTGACATATATAGTAGTGTCTCAATAAATAATTGATGAATG 3850
Db 26233 CAGATACCTTAAAAAACATCTACCACAATTCAGAAAGTATTCAAATTCCAAACCATGTAAA 26174
Qy 3851 CACAGCCTAGATATAAACTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTGCAGA 3910
Db 26173 CATCCAGTTATTTGGGCCCATGTAATTGCATTTGTCATTTATTTCGTACAGTTAAAAAAA 26114
Qy 3911 ATAAATACAATCTTGCA TTTCTTTTTCACCTTATCACCTTGTATGACTTTTTCATATT 3970
Db 26113 AAAAAAAAATCCCGGGACATTTCTTCTGGAATTAATGGTATTTGGCATTAGAGGAGTTC 26054
Qy 3971 GCCTCAAAACCTTTATTGTTACTGTTTTTTTTCATTTTCTACTATATTTTAGTCACTGAATAAT 4030
Db 26053 GCGAACAGTCTACATCAAAACCAGGGTGCTGA-AGTCTCTGTGCTCCTTCCAAAGCACAG 25995
Qy 4031 GGCTTAATTTGCTTATACATCCTCTCTGCTCCACTTTAGAAGGCCAAAATTTACAAATCTGA 4090
Db 25994 CCAGCCTTGGGGCACAGGAGGGAAGTGTCCAAGTGCCAAACACCTGCCCCACAGAGCATAT 25935
Qy 4091 TGAAGCTATGAACCTCTCTCCCCAGAGAAAATACACACACACACACTCACACA-CAG 4149
Db 25934 CAGTGTCTCACCATTTGTGTAAAAAGAAAACACAAAAGGATATAAACAGAACTGATGTG 25875
Qy 4150 TTTTTTTTAAATGTTGCAACTAAGACAAGAAACCTGCAATTAGAGGAT-GTTTGTTCATA 4208
Db 25874 ACTGTGATTTTGTTCCTAGGACTACTGAAAACACAGACCCACAAAACCTAGGCAGTTTCAA 25815
Qy 4209 TTAATTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCAAGTACTTTGGA 4268
Db 25814 AAAGTCCACAGTTCTGAGCCAGGCACACAACCTCACACCTGTAATCCCAGCACTTTGGG 25755
Qy 4269 AGTCCAAGGTGGGTGATCACTTGAGGTGAGAAGTTTCGAGACCAGCCTGGTCAATATGGT 4328
Db 25754 AGCCAAAGGCAGGAGAATCGCTTGAGCCCAAGGGGTTTAAGACCAGCCTGGGCAAGAAAT 25695
Qy 4329 GAAACCTTATCTCTACTAAAAATACAAAAAATTAGCTGGGTGTAGTGATGCATGCCGTAG 4388
Db 25694 GAGACTCCATCTCTGCAAAAAACACAAAAACTAGGAGGTGTAGTGGTGTGCACCTGTAG 25635
Qy 4389 TCCAGCTACTCGGGAGGTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGTTGC 4448
Db 25634 TCCAGCTACTTGTGAGGTGAGGTGGGAAGATCACTTGAGCCCAAGGATGTTGAGGCTGT 25575
Qy 4449 AGTGAGCCGAGATCCCAACA-----CTGCACCTCCAGCCTGGCGACACAGCGAGACT 4500
Db 25574 AGTGAGCCAAGATCACACTACCGCACTTCTGCACTTCAGGCTGGGTGAGACAGCGAGACT 25515

Qy 4501 CTATCTCAAAAAAAAAATAAAA 4522
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Db 25514 CTGTCTCAAAAAAAAAAAAAAA 25493

RESULT 27

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US-09-949-016-17289/c
; Sequence 17289, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17289
; LENGTH: 64518
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17289

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Query Match 8.1%; Score 406.8; DB 3; Length 64518;
Best Local Similarity 59.8%; Pred. No. 1.2e-82;
Matches 874; Conservative 1; Mismatches 548; Indels 39; Gaps 10;

QY	3081	CTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTTGTTGTTTGTAGAGACAGGGTCTTGCTC	3140
Db	26935	CCTAAAAGGTACAAAAACTTGCCTTTTTTTTTTTTTTTTTTTGTAGATGAAGTCTCACTC	26876
QY	3141	-TGTACCCAGGCATGAGCACAGTGGTGCAACCATAGTCTACTGCAGCCTCAACCTCCTG	3199
Db	26875	TTGTTGCCAGGCTGCAGTGCATGGTGCAATCTCGGCTCATTGCAACCTCCACCTCCCG	26816
QY	3200	AGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAC	3259
Db	26815	GGTTCAAGCGATTCTCCTGCCTCAGCCTCCGAGTAGCTGGGTTTACAGGCGCTGCCAC	26756
QY	3260	CACGCCTGGCTAATTAAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGG	3319
Db	26755	CACACCCAGCTAATTTTTTGTA--GTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGG	26698
QY	3320	CTTGCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGA	3379
Db	26697	CTGGTCTCGAACTCTTGACCTCAGGCGATCTGCCACCTCAGCCTCCCAAAGTGCTAGGA	26638
QY	3380	TTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAATAG	3439
Db	26637	TTACAGGCATGAGCCACCGTGCCCGAGCCAAAACCTTGCCCTATCTTTAGGCCT	26586
QY	3440	AATGTAAGATCCACAGAACAGGGAATTACTGCCTATTTTCTCTCTTTCTTTTTTGAGACAG	3499
Db	26585	ATTCTGGACTTACAAACAGCACAAACCTGGCCTTTTGTGTTTTTTTTTTTGTAGATGG	26526
QY	3500	AGTCTCACTCATCACTCAACCTCCGT-----TCAGTCACTGCAACCTCTGCCT	3550
Db	26525	AGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGATCTCGGCTCACTGCAACCTCCATCT	26466
QY	3551	CCCGGGTTCAAGYGATTCTCCTGCTTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCA	3610
Db	26465	TCCGGGTTCAAGCGATTCTCCTGTCTCAGCCTCCAAAAGTAGCTGGGACTACAGGCCACG	26406
QY	3611	CCACCATGCTTGGCTAATTTTTTGTATTTTTTAGCAGAGATGGGGTTTTTACCATGTTGCC	3670
Db	26405	CCACCATGGCT-----AATTTTTGTATTTTTTAGTAGAGACAGGTTTCACTTATTGGTC	26351


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; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 843
; LENGTH: 64518
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-843

Query Match      8.1%; Score 406.8; DB 3; Length 64518;
Best Local Similarity 59.8%; Pred. No. 1.2e-82;
Matches 874; Conservative 1; Mismatches 548; Indels 39; Gaps 10;

QY 3081 CTTGTAAGTGGTGACAGTTTGGGTTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTC 3140
Db 26935 CCTAAAAGGTACAAAAACTTGCCTTTTTTTTTTTTTTTTTTTTGGAGATGAAGTCTCACTC 26876

QY 3141 -TGTCACCCAGGCATGAGCACAGTGGTGCRAACCATAGGTCACCTGCAGCCTCAACCTCCTG 3199
Db 26875 TTGTTGCCCAGGCTGCAGTGCAATGGTGAATCTCGGCTCATTTGCAACCTCCACCTCCCG 26816

QY 3200 AGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCAACCAC 3259
Db 26815 GGTTCAAAGCGATTCTCTGCCTCAGCCTCCCGAGTAGCTGGGTTTACAGGCGCCTGCCAC 26756

QY 3260 CACGCCCTGGCTAATTAAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGG 3319
Db 26755 CACACCCAGCTAATTTTGTGA--GTTTTAGTAGAGACAGGGTTTACCATGTTGGCCAGG 26698

QY 3320 CTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGCTGGGA 3379
Db 26697 CTGGTCTCGAACTCTTGACCTCAGGCGATCGCCACCTCAGCCTCCCAAGTGCTAGGA 26638

QY 3380 TTACAGGGGTGAGCACCATGTGCGGCTACTTATTCTTTACATTCCATCTTTCCAATAG 3439
Db 26637 TTACAGGCATGAGCCACCGTGCCAGCCCAAACTTGCCATTTCCTTAGGCTT----- 26586

QY 3440 AATGTAAGATCCACAGAACAGGGAATTACTGCGCTATTTTCTTCCTTTCTTTTGTAGACAG 3499
Db 26585 ATTCTGGACTTACAAAACAGCACAAACCCTGGCCTTTGTTTTTTGTTTTTTTGGATGG 26526

QY 3500 AGTCTCACTTCACTCAACCTCCGT-----TCAGCTCACTGCAACCTCTGCCT 3550
Db 26525 AGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGATCTCGGCTCACTGCAACCTCCATCT 26466

QY 3551 CCCGGGTTCAAGYGAATTCTCCTGCCCTAAGCCTCCTGAGTAGCTGGGAATTACAAGCGTGCA 3610
Db 26465 TCCGGGTTCAAGCGAATTCTCCTGTCTCAGCCTCCAAAAGTAGCTGGGACTACAGGCACCAG 26406

QY 3611 CCACCATGCTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGGTTTTTACCATGTTGCC 3670
Db 26405 CCACCATGCGCT----AATTTTGTATTTTGTAGTAGAGACGAGGTTTTCACCTTATTGGTC 26351

QY 3671 AGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTCAGTCTCCCAAAGTGCTG 3730
Db 26350 AGGCTGCTCTCGAACTATTGACCTCAGGTGATCCACCCACCTAGGCTCCCAAAGTGCTG 26291

QY 3731 GAATTATAGGCGTGAGTCACGTGTCCTGGCCGATTACTGTCTATTTCTTTATTGCTATA 3790
Db 26290 GGATTACAGGCGTGAGCCACCATGCCCGGCC---AACCCTAGCCTGTCTTTATCTCTATG 26234

QY 3791 TCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATG 3850
Db 26233 CAGATACCTTAAAAAACAATCTACCACAATTCAGAAAAGTATTCAAATTTCCAAACCATGTAAA 26174

QY 3851 CACAGCCTAGATATAAACTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTGCAGA 3910
Db 26173 CATCCAGTTATTTGGGCCCATGTAAATTGCATTGTTCACTTTATTTCGFACAGTTAAAAAAA 26114

QY 3911 ATAAATACAATCTTGCAATCTGCTTTTTCACCTATATCACCTTGTGTTATGACTTTTTCATATT 3970
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Db 26113 AAAAAAAAATCCCGGACATTTCTTCTGGAATTAATGGTATTTTGGCATTAGAGGAGTTC 26054
QY 3971 GCCTCAAAACCTTTTATTGTACTGTTTTTTTTCATTGTTACTATATTTTAGTCACTGAATAATAT 4030
Db 26053 GCGAACAGTCTACATCAAAACCAGGGTGCTGA-AGTCTCTGTGCTCCTTCCAAAGCACAG 25995
QY 4031 GGCTTAATTTGCTTATACATCCTCTCTGCTCCACTTTAGAAAGGCCAAAATTTACAAAATCTGA 4090
Db 25994 CCAGCCCTGGGGCACAGGAGGGAAGTGTCCAAGTGCCAAACACCTGCCACAGAGCATAT 25935
QY 4091 TGAAGGCTATGAACCCCTCTCCCCAGAGAAAATACACACACACACACACTCACACA-CAG 4149
Db 25934 CAGTGTTTCTCACCATTTGTGTAAAGAAAACACAAAAAGGATAAAACCAGAAACTGATGTG 25875
QY 4150 TTTTTTTAAATGTTTGCAACTAAGACAAGAAACCTGTCATTAGAGGAT-GTTTGTTCATA 4208
Db 25874 ACTGTGATTTTGTCTTAGGACTACTGAAAACACAGACCACAAACTAGGCAGTTTCAA 25815
QY 4209 TTAATTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACAGTACTTTTGA 4268
Db 25814 AAAGGTCCACAGTTCTGAGCCAGGCACACAACCTCACACCTGTAAATCCCAGCACTTTGGG 25755
QY 4269 AGTCCAAAGGTGGTGATCACTTGAAGTGAGAGTTTCAAGACCAGCCTGGTCAATATGGT 4328
Db 25754 AGGCCAAGGCAGGAGAAATCGCTTGAGCCCGAGGGTTTAAAGACCAGCCTGGGCAAGAAAT 25695
QY 4329 GAAACCCCTATCTCTACTAAAAATAACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAG 4388
Db 25694 GAGACTCCATCTCTGCAAAAAACACAAAAACTAGGCCAGGTGTAGTGGTGTGCACCTGTAG 25635
QY 4389 TCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTTGCTTGAACCTGGGAGGCAGAGGTTGC 4448
Db 25634 TCCCAGCTACTTGTGAGGCTGAGGTGGGAAGATCACTTGAGCCCAGGATGTTGAGGCTGT 25575
QY 4449 AGTGAGCCGAGATCCCAACA-----CTGCACCTCAGCCTGGGCGACACAGCCGAGACT 4500
Db 25574 AGTGAGCCAAAGATCACACTACCGCACTTCTGCACCTTCAGGCTGGGTGAGACAGCCGACT 25515
QY 4501 CTATCTCAAAAAAATAATAAA 4522
Db 25514 CTGTCTCAAAAAAATAAAAAA 25493
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RESULT 29
US-09-949-016-16766/c
; Sequence 16766, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16766
; LENGTH: 32584
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16766
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Query Match      8.1%; Score 404.4; DB 3; Length 32584;
Best Local Similarity 61.4%; Pred. No. 3.2e-82;
Matches 884; Conservative 1; Mismatches 512; Indels 43; Gaps 13;

QY 3109 TTTTGTGTTGTTTAGACAGAGGGTCTTGCTCTGTCCACCCAGGCATGAGCACAGTGGTGC 3168
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Db 11475 CTGGATTACAGGCATGAGCCACCGTGCCAGCCT-----TGTTTTTTTTTTTGAG 11424
QY 824 ACAGAGTCTTGCTTTGTGCGCAAGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAA 883
Db 11423 ACAGAGTTTCACTCTGTGCGCCAGCTGGAGTGCACTGGCGGATCTTGGCTCACTGCAA 11364
QY 884 GCTCCACCTGCTGGTTACGCCATTTCTCCGCCTCAGCCTCCCGTAGCTGGGACTAA 943
Db 11363 GCTCCGCTCCCGGTTACGGCATTTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGGCTAT 11304
QY 944 AGCGCCTGCCACCACCGCCCGCTAAATTTTTTGTATTTTTTAATAAGACGGGTTTCAT 1003
Db 11303 AGGCACCTGCCACCATGCTCAGCTATATTTTTTGTATTTTTTAGTAAAGACGGGTTTCAC 11244
QY 1004 CGTGTTAGCAGGATGGTCTCGATCTCATGACCTTGTGATCCGCCTGCCTCGGCCCTCCA 1063
Db 11243 CGTGTTAGCAGGATGGTCTTGATCTCCTGACCTCGTGATCCGCCCATCTCGGCCCTCCA 11184
QY 1064 AAGTGCTGGATTACAGGCATGAGCCACCGTGCCCGCCTTATCACATTTATTATTATT 1123
Db 11183 ACGTGCTGGSATCACAGGCATAAGCCACCGTGCCCGGCCAAATTTTTTTTTTTTGAGACG 11124
QY 1124 GTTTTTCTCCTCCACTAGGTTGTAGCTCCATGAGGTTAGAGATTATTATTATTATT 1183
Db 11123 GAGTCTTGCTCGCTCGCCAGACTGGAGTGAATGGCATGATCGGGCTCACTCTGCCTC 11064
QY 1184 ATTATTATTATTATTATTATTATTATTATCTGTTCACTGCTGTATCTCTAGCTCCTAG 1243
Db 11063 CCGGTTTCRAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTATACGCATGTAC 11004
QY 1244 GACAGAGCCTGGCACATAGTAAAGTGTCAATAAATATTCACITGGATAAACAGTGCAGATA 1303
Db 11003 CACCAGGCCTGGC-----TAATTTTTGTATTTTTTAGTAGAATG 10965
QY 1304 GTTTAAACTATCTGACCTAGGAGGCTGAGGCAGGAGAAATGGCGTGAAACCCGGGAAGCA 1363
Db 10964 GGGTTTCACTTGTGTCAGGCTGGTCTCGAACTCCTGACCTCGTGATCTGCCTGCCTC 10905
QY 1364 GAGTTTGCACTGAGCTGAAATCGTGTCACTGCACCTCCAACTGGGCAACAGAGCAAGACT 1423
Db 10904 AGCCTCCCAAAGTGTGGGATTACAGGAGTGAGCCACCACCCCGGATTTTCAGAAAAATA 10845
QY 1424 CCATCTCAAAAAAAAAAAAAAATACTATCA---GGCCTAGCTGGGTGGCACATGCCCTGTA 1479
Db 10844 TTTATAGAAAAAGTAGTACATGGTTTATTTTATACAGCTTTATTGTTTTCGTAAAACTTATA 10785
QY 1480 ATCCTAGCTGAGCGGTAGGGTCCCAAGAAGAAGAAGAAAAAGAAAAAGAGATATAT 1539
Db 10784 CATGCTCATAGAAAAATGAAATTCAATCAAAACAGTTTTTATTTTITAGAGAGAGGTCTTG 10725
QY 1540 ATATATATACACACACAAAGATATAAACTTTATATATATAAAGTTTTTCATTTAAAAAAA 1599
Db 10724 CTCTGTTACCGGGCTGGAGTGCAGTGGTACAATTATAACTCACCACAGACTTGAATTCC 10665
QY 1600 AAAAAAACCTCTACCCACT--TTCACTTTACCAGGTTCTGGGTCCAACGGTCTTTCAGA 1657
Db 10664 TGAGCGCAAGTGATCCTCCTGCTTCAAGTTCCTCAGGTAGCCGGGACTACAGGCATGCACC 10605
QY 1658 GGAGGCAGCTGGCAGGGGTGAGGAGGCAGCGTGGGACCCGAGGAGCAGGAAGGCAGTG 1717
Db 10604 ATGAGGCCTGGCTAAATTTTTTCTTTAAAAAATAAATAAAAAATTTTTTAAAGAAAAAGTTTTT 10545
QY 1718 --TGTCCTCCGGGTGCTGGCAGACCGATTGAACTCTGGCTATGCTTCTTTGAGTGGCC 1775
Db 10544 AAAGATGGCTGGGCACAGTGACTCACGCCGTGTAATCCCAACACTTTGGGAGGCCGAGACG 10485
QY 1776 GCCGCCGMCAGCGGCATCAGCCCTCGSGCGGTGTGGCAGTTCCGCAAAATGATCAAGTGC 1835
Db 10484 GGTGGATCACCCTGAGGTGAGGAGTTTGAGAG-CAGCCTGGCCAAACATGGTGAAACTGCCG 10426
QY 1836 GTGATCCCGGGGAGTGACCCCTTYYTTGGAATACAACAACTACGGCTGCTACTGTGGCTTG 1895

Db 10425 CTCTACTAAAAATACAAAAAATTAGCCAAGCATGGTGGCAGGCACCTGTAAATCCAGCTA 10366
QY 1896 GGGGGCTCAGGCACCCCGTGGATGAACCTGGACAAGTAAGTGATCCGCCCTGCAGGAAAAAT 1955
Db 10365 TTCGGAGGCTAAGCAGGAGAAATCGCTTGAACCTCGCGGTGGAGGATGCAGTGAGCCAA 10306
QY 1956 TGGAGTGCCTGCCGGGGCGGGTGGGGGCACACGCCAAGGATCTCACGAGGCATACAAAG 2015
Db 10305 GATTGCACCATTGCACTCCAGCCTGGGCAACGAGATCAAAACTCTGTCTCCAAAAAANA 10246
QY 2016 GGGACTTGCCATATCTGCTAAGGATAACATATTTTTCACCTCTTGTCAAATAAACAAATATG 2075
Db 10245 AAAAAAGTTTTTTTTTAGAGATGCAGTCTCACTATGTTGCCCTAGGCTCTCAAACTCCT 10186
QY 2076 TTCCAAGAGGACCTGTAGCGAACGCACCCCGTTAGAGATGGAACAATAGCCGACGTGC 2135
Db 10185 GGCCTCAAGTGATCCTCCTGCCTCTGTAGTAGCTAGGATTACAGGCATAAGCCACAGCAC 10126
QY 2136 AAAACAGTGGCGATGCTGCCCTCCAGTGGCAGAATGTAGCAACAGTAAACATCACAGCA 2195
Db 10125 CAGGCAAAAAAAATTTTAATTGTCACTTAATTCCTATTTCCCCAAAAATAACTACC 10066
QY 2196 ACTATCCACGTGTCAATTTTCTAGCAGTGGTTGTCACTGCACCTTCTGAATACAGGATTTT 2255
Db 10065 ATTAGCATTTGGTGAACATTATTCAAGACGCTCTCTCAATGCATTTATATAAAAAAACTGA 10006
QY 2256 ACTGTATTCTTGC-----AACCATGTTTAAAAATCGCTTTCAGGCCAGGGCGGTGGC 2307
Db 10005 GACATAGACTAACTTTAACTGCTTCCATAAAATAAAAAGTATTTCAGTCGGGCGGAGTGGC 9946
QY 2308 TCATGCCCTGTAATCCAGCACACTTTTGGGAGGCCGAGCGGGCGGATCACTTGAGGTCAGGA 2367
Db 9945 TCACGCCTGTAGTCCAGCACACTTTGGGAGGCTGAGGCGGATGGATTGCCCTGAGGTCAGGA 9886
QY 2368 GTTCGAGACCAGCCTGGCCAAACATGGTGAACCCCTGTCTCTACTAAAAAATACAAAAATT 2427
Db 9885 GTTCGAGACCAGCCTGGCCAAACATGGAGAAACCCCTGTCTCTACT-AAAAATACAAAAACT 9827
QY 2428 AGCCGGACATGGTGGCAGCGCCTGTAAACCCAGCTACTTGGGAGACTGA-GTTGGAGGT 2486
Db 9826 AGCCGGCATGGTGTAAGTGCCTGTAAATCCAGCTACTCAGGGGCTGAGGCGAGAGAA 9767
QY 2487 TTCAGTGAGCCCAAGGTGCTGTCACTGCTGTCCAGCCTGGGTAAC-----AGAGCAACT 2539
Db 9766 TTGCTTGAACCCAGGAGGAGAGGTTGCAGTGAGCTGAGATCATTTCCACCACCAACTCAAGC 9707
QY 2540 CTGTCTCAAAAAAANAANTGCTTTTCAATAAATATATGATAAAAGGACTTATATTTTTTC 2599
Db 9706 CTGGGTGACAGAGCGGAGACTCCATCTCAAAAAAGTAATAAATAATATATATAATTA 9647
QY 2600 AAGCCATAGGATCATTTCTCCTGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCCTGAG 2659
Db 9646 ATAAAAATAAAAAGTATTCAAATATAATTTTATT--TGAAATTACATATTATAGTTTTCAGAA 9589
QY 2660 AGTGGCAGGTGAGGCTGACCTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCCTCC 2719
Db 9588 AAAAACTCAATTATTTAGAACATGTTGAGGTTTCAGATACACATCTTTCTTTTATGAAAA 9529
QY 2720 CACTTTCAGGTTGCTGCCAGACACATGACAACTGCTAYGACCAGGCCAAGAAGCTGGACA 2779
Db 9528 CTATGAC---TTAAAAATATACTTGTACAAGCTGTTGAGGTAGCTCTAGACGGACAAAA 9473
QY 2780 GCTGTAAATTTCTGCTGGACAMMCCGTACACCCACACCTTATTCATACCTCGTCTCGCT 2839
Db 9472 GCCAGAAATACTGTCTTGACAA-----AGACAGATCTCATGACACAATTTGTTTGGC- 9421
QY 2840 CGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCCTTGACCTATGAATTCATGTTGTTTC 2899
Db 9420 -----AAATTTTGTTTTTTCTTCTTATTTTAAAAAGGTCAAAAATCCCA 9375
QY 2900 TCAGTAGGCCGGGGGAAATAATAGTAAACAACAGCCATGATTTTAGTGTAAATTTTCTTGG 2959
Db 9374 GGGTCTTGATAJCTGGCAGTTGGTTTTCAGCAGTGCTGAGACAGTTACTTATACTTCTTGT 9315

QY	3166	TGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGC	3225
Db	11280	CTTGATCTCAACTCACTCGGCCCTCAACCTCCAGGCTCAAGCAATCCTCCCACCTTAGT	11339
QY	3226	CTCCCAAGTAGCTGGGACTACGAGCGTGACCAACCACCGCTGGCTAA-TTAAAAAAATTT	3284
Db	11340	CACCTGAGTAGCAGGGACCAACAGCGTGGCCACCAACACCTGGCTAAATTTTGTATTTT	11399
QY	3285	TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTG-TCTTAAACTCCTGGCTCAA	3343
Db	11400	TTTTGTGGAGACAGGTTTCAACACGTTGCCAGGCTGGCTCTTGAACCTCCTGGACTAA	11459
QY	3344	GCAATCCTCCTACTTGGCATCCCAAGTGCTGGATTACAGSGGTGAGCCACCATGTGC	3403
Db	11460	ACGATCCTCCTGCTCGGCCTCCCAAAGTGTGGATTACAGCGTGAGTACCACACCT	11519
QY	3404	GGCTACTTATTTTACATTCCTTCCCAATAGAATGTAAGATCCACAGAACAGGGA	3463
Db	11520	GGCCACTGACTATTCCTCTTTTTTTTTT-----	11547
QY	3464	TTACTGCCCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCT	3523
Db	11548	TTTTTTTTTTTCTGAGACAGTTCCTCTTGTGCCAGGCTGGAGTGCAATGGCGT	11607
QY	3524	CGTTTCAGTCACTGCAACCTCTGCTCCCGGGTTTCAAGYGATCTCTCCTGCTAAGCCTC	3583
Db	11608	GATCTCAGTTCACTGCAGCCTCCCCCTCCTGGGTTCAAGTATCTCTGCTCAGCCTC	11667
QY	3584	CTGAGTAGCTGGAATTACAAGCGTGCAACCATGCTTGGCTAAATTTTGTATTTTAG	3643
Db	11668	CTGAGTAGCTGGATTACAGGCATGTACCACCATCCAGCTAA--TTTTGTATTTTAG	11725
QY	3644	CAGAGATGGGGTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC	3703
Db	11726	TAGAGACGGAGTTCTTTCATGTTGGTCAGGCTGGTCTTGAACCTCCTGACCTCAGGTGATC	11785
QY	3704	TGCCTGCCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACCTGTGCTGGCCGA	3763
Db	11786	CACCTACCTCAGCCTCCCAAAGTGCTGGGATTACAGGTGTAGCCACCACGCCCGGCCAA	11845
QY	3764	TTA-----CTGTCTATTTTCTTTATTGCTAT	3789
Db	11846	CTATTCCATTTTGTGGCGAGATTTTGTGTTTGTGTTTAAATCTCTCCTTC	11905
QY	3790	ATCCCCAGATCTAGACAGTGTCTGCACATATAGTGGTGCTCAATAAATAATATGATGAAT	3849
Db	11906	TTAGGAGCTGTAAGACTATTTCAGAGAGTTCAGAAAGGCACAAAATGGAAGTAAATGSGT	11965
QY	3850	GCACAGCCTAGATATAAACTTTCT-----TTTTCTTTTTTTTAAACCAATC	3894
Db	11966	TCCACTCTTTCTTAAAGGAACCTACTAAATACAGTGTCTTGGGTATTTTCTAAAGTTT	12025
QY	3895	TTGACAACTTTGCAGAATAAATACAATCTTGCACTTCTGCTTTTCACTTATCACCTTGT	3954
Db	12026	TTAAAAAATGAAATTATTTTGCATTTTGTTCACCTTGGTAAATTTTGGAGGTCACTCATC	12085
QY	3955	ATGACTTTTTCATATTGCCTCAAACTTTATTTGTACTGTTTTTTCATTTTACTATTTT	4014
Db	12086	AGTATATTTATCTTCGCATGTTTTTCTAGGAGTTATGTGGTTTTTACATTGTGAAGAATT	12145
QY	4015	AGTCACTGAATAATATGGCTTAATTTTGCTTATACATCCTCCTGCTCCACTTTTAGAAGCC	4074
Db	12146	TAGAAAAATACATTTAGCCAGTTCTGTAAACACTGAAATTGTATACTAGGTTTTTAGCTGACA	12205
QY	4075	AAATTTACAAATCTGATGAAAGCTATGAACC--CTCTCCCCAGAGAAATACACACACAC	4131
Db	12206	TAAGCAGTGTGTAGTCCCTTTTATATGTACCTATTTGTGTAGGTACAACCTGGTCCCTGGC	12265
QY	4132	ACACACACTCACACACAGTTTTTTTTTTTAAATGTTTGCAACTAAGACAAGAAACCTGCA--	4188
Db	12266	TTATGAAGTTTGACCTGATTTTTTTTTTCGACTTTACAATGGTGTAATAACCATACTTTTGAGCA	12325

QY	4189	-TTAGAGGATGTTTTGTTCATAATTAAATAAAAA-----TAACCTCAGTTGGGCACAGTGA	4240
Db	12326	CTCACACGTTGTTTTTTTTTCTTCTTTAAGAGACAGGGTCTCTGGCTGGGAGCAGTGG	12385
QY	4241	CTCAAGCCCTGTAACACACAGTACTTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGA	4300
Db	12386	CTCAGGCCCTGTAATCCCACAACACTTTTGAGAGGCCAGGGT-GGCGGATCACTTGAGCTCAGG	12444
QY	4301	AGTTCGAGACCAGCCTGGTCAATATGGTGAAAACCCCTATCTCTACTAAAAATACAAAAATT	4360
Db	12445	GGTTTGAGAACACAGCCTGGGCAACATAGTGAGACCTTGTCTCTAAAAAACACA-AAAAATT	12503
QY	4361	AGCTGGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAA	4420
Db	12504	AGCCTGGTGTAGTGGCACGCACCTGTGTGTTCCAGGTACTCAGGAGGCTGAGGTGGGAGAG	12563
QY	4421	TGCTTTGAACCTGGAGGCAGAGGTTGCAGTAGCCGAGATCCCACCACCTGCACCTCCAGC	4480
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QY	4481	CTGGGGCACACAGCGAGACTCTATCTCAAAAAATAAAATAAAATAAAG	4532
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RESULT 32
US-09-949-016-13968
; Sequence 13968, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13968
; LENGTH: 68444
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(68444)
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13968


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QY 3718 TCCCAAAGTCTGGAATTATAGGCGTGAGTCACTGTGCCCTGCGCGATTACTGTCTATTTT 3777
|||
Db 4091 TCCCAAAGTCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCCAA-----ACCTTT 4040
|||
QY 3778 CTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAA 3837
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Db 4039 TTTCTTTAAGAAACATTTTCATGGTGAAAAGTCTCTCACATTTTGCTCTCCAGTCATCCAA 3980
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QY 3838 TAATTGATGAATGCACAGCCTAGATATATAAACTTTCTTTTCTTTTAAACAACTTTG 3897
|||
Db 3979 TTCTT-----CTCCCAAGAACCAATTTCTTGTGTAGAAATGTACCTT 3934
|||
QY 3898 ACAACTTTGCAGAAATAAATACAATCTTGCAATCTGTCTTTTCACTTATCACCTTGTATG 3957
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Db 3933 AAACATGCATTTTCATTAAGTACTAGTCAAAATTTCCATATTAACGGTCTCATCAGATAAA 3874
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QY 3958 ACTTTTTCATATTGCCCTCAAACCTTTATTTGTTACTGTTTTTTCATTTTACTATTTAGT 4017
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Db 3873 CACTATTCTCCACCCT-----TGGTAACTGTGTAGG 3841
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QY 4018 CACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAACGCCAAA 4077
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Db 3840 CAGATAAAA-----ACCTACTACCATTTCCCTGAGAGCC 3806
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QY 4078 TTTACAAATCTGATGAAAGCTATGAACCTCTCTCCCGAGAGAAATACACACACACACAC 4137
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Db 3805 TCTCTCCACTAGTCTTCTCTGTCAAGCTTTCTCAGAGCAGTAAAGAACCCACTCAAAC 3746
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QY 4138 ACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAGAAACCTGCAATTAGAGGAT 4197
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Db 3745 TTTTCATCTCAGGCTCTAGCTAAATTTCTGTTCTACTGAGAGGATGCTCCTAAATAGCCA 3686
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QY 4198 GTTTGTTCATATTAATTAATAAATAACTCACTGTTGGCACAGTGACTCAAGCCTGTAAACCAC 4257
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Db 3685 GAATTCATTTTATATTAATAAATAAATCTGGACGGACGCGAGTGCACACCTGTAATCCC 3626
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QY 4258 AGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTG 4317
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Db 3625 AGCACTTTGGGAGGCGGAGGCAGGTGGATCACCTGAGGTTGGAGTTTGAGACCAGCCTG 3566
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QY 4318 GTCATATGTTGAAACCCCTATCTCTACTAAAAATACAAAAATAGCTGGGTGTAGTGATG 4377
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Db 3565 ACCAACATGGAGAAACCCCGTCTCTACTAAAAATAC-AAAAATAGCCGGGCATGGTGGCG 3507
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QY 4378 CATGCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAAATGCTTGAACCTGGGAG 4437
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Db 3506 CATGCTGTAAATCCCAGCTACTCGGAAGGCTAAGGCAGGAGAAATCACTTGAACCCGGGAG 3447
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QY 4438 GCAGAGTTGCAGTGAGCCGAGATCCACCCACTGCACCTCCAGCTGGCGGAC-ACAGCGA 4496
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Db 3446 GTGGAAGTTGCAGTGAGCCGAGATCAGCCCACTGCACCTCCAGCCTGGCAACAAGAGCAA 3387
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QY 4497 GACTCTATCTCAAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAAACTAATA 4556
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Db 3386 AACTCCGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3327
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QY 4557 AGATTCCT 4564
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Db 3326 AGTTTCTT 3319
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RESULT 35
US-09-791-105B-32/c
; Sequence 32, Application US/09791105B
; Patent No. 6723508
; GENERAL INFORMATION:
; APPLICANT: EPIDAUROS Biotechnologie AG
; TITLE OF INVENTION: Method for detecting the presence of at least one single allele of a gene
; TITLE OF INVENTION: deletion mutant
; FILE REFERENCE: US 09,791,105
; CURRENT APPLICATION NUMBER: US/09/791,105B
; CURRENT FILING DATE: 2001-02-22

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; PRIOR APPLICATION NUMBER: EP20000103844 20000224  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32  
; LENGTH: 118999  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(118999)  
; OTHER INFORMATION: Homo sapiens genomic DNA, chromosome 22q11.2, clone KB226F1, Genb  
; OTHER INFORMATION: ank accession number AP00351.2 GI:5420485  
US-09-791-105B-32
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Query Match 8.0%; Score 397.6; DB 3; Length 118999;  
Best Local Similarity 53.7%; Pred. No. 2.1e-80;  
Matches 1301; Conservative 2; Mismatches 941; Indels 180; Gaps 16;  
  
QY 2278 AAAAAATCGCTTTCAGGCCAGGCGGTGGTCTCATGCTGTAAATCCCAGCACCTTTGGGAGG 2337  
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Db 88925 AAAAAAAGGCCAGGTGCGTGTGCTTATACGTGTAAATCACAGCACCTTTGGGAGG 88866  
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QY 2338 CCGAGGCGGCGGATCATTGAGGTGAGGTTCAGAGCAGCCTGGCCAAACATGTTGAA 2397  
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Db 88865 CCGAGGCGGCGAGATCAC--AAGTTCAGGAGTTCGAGACCATCTCTGGCTAATATGTTGAA 88808  
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QY 2398 ACCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGGAGCGCCTGTAAAC 2457  
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Db 88807 ACCCCATCTCTACTAAAAAATACAAAAAATTAGCCAGCATGGTGGCACCGCACCTGTAGTT 88748  
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QY 2458 CCAGCTACTTTGGGAGACT-----GAGTTGGAGGTTTCAG 2491  
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QY 2492 TGAGCCAAGGTGCTGCTACTGCTGTCCAGCCTGGTAAACAGAGCAACTCTGTCTCAAAA 2551  
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QY 2552 AAAAAAATGCTTTTCAATAAATATATGATAAAAGGACTTATATTTTCAAGCCATAGGAT 2611  
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Db 88627 AAAAAAAGCGACTATGTATGAAATACCCAGCACAGTGCCCTTCCCTTACCCATCAT 88568  
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QY 2612 CATTTCTCTGAAGCATCTTGGC-----GAAGTCATCCCC 2646  
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Db 88567 GACCCCCACACCCACAGTGTGGCCATCCTGTCTACCTGACGGCAAAATATAAGGTCCCT 88508  
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QY 2647 ACCTGTTCTGAGAGTGGGCGAGGTGAGGCTGACCTATTGCTCTGCACCTTACTCTATCT 2706  
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Db 88507 GACTACTGTTACCTCAGGACCTGCAGGCCCGTGCCTGTGGATGAGTACCTGGCATGG 88448  
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QY 2707 CAGCTGTCCCTCCCACTTTCCAGGTGTGCCAGACACATGACAACTGCTAYGACCAGGCC 2766  
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Db 88447 CAGCACAGCACTCTGCGAGAGAGCTGCCCTCCGGGC-CTTGTGGCATAAGGTGAGGCTGGG 88389  
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QY 2767 AAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCACACCTATTTCATAC 2826  
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Db 88388 AATGTGGGGGGCGGACGAGAGCATTTCCCAAAAGGTGTTTCAGGCACCAGTCTCTTCTT 88329  
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QY 2827 TCGTGTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCCTTGACCTATGAA 2886  
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Db 88328 TCAGTTTGGATTATTCTACTGACCTGTCTTTGGCCTTCACAGATTCTTTCTCTGTGT 88269  
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QY 2887 TTCTAGTTGGTTCTCAGTAGGCCGGGGGAAATAATAGTAAACACAGCCATGATTTAGTG 2946  
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Db 88268 GCCAAATTGCTATTAGCCCATCCAATACATCTCTTGTGTTGAGATATGATTTTTCAGCT 88209  
|||  
QY 2947 TTAATTTTCTGGGCGAGTGTCTCTCTTTAATCTCAGAACAAACACTATGGGATAG 3006  
|||  
Db 88208 CTGGAATTCATTTGGTGTGTTTTTAGAATTTCCACTTCTCTGATGAAATTCACCATCT 88149  
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QY 3007 GTACAATTATCTCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAAGGCTGA----- 3057  
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Db	88148	GTTCAATCCATTTATCTGTCTTTTCTTGTAATAATCTTTAAACAATATTATCACTGTTACCT	88089
Qy	3058	-----GCTAATTTGCCCAAGATCACACAGCTTGTAAGTGGTGACAGTTTGGTTTTTTTTT	3111
Db	88088	AAAAATCTTTGTCAACTAATTTTCAACACGTAGGTGTTCTGTGGGTCTGTTTTTTTGTTT	88029
Qy	3112	TGTTGTTGTTTAGAGACAGGGTCTTGCTGTGTCAACAGGCTAGGATGAGCACAGTGGTGCAAC	3171
Db	88028	TGTTTTGTTTTGAGATGGGTCTCACTCTGTCAACCCAGGC-TGAGTGCAATGGTGGAT	87970
Qy	3172	CATAGGTCACCTGCAGCCTCAACCTCTGAGCTCAAGGGATCTGTGACCTCAGCCTCCCA	3231
Db	87969	CTCAGCTCACTGCAACCTCCACCTCCCAGGCTCAAGCGATTCTCTGCTCAGCCTCCTG	87910
Qy	3232	AGTAGCTGGGACTACGAGCGTGCACCAACCGCCTGGCTAATTAAAAAAATTTTTTTGTA	3291
Db	87909	CGTAGCTGGGATTACAGGCACCCACAGCACACCTGGCTAACTTTTGTTA-TTTGTAGTG	87851
Qy	3292	GAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCTCGGCTTCAAGCAATCCT	3351
Db	87850	GAGACCGGTTTACCATGTTGGCCAGGCTGTTTCGAACTCTCCACCTGAAGTGATTCTG	87791
Qy	3352	CCTACCTTGGCATCCCAAGTGTGGGATTACAGGGTGAGCCACCATGTGCGG-----	3405
Db	87790	TCCTCCTTGGCTTCCCAAAGTGTGGGATTACAGGCATGAGCCACCATACCCAGCCTACG	87731
Qy	3406	-----CTACTTATTTCTTTACATTCACATCTTTCCATCTTTCCAATAGAAATGAATCCACAGA	3456
Db	87730	GGTCTATTTCTATTGATTGTTGTTTCTCCCTCTTGATTATGGGTACATTTGCTGCTT	87671
Qy	3457	ACAGGGATTACTGCCTAT-----TTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACT	3508
Db	87670	CTTTGCATGTCTCATGTGATTATCATATATTTTTTATTTTTTTTGAGACGGACTCTCACT	87611
Qy	3509	TCATCACCTCAACCTCCGTTCA-----GCTCACTGCAACCTCTGCTCCCG	3554
Db	87610	CCATTGCCCAGGCTGGCGTGCAATGGCACGATCTTGGCTCACTGCAACCTCCGCTCCTG	87551
Qy	3555	GGTTCAAGYGATTTCTCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCAC	3614
Db	87550	GGTTCAAGCGATTCTCCACCTCAGCCTCCCAAAGTAGCTAGAAATTACAGGCACCTGCCAT	87491
Qy	3615	CATGCTTGGCTAATTTTGTATTTTATAGCAGAGATGGGTTTTTACCATGTTGCCCAGGC	3674
Db	87490	CATGCCCTGGCTAAATTTT--GTATTTTGTAGAGACAGGGTTTACCATGTTGGCCAGGC	87433
Qy	3675	TGGTCTCAAACCTCCTGACCTCAAGTGATGTGCCTGCCTCAGTCTCCCAAAGTGTGGAAT	3734
Db	87432	TGGTCTTGAACTCCTGACCTCAGGTGATCCTCCCATCTCGGCCCTCCCAAAGTGTGGAT	87373
Qy	3735	TATAGGCGTGATCACTGTGCCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCCC	3794
Db	87372	TGTAGGCATGAGCCACCATGCCCGCCTCATGATGTATCCTTGTGTGCCAGACATTATGA	87313
Qy	3795	CAGATCTAGAGAGTGTCTGCACATATAGTAGGTGCTCAATAATAATGATGAATGCAC-	3853
Db	87312	TAAAAGAAGAGCAGAGATTGAATTGCATAATAAACACCCCAAGAAAGGGCTTGCACTTC	87253
Qy	3854	-----AGCCTAGATATAAACTTCTTTTCTTTTAAAAACAATCTTTGACAA	3901
Db	87252	CCTGTGTCAGGTAGCCAGGATGTGAGGCTGTCTCTTCTTAAGCTAATCAGGAGTGGCT	87193
Qy	3902	CTTTGCAGATAAATAACAATCTTGCAATCTGCTTTTTTTCACCTTATCACCTTGTATGACTT	3961
Db	87192	GGGTTGCAGGTTTAGTTGGTTTCAGTTTATCTTTGGTTTCAATATCTTGAATGTGAGAT	87133
Qy	3962	TTTCATATTGCTCAAACCTTTATTGTTACTGTTTTTTTCATTGTTACTATTTTAGTCACT	4021
Db	87132	CAGGTCACTAGCTCAGTCTAGCATGGCTTTGGAATCTAATCACCAACTACGATGTTGCCT	87073
Qy	4022	GAATAATATGGCTTAATTTGCT-----TATACATCCTCCTGCTCCACTTTAGA	4069
Db	87072	GTAAGATCTCTCTGCTTTTTCATCCCTGCCCCCAGTTTCCCAAACCTGCTGCTCAGTCAGAAA	87013

Qy	4070	AGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCTCCCAG-----AGA	4118
Db	87012	AGCCCATGCCTGTGACAGTCTTTCTCCCAGCCTGCTGGGCCCAAGGAAATGAAATTGGA	86953
Qy	4119	AATACACACACACACACACTCAACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAA	4178
Db	86952	ATGAAAGTAGCTCATCTAGGAAACGGCTTATGCCCTCTCTGGAAATTTAGTTTCATTAGTCAA	86893
Qy	4179	GAAACCTGCATTAGAGGATGTTTGT-----C	4205
Db	86892	GTGCTGTCCGATAGAAAGTATAAAGTGAGCCACATACGTAATTTTAAATTTTCTAGTAGGC	86833
Qy	4206	ATATTAATTAATAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACACAGTACTTT	4265
Db	86832	ACATTTAAAAAGTAAAAAGAGTCCAGGCACAGTGGCTCATGCCAATAATCCTAGCACTTT	86773
Qy	4266	GGAAGTCCAAGGTGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCGCCTGGTCAATAT	4325
Db	86772	GGGAGGCCAAGG-CAGTGGATCACCTGAGTCAAGGTCAAGAGTTCGAGACCGCCTGGTCAACAT	86714
Qy	4326	GGTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTAGTGCATGCCTG	4385
Db	86713	GGGGAACCTTGTCTCTACTAAACCAACCAAAATTAGCCAGGCTTGGTGGCCTGTGCCTA	86654
Qy	4386	TAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGT	4445
Db	86653	TAATCCCAGCTACTCAGGATGCTGAGGCAGGAGAAATTGCTTGAACCCAGGGGGCAAGTT	86594
Qy	4446	TGCAGTGAGCCGAGATCCCACCACTGCATCCAGCCTGGCGACACAGCGAGACTCTATC	4505
Db	86593	GGCAGTGTCCGAGATGGTGCCACTTCACTCCAGCCTGGGTGACAGAGCTGAACACTGTC	86534
Qy	4506	TCAAAAAATAATAATAAAAAATA	4529
Db	86533	TCAAAAGAAAAAATAAGTAAAA	86510

RESULT 36

US-09-949-016-15970/c
; Sequence 15970, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15970
; LENGTH: 181251
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15970

Query Match	7.9%;	Score 397.2;	DB 3;	Length 181251;
Best Local Similarity	56.9%;	Pred. No. 3.1e-80;		
Matches 927;	Conservative 2;	Mismatches 645;	Indels 54;	Gaps 9;
Qy	3087	AGTGGTGACAGTTGGGTTTTTTTTTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAAC	3146	

Db 112160 CCTGGCTGAGTGCAGTGGCGCAATCTTGACTCACTGTAACCTCCACCTCCCCGGTTCAA 112101

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Db 112100 GCAATTCCTGCCTCAGTCTCCCAAGTAGCAGGGAATTACAGTGTCATGTACCACCTCC 112041

Qy 3267 GGCTAATTAAAAAATTTTTTTGTAGAGACTGGGTCTTTACTACGTTGGCCAGGCTTGCT 3326

Db 112040 GGCTAATTTTGTGTA--TTTTCTGTAGAGGTAGGGTTTTCACCATGTTGGCCAGGCTGGTCT 111983

Qy 3327 TAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGTCTGGGATTACAGG 3386

Db 111982 CAAACTCCTGACCTCAGGGGATCCACCACCTCGGCCCTCCCAAGTGTCTGGGATTATA-G 111924

Qy 3387 GGTGAGCCACCATGTGCGGCTACTTTATTCTTTTACATTCCATCTTTTCCAATAGAATGTAA 3446

Db 111923 GGTAAAGTCACCATGCCCGC-----CAAGATTGGAGATTTTTTTGTG 111882

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Db 111881 TGATTTGGTCTTTTCGCTTTTTTTTTTTTGTGACGGAGTTTGTCTCTTGTGCTAGG 111822

Qy 3507 CTTCAATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCTCCCGGTTTCAAGYGAT 3566

Db 111821 CTGGAGTGCATGTTGCAACCTCGGCTCACCACAACCTCCACCTCATGGTTTCAAGTGAT 111762

Qy 3567 TCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCACCATGCTTGGCTA 3626

Db 111761 TCTCCTGCTTAGCCTCCCAAGTAGTGGGATTCAGGCTGCGCCACCATGCGCAGCTA 111702

Qy 3627 ATTTTTTGTATTTTAGCAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACT 3686

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Qy 3687 CCTGACCTCAAGTGATCTGCCCTCAGTCTCCCAAGTGTGGAATTATAGGCGTGAG 3746

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Qy 3747 TCACTGTGCTGGCCGATTACTGTCTATTTTCTTTTATTGCTATAT-CCCCAGATCTAGAG 3805

Db 111583 CCACTGGCCTGGCCTGCTTTTTTTGTTTTTTTAAACCCCGCAGGTAGTAAAGATGTAGAG 111524

Qy 3806 CAGTGTCTGACATATAGTAGTGTCTCAATAAATAATTGATGAATGCACAGCCTAGATATA 3865

Db 111523 GTAATATAACAAAAAATGGAGTGTCCAAGAAATTGTAGTTCTCTGAAATTTTGTGTTCTG 111464

Qy 3866 AACTTTTCTTTTCTTTTTTTTAAACAATCTTGACAACCTTTGCAGAAATAAATACAATCTTG 3925

Db 111463 AATAGAGTCATTTGTGGGCTGGAGCACATAGTGCAGACTGAGCTGATGCAAGAGATGATG 111404

Qy 3926 CATTCGTCTTTTTCACTTATCACCTTGTTA--TGACTTTTTTCATATTGCCCTCAAACTT 3982

Db 111403 CGAGACAAAAAATACAGGCACACAAGCCACGTTAAAGAGTCTAGAGTTTATCCTTAGGG 111344

Qy 3983 TATTGTACTGTTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTGC 4042

Db 111343 TAATGGAAAAAAGAAGGGTTTTTGAGCTAAGTTACATCATTTGCTAATAATATTAGTTAAGTGCC 111284

Qy 4043 TTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAAATTTACAATCTGATGAAAGCTATGA 4102

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Qy 4438 GCAGAGGTTGCAGTGAGCCGAGATCCCACTGCACTCCAGCCTGGGCGACACAGCGAG 4497

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Db 110685 CCCATAATTTATTGTCCAAACTAATTTTGAGAGTGAAAGAGGCTAATAGTGAAAAAACTG 110626

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RESULT 37

US-09-949-016-12511

; Sequence 12511, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12511

; LENGTH: 100463

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(100463)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12511

Query Match 7.9%; Score 396.4; DB 3; Length 100463;

Best Local Similarity 59.4%; Pred. No. 3.7e-80;

Matches: 872; Conservative 1; Mismatches 522; Indels 73; Gaps 9;

Qy 3096 AGTTTGGGTTTTTTTTTGTGTTGTTTGTAGAGACAGGGTCTTGTCTGTCAACCCAGGCATG 3155

Db 15375 AGTTTGTGTTTGTGTTTGTGTTTGTGAGATGAGTCTTGTCTGTGCGCCAGGCTGG 15434

Qy 3156 AGCACAGTGGTGCACCAACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGATCTGC 3215

Db 15435 AGTCAGTGGCGCAATCTCGGCTCACTGCAAGCTCGGCCTCCGGGTTTCATGCCAATCTC 15494

Qy 3216 TGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACACCGCTGGCTAATTA 3275

Db 15495 CTGCCTCAGCCTCCTGAGTAGCTGGGACTACAGGCGCCCGACACACCGCCGGCTAATTT 15554

Qy 3276 AAAAAATTTTTT---GTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACT 3332

Db 15555 TTTTGTTTTTTTTCAGTAGAGACGGGGTTTCACTGTGTTAGCCAGGATGGTCTCAATCT 15614

Qy 3333 CCTGGCTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAG 3392

Db 15615 CCTGACCTC--GTGATCTGCCCGCCTTGGCCTCCCAAAGTGTGGGATTACAAGCGTGAG 15672

Qy 3393 CCACCATGTGGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCA 3452

Db 15673 CCACCGTGCCAGCCTTGTTCTTTTTTTTTTTTTTTTTTTTT----- 15712

Qy 3453 CAGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTTTGAGACAGAGTCTCACTTCAT 3512

Db 15713 -----TTTTTTTGAGACAGTGTTCACCTCTTGGCACCCAGGCTCCAGGCTGGAG 15761

Qy 3513 CACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCCTCT 3572

Db 15762 TGCAGTGGCACAATCTGAGCTCACCTGCAACCTCTGCCTCCCAAGTTCAAGCGATTCCTCT 15821

Qy 3573 GCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCT--AATTT 3630

Db 15822 GTCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGTGCTCCAATATGCTTGGCTGGCTACATTT 15881

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Qy 3691 ACCTCAAGTGATCTGCCTGCCTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGGAGTCTCAC 3750

Db 15942 ACCTCAGGTGATCCACCTGCTTCGGTCTCCCAAAGTGTGGGATTACAGGTGTGAGCCAC 16001

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Db 16061 GCTGGAGTGCAGTGGCACCATCACAGCTCACTGCAGCATTAACCTCCTGGGCTCAAA--- 16117

Qy 3871 TCTTTTTCTTTTTTAAACAATCTTGACAACTTTGCAGAAATAAATACAATCTTGCATTC 3930

Db 16118 ---TGATCTCCCAACCCAGCCTCCCAACTAGCTGGGACTACAGTTGCAAAACCACTATC 16174

Qy 3931 TGCTTTTTTCACTTATCACCTTGTTATGACTTTTTTTCATATTGCTCAAAACCTTTATTGTTA 3990

Db 16175 CTGGCTAATTTTGTTTTTTTGATTTTGTGTTTCATTTGTTTGTAGCGATGGGGTTT 16234

Qy 3991 CTGTTTTTCAATGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACAT 4050

Db 16235 ACCATATGGCTCAGACTGGTCTCAAACTCTGGGCTCAAGCAGTCTCCTCCTCGGCCT 16294

Qy 4051 CCTCCTGCTCCACTTTAGAGGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTC 4110

Db 16295 CCCGAAGCGCTGGGATTACAAGTGTAGGCCATTACACCCAGCCCAACCTTAGCTGCAATA 16354

Qy 4111 CCCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTTAATGTTTG---- 4166

Db 16355 GGCAGAGAATAGGTCCCTGACATCTTGTCTCCCCAACCTCAGTTTACCCGTCTGTACA 16414

Qy 4167 -----CAACTAAGACAAGAAACCTGCATTTAGAGGATGTTTGTTCAT 4207

Db 16415 ATGGGTTGTCCATGAGCCTCCACCTGGCCCCCTTAGCTTGCTCCATCTGCAATGCTGGGT 16474

Qy 4208 ATTAATTAATAAATACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCAAGTACTTTGG 4267

Db 16475 TCAACATAGGTCTCCACGGCTGGGCATGGTGGCTCACACCTGTCTCATCCAGCACTTGGG 16534

Qy 4268 AAGTCCAAG-----GTGGGTGGATCACTTGAGGTGAGAAAGTTTCGAGACCAGCCTGGTCAAT 4323

Db 16535 GAGGCCGAGAGCCGAGCGGGCGGATCAGAGGTCAGGAGATCGAGACCATCCTTGCCAAAC 16594

Qy 4324 ATGGTGAACCCCTATCTCTACTAAAAATACAAAAATAGCTGGGTGTAGTGATGATGCC 4383

Db 16595 ATGGTGAACCCCATCTTCTTAAAAATACAAAAATAGCTGGGCGTGGTGGGCGATC 16654

Qy 4384 TGTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAAATTGCTTGAACCTGGGAGGAGAG 4443

Db 16655 TGTAATCCTAGCTACTCGGAGGCTGAGGCAGGAGAAATCGCTTGAACCCGGGAGGTGAG 16714

Qy 4444 GTTGCAGTGAGCCGAGATCCCAACCACTGCACCTCCAGCCTGGGCG-ACACAGCGGAGACTCT 4502

Db 16715 GTTGCAGTGGGCCGAGATTGCGCCACTGCACCTCCAGCCTTAGCGTTAAGAGCAAGACTCC 16774

Qy 4503 ATCTCAAAAAAATAAATAAAATAAAATAA 4530

Db 16775 GTCTCAAAAAAATAAATAAATAAATAAATGA 16802

RESULT 38

US-09-949-016-13725

; Sequence 13725, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13725

; LENGTH: 100468

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(100468)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13725

Query Match 7.9%; Score 396.4; DB 3; Length 100468;

Best Local Similarity 59.4%; Pred. No. 3.7e-80;

Matches 872; Conservative 1; Mismatches 522; Indels 73; Gaps 9;

Qy 3096 AGTTTGGGTTTTTTTTTTTGTGTTGTTTAGAGACAGGCTCTGTCTGTCACCCAGGCATG 3155

Db 15375 AGTTTTTTTGTGTTTTTGTGTTTTTTTGAGATGGAGTCTTGCTCTGTGCGCCAGGCTGG 15434

Qy 3156 AGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCTCTGAGCTCAAGGGATCTGC 3215

Db 15435 AGTCAGTGGCGCAATCTCGGCTCACTGCAAGCTCCGCCCTCCGGGTTTCATGCCAATCTC 15494

Qy 3216 TGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACCAACCGCTGGCTAATTA 3275

Db 15495 CTGCCTCAGCCTCCTGAGTAGCTGGGACTACAGGCGCCCGACACCAACCGCCGGCTAATTT 15554

Qy 3276 AAAAAATTTTTT---GTAGAGACTGGGTCTTACTAGCTTGGCCAGGCTTGTCTTAAACT 3332

Db 15555 TTTGTTTTTTTTTCAGTAGAGACGGGGTTTTCACGTGTGTAGCCAGGATGGTCTCAATCT 15614

Qy 3333 CTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAG 3392

Db 15615 CCTGACCTC--GTGATCTGCCCGCCTTGGCCTCCCAAAGTGTGGGATTACAAGCGTGAG 15672

Qy 3393 CCACCATGTGGGCTACTTATTTCTTTACATTCCATCTTTCCAATAGAATGTAAGATCCA 3452

Db 15673 CCACCGTGCCAGCCTTGTTCTTTTTTTTTTTTTTTTTTTTT----- 15712

Qy 3453 CAGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTTTGAGACAGAGTCTCACTTCAT 3512

Db 15713 -----TTTTTTTGAGACAGTGTTCACCTCTTGGCACCCAGGCTCCAGGCTGGAG 15761

Qy 3513 CACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCCTCT 3572

Db 15762 TGCAGTGGCACAATCTGAGCTCACCTGCAACCTCTGCCTCCCAAGTTCAAGCGATTCCTCT 15821

Qy 3573 GCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCT--AATTT 3630

Db 15822 GTCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGTGCTCCAATATGCTTGGCTGGCTACATTT 15881

Qy 3631 TTTGTATTTTACGAGAGATGGGGTTTACCATGTTGCCCAAGTGTGGTGTCTCAAACTCCTG 3690

Db 15882 TTTGTATTTTATAGTAGGACGGGGTTTGGCCATGTTGGCCGGGCTGTCTCAAGCTCCTA 15941

Qy 3691 ACCTCAAGTGATCTGCCTGCCTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGGAGTCTCAC 3750

Db 15942 ACCTCAGGTGATCCACCTGCTTCGGTCTCCCAAAGTGTGGGATTACAGGTGTGAGCCAC 16001

Qy 3751 TGTGCCTGGCGGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTG 3810

Db 16002 TGCGCCCAGCCTTTTTTTTTTTTTTTTTTTTTTTTGTGACA-GTCTGTCTGTGCCCCAG 16060

Qy 3811 TCTGACATATAGTAGGTGCTCAATAATAATATGATGAATGCACAGCCTAGATATAAACTT 3870

Db 16061 GCTGGAGTGCAGTGGCACCATCACAGCTCACTGCAGCATTAACCTCCTGGGCTCAAA--- 16117

Qy 3871 TCTTTTTCTTTTTTAAACAATCTTGACAACTTTGCAGAAATAAATACAATCTTGCATTC 3930

Db 16118 ---TGATCTCCCAACCCAGCCTCCCAACTAGCTGGGACTACAGTTGCAAAACCACTATC 16174

Qy 3931 TGCTTTTTTCACTTATCACCTTGTTATGACTTTTTTTCATATTGCTCAAAACCTTTATTGTTA 3990

Db 16175 CTGGCTAATTTTGTTTTTTTGATTTTGTGTTTCATTTGTTTGTAGCGATGGGGTTT 16234

Qy 3991 CTGTTTTTCAATGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACAT 4050

Db 16235 ACCATATGGCTCAGACTGGTCTCAAACTCTGGGCTCAAGCAGTCTCCTCCTCGGCCT 16294

Qy 4051 CCTCCTGCTCCACTTTAGAGGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTC 4110

Db 16295 CCCGAAGCGCTGGGATTACAAGTGTAGGCCATTACACCCAGCCCAACCTTAGCTGCAATA 16354

Qy 4111 CCCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTTAATGTTTG---- 4166

Db 16355 GGCAGAGAATAGGTCCCTGACATCTTGTCTCCCCAACCTCAGTTTACCCGTCTGTACA 16414

Qy 4167 -----CAACTAAGACAAGAAACCTGCATTTAGAGGATGTTTGTTCAT 4207

Db 16415 ATGGGTTGTCCATGAGCCTCCACCTGGCCCCCTTAGCTTGCTCCATCTGCAATGCTGGGT 16474

Qy 4208 ATTAATTAATAAATACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCAAGTACTTTGG 4267

Db 16475 TCAACATAGGTCTCCACGGCTGGGCATGGTGGCTCACACCTGTCTCATCCAGCACTTGGG 16534

Db 15615 CTGACCTC--GTGATCTGCCCGCCTTGGCCTCCAAAGTGCTGGGATTACAAGCGTGAG 15672

Qy 3393 CCACCATGTGGGCTACTTATTTCTTTTACATTCATCTTTCCAATAGAAATGTAAGATCCA 3452

Db 15673 CCACCGTGCCAGCCTTGTTCTTTT----- 15712

Qy 3453 CAGAACAGGGATTACTGCCTATTTTCTTCTCTTTTGAGACAGAGTCTCACTTCAT 3512

Db 15713 -----TTTTTTGAGACAGTGTTCACCTCTTGGCACCCAGGCTCCAGGCTGGAG 15761

Qy 3513 CACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCCTCCGGGTTCAAGYGATTCCT 3572

Db 15762 TGCAGTGGCACAATCTGAGCTCACTGCAACCTCTGCCCTCCAGGTTCAAGCGATTCCT 15821

Qy 3573 GCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCACTGCTTGGCT--AATTT 3630

Db 15822 GTCTAGCCTCCTGAGTAGCTGGGATTACAGGTGTGCTCCAATATGCTGGCTACATTT 15881

Qy 3631 TTTGTATTTTATAGCAGAGATGGGTTTTTACCATTGTTGCCAGGCTGGTCTCAAACTCCTG 3690

Db 15882 TTTGTATTTTATAGGACGGGTTTGGCCATGTTGGCCGGGCTGGTCTCAAGCTCCTA 15941

Qy 3691 ACCTCAAGTGATCTGCCCTCAGTCTCCCAAGTGCTGGAATTATAGGCGTGAGTCAC 3750

Db 15942 ACCTCAGGTGATCCACCTGCTCGTCTCCCAAGTGCTGGGATTACAGGTGTAGCCAC 16001

Qy 3751 TGTGCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTG 3810

Db 16002 TGGGCCCAGGCTTTTTTTTTTTTTTTTTTTTTTTTGTGACA-GTCTGTCTGTGCGCCAG 16060

Qy 3811 TCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTT 3870

Db 16061 GCTGGAGTGCAGTGGCACCATCACAGCTCACTGCAGCATTAAACTCCTGGGCTCAAA--- 16117

Qy 3871 TCTTTTCTTTTTTAAACAAATCTTTGACAACTTTTGAGAAATAAATACAATCTTGCATTC 3930

Db 16118 ---TGATCCTCCACCCAGCCTCCCAACTAGCTGGGACTACAGTTGCAAAACCACCATAC 16174

Qy 3931 TGCTTTTTCATTATCACCTTGTTATGACTTTTTTCATATTCCTCAAACTTTAATGTTA 3990

Db 16175 CTGGCTAATTTTGTGTTTTTTGATTTGTGTTGTTCAATTTGTTGTAGCGATGGGTTTT 16234

Qy 3991 CTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATAATGCGTTAATTTGCTTATACAT 4050

Db 16235 ACCATATGGCTCAGACTGGTCTCAAACTTCTGGGCTCAAGCAGTCTCCTCCTCGGCT 16294

Qy 4051 CCTCCTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGTGAAAGCTATGAACCTCTC 4110

Db 16295 CCCGAAGCGCTGGGATTACAAGTGTAGGCCATTACACCCAGCCCCAACCTAGCTGCAATA 16354

Qy 4111 CCCGAGAAATACACACACACACACTCACACACAGTTTTTTTTTAATGTTT----- 4166

Db 16355 GGCAGAGAAATAGGTCCCTGACATCTTGTGTTCTCCCAACCTCAGTTTACCCTGTGTACA 16414

Qy 4167 -----CAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCAT 4207

Db 16415 ATGGTTGTTCATGAGCCTCCACCTGGSCCCTTAGCTTGTCTCCATCTGCATGCTGGGTT 16474

Qy 4208 ATTAATTAATAAATAACTCAGTTGGSCACAGTGACTCAAGCCTGTAAACCACAGTACTTGG 4267

Db 16475 TCACATAGGTCTCCACGGCTGGGCATGGTGCTCACACCTGTCTATCCCGACTTGGG 16534

Qy 4268 AAGTCCCAAG---GTGGGTGGATCACTTGAGGTGAGAAGTTTCAGACCCAGCCTGGTCAAT 4323

Db 16535 GAGGCCGAGAGCCGAGGCGGCGGATCAGAGGTCAGGAGTCAGAGACCATCTCGGCCAAC 16594

Qy 4324 ATGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTAGTGATGCATGCC 4383

Db 16595 ATGGTGAACCCCATCTTTCCTAAAAATACAAAAAATTAGCTGGGCGTGGTGGGCGATC 16654

Qy 4384 TGATGCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAG 4443

Db 16655 TGTAATCTAGCTACTCGGGAGGCTGAGGCAGGAGAAATCGCTTGAAACCCGGAGGTGGAG 16714

Qy 4444 GTTGCAGTGAGCCGAGATCCCACTGCACTCCAGCCTGGGCG-ACACAGCGAGACTCT 4502

Db 16715 GTTGCAGTGGCCGAGATTGGCCACTGCACTCCAGCCTTAGCGTTAAGAGCAAGACTCC 16774

Qy 4503 ATCTCAAAAAATAAATAAATAAATAA 4530

Db 16775 GTCTCAAAAAAATAAATAAATAAATAA 16802

RESULT 39

US-09-949-016-16487

; Sequence 16487, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16487

; LENGTH: 12082

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-16487

Query Match 7.9%; Score 396; DB 3; Length 12082;

Best Local Similarity 53.6%; Pred. No. 1.8e-80;

Matches 1300; Conservative 2; Mismatches 942; Indels 180; Gaps 16;

Qy 2278 AAAAATCGCTTTCAGSCCAGGCGGGTGGCTCATGCTGTAATCCCAGCACCTTTGGGAGG 2337

Db 6336 AAAAAAAGCCAGGTGCGTTGCTTATACGTGTAATCACAGCACCTTTGGGAGG 6395

Qy 2338 CCGAGGCGGGGATCACTTGAGGTGAGGATTCGAGACCAGCCTGGCCCAACATGGTGAA 2397

Db 6396 CCGAGGCAGGCAGATCAC--AAGGTGAGGATTCGAGACCATCCTGGCTAATATGGTGAA 6453

Qy 2398 ACCCTGTCTCTACTAAAAATACAAAAAATTAGCCGACATGGTGGCAGCGCCTGTAAACC 2457

Db 6454 ACCCATCTCTACTAAAAACTACAAAAAATTAGCCAGGCATGGTGGCAGCACCTGTAGTT 6513

Qy 2458 CCAGCTACTTGGGAGACT-----GAGTTGGAGGTTTCAG 2491

Db 6514 CCAGCTACTTGGAGGCTGAGGCAGGAGAAATCACTTGAAACCCGGAGGTGGAGGTTGCAG 6573

Qy 2492 TGAGCCAAGGTCGTGTCACTGTGTCCAGCCTGGTAAACAGAGCAACTCTGTCTCAAAAA 2551

Db 6574 TGAGCCAAGATCGCACCACTGCATCCAGCCTGAGCGACAGAGCGAGACTCCGTATCAAA 6633

Qy 2552 AAAAAAATGCTTTCAATAAATATATGATAAAGGACTTATATTTTCAAGCCATAGGAT 2611

Db 6634 AAAAAAAGCGACTATGTATGAAATACCCAGCACAGTGCCCTTCCCTTACCCATCAT 6693

Qy 2612 CATTTCTCTGAAGCATCTTGGC-----GAAGTCATCCCC 2646

Db 6694 GACCCCAACACCCACAGTGTGGCCATCCTGTCTACCTGACGGCAAAATATAAGGTCCCT 6753

Qy 2647 ACCTGTTCTGAGAGTGGGCAGGTGAGGGCTGACCTATTGCTCTGCACCTACTCCTATCT 2706

Db 6754 GACTACTGGTACCTTCAGGACCTGCAGGCCCTGCGCCGTGTGGATGAGTACCTGGCATGG 6813

Qy 2707 CAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACATGACAACTGCTAYGACAGGCC 2766

Db 6814 CAGCACACGACTCTGCGGAGAAAGCTGCCTCCGGGC-CTTGTGGCATAAAGGTGAGGCTGGG 6872

Qy 2767 AAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCACACCTATTTCATAC 2826

Db 6873 AATGTGGGGCGGACGAGAGCATTCGCCAAAGGTGTTCCAGSCACCAGTCTCTTCTTT 6932

Qy 2827 TCGTGTCTGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCTTGACCTATGAA 2886

Db 6933 TCAGTTTGGATATTTCTACTGACCCTGTCTTGCCTTCACAGATTTCTTCCCTCTGTTGT 6992

Qy 2887 TTCTAGTTGGTCTCAGTAGGGCGGGGGAATAATAGTAACAACAGCCATGATTTAGTG 2946

Db 6993 GCCAAATTGCTATTAAAGCCCATCCAATACATTTCTTGTGTTGAGATATGATTTTTCAGCT 7052

Qy 2947 TTAATTTTCTGGTTCTGGGAGTGTCTCCTTTAATCCTCAGAAACAACACTATGGGATAG 3006

Db 7053 CTGGAAATTCATTTGGTTGTTTTTGTAGAAATTTCCACTTCTCTGATGAAATTCACCATCT 7112

Qy 3007 GTACAATTAATCCTCACTTAACAGATAAGAAAAACTGAGGCTCAGAAGGCTGA----- 3057

Db 7113 GTTCATCCATTTATCTGTCTTTTCTGTAAATTTCTTTAACAATTTATCACTGTTACCT 7172

Qy 3058 -----GCTATTGCCCCAAGATCACACAGCTTGTAAGTGGTGACAGTTTGGGTTTTTTTT 3111

Db 7173 AAAAAATCTTTGTCAACTAATTTCAACACGTAGGTGTTCTGTGGGTCTGGTTTTTTTGTT 7232

Qy 3112 TGTGTTGTTTAGAGACAGGGTCTTGTCTGTCACCCAGGCATGAGCACAGTGGTGCAC 3171

Db 7233 TGTTTTGTTTTGAGATGGGGTCTCACTCTGTCACCCAGGC-TGAGTGCAATGGTGGCAT 7291

Qy 3172 CATAGGTCACCTGACGCCCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCA 3231

Db 7292 CTCAGCTCACTGCACACCTCCACCTCCAGGCTCAAGCGATTCTCTGCCTCAGCCTCCTG 7351

Qy 3232 AGTAGCTGGACTACGAGCGTGCACCAACGCTTGCTTAAACTCTCGGTTCAAGCAATCCT 3291

Db 7352 CGTAGCTGGATTACAGGCACCCACCAGCACACCTGGCTAACTTTGTGA-TTTGTAGTG 7410

Qy 3292 GAGACTGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCTCGGTTCAAGCAATCCT 3351

Db 7411 GAGACCAGGTTTCAACCATGTTGGCCAGGCTGTTTCGAACTCTCCACCTGAAGTGATCG 7470

Qy 3352 CCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGG----- 3405

Db 7471 TCCCTCCTTGGCTTCCCAAAGTGTGGGATTACAGGCATGAGCCACCATACCCAGCCTACG 7530

Qy 3406 -----CTACTTATTTCTTTACATTCCTATCTTTCCAAATAGAATGTAAGATCCACAGA 3456

Db 7531 GGTCTATTTCTATTGATTGTTGTTTCTCCCTCTTGATTATGGGTCACATTTGCCCTGCTT 7590

Qy 3457 ACAGGGATTACTGCCCTAT-----TTTCTTCTTTTCTTTTGTAGACAGAGTCTCACT 3508

Db 7591 CTTTGCATGTCTCATGATGATTAATCATATTTTATTTTATTTTGTAGACGGACTCTCACT 7650

Qy 3509 TCATCACCTCAACCTCCGTTCA-----GCTCACTGCAACCTCTGCCTCCCG 3554

Db 7651 CCATTGCCCAGGCTGGCGTGCAATGGCACGATCTTGGCTCACTGCAACCTCCGCCTCCTG 7710

Qy 3555 GGTTCAGYGATTTCTCTGCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCAC 3614

Db 7711 GGTTCAGCGATTCTCCACCTCAGCCTCCCAAGTAGCTAGAATTACAGGCACCTGCCAT 7770

Qy 3615 CATGCTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGGTTTACCATGTTGCCCAGGC 3674

Db 7771 CATGCCCTGGCTAATTTT--GTATTTTGTAGAGACAGGGTTTCACCATGTTGGCCAGGC 7828

Qy 3675 TGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCCAAAGTGTGGAAT 3734

Db 7829 TGGTCTTGAACCTCCTGACCTCAGGTGATCTCCCATCTCGGCTCCCCAAAGTGTGGGAT 7888

Qy 3735 TATAGGCGTAGTCACTGTGCCTGGCCGATTACTGTCTATTTCTTTTATTGCTATATCCC 3794

Db 7889 TGTAGGCATGAGCCACCATTGCCCGGCTCATGATGTATCCTTGTGTGCCAGACATTATGA 7948

Qy 3795 CAGATCTAGAGCAGTGTCTGCACATATAGTAGGTCTCAATAAAATAATTGATGAATGCAC- 3853

Db 7949 TAAAAAGAGAGCAGAGATTGAATTGCATAATAAACACCCCCAAGAAAGGCTTGCACTTC 8008

Qy 3854 -----AGCCTAGATATAAAACTTTTCTTTTCTTTTAAAAACAATCTTGACAA 3901

Db 8009 CCTGTGTCAGGTAGCCAGGATGTGAGGCTGTTCTCTTCTAAGCTAATCAGGAGGTGGCT 8068

Qy 3902 CTTTGCAGAAATAAATAACAATCTTGCAATCTCTGCTTTTTCACCTTATCACCTTGTATGACTT 3961

Db 8069 GGGTGCAGGTTTAGTTGGTTTCAGTTTATCTTTGGTTTCAAAATATCTTGAATGTGAGAT 8128

Qy 3962 TTTTCATATTGCCCTCAAAACCTTTTATTGTTACTGTGTTTTTTCATTGTTACTATTTTAGTCACT 4021

Db 8129 CAGGTCACCTAGCTCAGTCTAGCATGGCTTTTGGAACTTAATCACCAACTACGATGTTGCCT 8188

Qy 4022 GAATAATATGGCTTAATTGCT-----TATACATCCTCCTGCTCCACTTTAGA 4069

Db 8189 GTAAGATCTCTCTGCTTTTCATCCCTGCCCCAGTTCCTCAAAACTGCTGCTCAGTCAGAAA 8248

Qy 4070 AGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCTCCCAG-----AGA 4118

Db 8249 AGCCCATGCTGTGACAGTCTTTCTCCCAGCCTGCTTGGGCCCAAGGAAATGAATTTGGA 8308

Qy 4119 AATACACACACACACACACTCACACACAGTTTTTTTTTTTAAATGTTTGCAACTAAGACAA 4178

Db 8309 ATGAAAGTAGTCTCATCTAGGAACGGCTTATGCCTCTCTGGAATTTTAGTTCAATTAGTCAA 8368

Qy 4179 GAAACCTGCATTAGAGGATGTTTGT-----C 4205

Db 8369 GTGCTGTCCGATAGAAGTATAAAGTGAGCCACATACGTAATTTTAAATTTTCTAGTAGGC 8428

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Db 8429 ACATTTAAAAAGTAAAAAGAGTCCAGGCACACAGTGGCTCATGCCAATAATCCTAGCACTTT 8488

Qy 4266 GGAAGTCCAAGGTGGTGGATCATTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATAT 4325

Db 8489 GGGAGGCCAAGG-CAGTGGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGGTCAACAT 8547

Qy 4326 GGTGAAACCTTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTATGCATGCCTG 4385

Db 8548 GGGGAAACCTTGTCTCTACTAAAAACCAAAAAATTAGCCAGGCTTGGTGGCCTGTGCCTA 8607

Qy 4386 TAGTCCCAGCTACTCGGAGGCTGAGGCAAGAAATGCTTGAACCTGGGAGGCAGAGGT 4445

Db 8608 TAATCCCAGCTACTCAGGATGCTGAGGCAGGAGAAATGCTTGAACCCAGGGGCAAGATT 8667

Qy 4446 TGCAGTGAGCCGAGATCCCACCACCTGCACCTCCAGCCTGGCGACACAGCGAGACTCTATC 4505

Db 8668 GGCAGTGTCCCGAGATGGTGCCACTTCACTCCAGCCTGGGTGACAGAGCTGAACACTGTC 8727

Qy 4506 TCAAAAAAATAAATAAATAAATA 4529

Db 8728 TCAAAAGAAAAAAGTAAAA 8751

RESULT 40
US-08-814-095-7/c
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills

/	NAME/KEY:	exon																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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QY	3749	ACTGTGCCTGGCCGATTACTGTCTATTTTCTTATTGCTATATCCCCAGATCTAGAGCAG	3808
Db	10568	ACGGCACCCAGCCCGAAGCATCTTTTTTCTGTGTTGTTTTGTTT-----GTTTGAGACGG	10515
QY	3809	TGTCTGACATATAGTAGGTGCTCAATAAATAAATTGATGAATGCACAGCCTAGATATAAAC	3868
Db	10514	AGTTTGTCTCCTGTGCCCCAGGATGGAGTGCCATGGTGCAATCTCAGCTCA---CTACAA	10458
QY	3869	TTTCTTTTTTCTTTTTTAAACAAATCTTGACAACTTTGCAGAAATAAATACAACTTGCAT	3928
Db	10457	TCTCTGCCTCCCGGTTCAAGCAATTTCTCCTGCCTCAGCCTCCTGAGTAGTGGGATTAC	10398
QY	3929	TCTGCTTTTTCACCTTATCACCTTGTATGACITTTTTTCATATTTGCCCTCAAACTTTATTGT	3988
Db	10397	AGGCATGCGCCACCAACCTGGCTAAATTTTGTATTTTGTAGTAGAGATGGGGTTTCACTA	10338
QY	3989	TACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATAC	4048
Db	10337	TGTTGGTCAGGCTAGTCTCGAACTCCTGACCTGAAAGTGATCCACCTGCCTCGGCTTCCCA	10278
QY	4049	ATCCTCCTGCTCCACTTTTAGAAGGCCAAATTTTACAAATCTGATGAAAGCTATGAACCTC	4108
Db	10277	AAGTGCTGGGATTACAGCGCTGAGCCACCCACCGCTGGCCGGAAGCATCTTAAATGTAAA	10218
QY	4109	TCCCCAGAGAAATACACACACACACACACTCACACACAGTTTTTTTTTTAATGTTTGCA	4168
Db	10217	ACTGCAGATGCAGGTTTAGCAATTTTAGACGCTTGCACCCCAAGATGCACATATTACTAGAG	10158
QY	4169	ACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAATAATAACTCAGT	4228
Db	10157	CAATGCCAAACAATAATGTGATTTCTGTGGGTTTCTGTTGATTTTTTAATTTGGAAGGATT	10098
QY	4229	TGGGCACAGTGA----CTCAAGCCTGTAAACCACACAGTACTTTTGAAGTCCAAGGTGGTG	4283
Db	10097	CTGGCTGAGTGAGGTGGCTCACATCTGTAAATCCACAGCACTTTGGGAGGCTGAGGTGGCA	10038
QY	4284	GATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTTA	4343
Db	10037	GATCACTTGAGGCCAGGATTTTGAGACCAGCCTGGCCAAACATGGTGAAACCCCTGTCTTA	9978
QY	4344	CTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGG	4403
Db	9977	CTGAAATTATAAAAATTAGCTGGGCATTTGTGTGGGCACCTGGTAATCCCAGCTATTGGG	9918
QY	4404	AGGCTGAGGCAAGAAATTGCTTGAAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCC	4463
Db	9917	AGGCTGACACAGGAAAAATGCTTGAAACCTGGTGGCAGAGGTTGCAGTGAGCCGAGATTG	9858
QY	4464	CACCACTGCACCTCCAGCCTGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAT	4523
Db	9857	TGCCACTGCACCTCCAGCCTGGCGATAGAGCGGAGACTCCGTCTCAAAAGAAAAAGATTCT	9798
QY	4524	AAAATAAAGGATCGGAGAGAAACAAA	4549
Db	9797	AAGGCATGGCAAAATAAGATTTAAAAA	9772

RESULT 41

US-09-949-016-17394/c
; Sequence 17394, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03


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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17394
; LENGTH: 145241
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17394

      7.9%;   Score 394.2;   DB 3;   Length 145241;
Query Match
Best Local Similarity 59.1%;   Pred. No. 1.4e-79;
Matches 882;   Conservative 1;   Mismatches 554;   Indels 56;   Gaps 10;

QY 3098 TTTGGGTTTTTTTTTGTGTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAG 3157
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
22191 TTTTGTTCATTTTTTGTCTTTTGAGATGGAGTCTTGCTCTGTGCCAGG----- 22138

QY 3158 CACAGTGGTGCAACCATAGTCACTGCGAGCCCTCAACCTCTGAGCTCAAGGGATCTGCTG 3217
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
22137 --CAGTGGTGCAATCTCAGCTCATTTGCAAGCTCCACCTCCAGGTTCAAGTGATCTTCT 22080

QY 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACACGCTGGCTAAATAA 3277
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
22079 GCCTCAGCCTCCCAAGTAGCTGGGACTATAGGCGCCCAACCAACACGCTCCGGCTAATTTT 22020

QY 3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGG 3337
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
22019 GTA--TTTTAGTAAAGACAGAGTTTCACCAATATTGGCCAGGCTGGTCTCGAACTCTGA 21962

QY 3338 CTTCAAGCAATCCTCCTACCTTGCGATCCCAAGTGTCTGGGATTACAGGGGTGAGCCACC 3397
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21961 CCTC--GTGATCTGCCTGCCTTGGCTCCCAAGTGTCTGCGATTACAGGCGTGAGCCACC 21904

QY 3398 ATGTGGGGTACTTATTTCTTTTACATTCCA-----TCTTTCCAATAGATGT 3444
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21903 ACACCAGCCTGGACCTCTTTTTTTTTTTTAAATCCAAAGCAATTTATGCTGAAGGAATAGT 21844

QY 3445 AAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCTTCTTTTGTGAGACAGAGTCT 3504
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21843 TTGCTAGAAAAATACAAAAGTGTTTTTTTGTGTTTTTGTGTTTTTTTGAGACCGAGTCT 21784

QY 3505 CACTTCATCACCTCAACCTCCGT-----TCAGTCACTGCAACCTCTGCCT 3550
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21783 TACTCTGTGCCCCAGGCTGGAGTGTAGTGGCAAGATCTTGGCTCATGGCAACCTCCGCCT 21724

QY 3551 CCCGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGTGAATTACAAGCGTGCA 3610
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21723 CCTGGCTCAAGTGATTCTCCTACTTCAGCCTTCCGAGTAGTGGGATTACAGGTGCACA 21664

QY 3611 CCACCATGCTTGGCTAATTTTTTGTATTTTTTAGCAGAGATGGGGTTTTTACCATGTTGCC 3670
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21663 TCACCACACCCAGCT-AGTTTTTGTACCCCTTAGTAGAGATGGGGTTTTTGTCTATGTTGCC 21605

QY 3671 AGGTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTGCCTCAGTCTCCCAAAGTCTG 3730
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21604 AGGTAGTCTTGAACCTCCTGGCCTCAGTTGATCTG-CTGCCCTAGCCTCCCAAACCTGCTG 21546

QY 3731 GAATTATAGCGGTGAGTCACTGTGCTGGCCGATTACTGTCTATTTTCTTTATTGCTATA 3790
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21545 GGATTACAGGCATGAGCCACCAACCCAGCC--CTAGAAAAATAAAATTATAAAACAAGAC 21488

QY 3791 TCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATG 3850
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21487 AGGCAATTAAATCTCACTTGCTAGTACCTACTATCAAAATGCTGTACTAGGTGCTTAAGA 21428

QY 3851 CACAGCCTAGATATAAACTTTTCTTTTCTTTTAAAAACAATCTTGACAACITTTGCAGA 3910
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21427 ACCACAAATATTTAAAAAGTCACAGGACTTGAAATCCAAATGGTTGAAGCAAAACCAAAAT 21368

QY 3911 ATAAATACAAATCTTGCAATCTGCTTTTTCACCTTATCACCTTGTTATG-----ACTTTT 3964
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21367 ATTACAGAAATTTATCAGCTAGAAATGCAACAAGTCAAAATATTAAGGAAAAAATTTTCAG 21308
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QY 3965 CATATTGCCCTCAAACTTTTATTGTTACTGTTTTTTTCTATTGTTACTATTTTAGTCACTGAA 4024
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21307 TTTAGGATTCCACACCCAGTAAACAATCTTTCAAATGGAGACTTTTATCAGACATAGAA 21248

QY 4025 TAA-----TATGGCTTAATTTGCTTATACATCCTCTCTCCACTTTTAGAAGGCCAAA 4077
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21247 AAAGCAGACCTACATAATAAAAAATGTTCAAAGCCATTCTCCAGCCAGAGGAAAAATGAT 21188

QY 4078 TTTACAAATCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAAAAATACACACACACAC 4137
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21187 ACTACATGGAAAGTTGGATCTGTAAAAAAGGAAAGCATTTGAAAAAGGTAACATTTGAGT 21128

QY 4138 ACTCACACACAGTTTTTTTTTAAATGTTTGCAACTAAGACAAAGAACCTGCTATAGAGGAT 4197
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21127 AAATATAAGTGCCTCTCTCATTTTAAATTTTATGTTCTGTATTTAACACACATACACCAT 21068

QY 4198 GTTTGTTCATATTAAATAAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCCAC 4257
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21067 GCAAAACAGACATAAAACAGATGACAACAGGCCAGCGCAGTGGCTCATGCCTGTAATCCC 21008

QY 4258 AGTACTTTTGGAAAGTCCAAGGTGGTGGATCATTGAGGTGAGAAGTTTCGAGACCCGCTG 4317
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
21007 AGCACTTTGGGAGGCTGAAGTGGTGGATCATTGAGGTGAGGATTTCAAGACCAAGCCTG 20948

QY 4318 GTCAATATGGTGAACCCCTATCTCTACTATAAAATACAAAAATTAGCTGGGTGTAGTGATG 4377
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
20947 GCCAACAGGTGAAATCCAGCTCTACTAAAAAATACAAAAATTAGCTGGCGGTGGTGCA 20888

QY 4378 CATGCTGTAGTCCCAGTACTCGGGAGGCTAGGCAAGAGAAATTGCTTGAACCTGGGAG 4437
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
20887 CATGCTGTAAATCCAGCTACTGGGAGGCTGAGCAAGAGAAATTGCTTGAACCTGGGAG 20828

QY 4438 GCAGAGGTTGCAGTGAGCCGAGATCCCACCCTGCACTCCAGCTGGGCGACACAGCGAG 4497
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
20827 GCGGAGGTTGCAGTGAGCCAAGATCATGCCATTGCATTCAGTCTAGACGAAGAAGTAAG 20768

QY 4498 ACTCTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAA 4550
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
20767 ACTCCGTCTCAAAAAAAGATGACAACAGTACAAAAGACAAGATGAAAA 20715
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RESULT 42

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US-09-949-016-17395/c
; Sequence 17395, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17395
; LENGTH: 145241
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17395
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Query Match 7.9%;   Score 394.2;   DB 3;   Length 145241;
Best Local Similarity 59.1%;   Pred. No. 1.4e-79;
Matches 882;   Conservative 1;   Mismatches 554;   Indels 56;   Gaps 10;

QY 3098 TTTGGGTTTTTTTTTGTGTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAG 3157
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 22191 TTTTGTTCATTTTTTGTCTTTTGAGATGGAGTCTTGCTCTGTGCCCAGG----- 22138

Qy 3158 CACAGTGGTGCAAACCATAGGTCACTGCAGCCTCAACCCTCCTGAGCTCAAGGGATCTGCTG 3217

Db 22137 --CAGTGGTGCAAATCTCAGCTCATTCGAAGCTCCACCCTCCAGGTTCAAGTGATCTTCT 22080

Qy 3218 ACCTCAGCCTCCAAAGTAGCTGGGACTACGAGCGTGCACCAACACAGCCTGGCTAAATAAA 3277

Db 22079 GCCTCAGCCTCCCAAGTAGCTGGGACTATAGGCGCCCAACCAACGCTCCGGCTAATTTT 22020

Qy 3278 AAAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGG 3337

Db 22019 GTA--TTTTAGTAAAGACAGAGTTTCACCATATTGGCCAGGCTGGTCTCGAACTCCTGA 21962

Qy 3338 CTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGGTGAGCCACC 3397

Db 21961 CCTC--GTGATCTGCCTGCCTTGCCCTCCCAAAAGTGCTGCGATTACAGGCGTGAGCCACC 21904

Qy 3398 ATGTGCGGTACTTATTTCTTTTACATCCA-----TCTTTCCAATAGAAATGT 3444

Db 21903 ACACCCAGCCTGGACCTCTTTTTTTTTTAATCCAAAGCAATTTATGCTGAAGGAATAGT 21844

Qy 3445 AAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTGTAGACAGAGTCT 3504

Db 21843 TTGCTAGAAAAATACAAAGTGTTTTTTTGTGTTTTTGTGTTTTTGTAGACCGAGTCT 21784

Qy 3505 CACTTCATCACCTCAACCTCCGT-----TCAGCTCACTGCAACCTCTGCCT 3550

Db 21783 TACTCTGTGGCCAGGCTGGAGTGTAGTGGCAAGATCTTGGCTCATGGCAACCTCCGCT 21724

Qy 3551 CCCGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCA 3610

Db 21723 CCTGGGCTCAAGTGATTCTCCTACTTCAGCCTTCCGAGTAGCTGGGATTACAGGTGCACA 21664

Qy 3611 CCACCATGCTGGCTAAATTTTTTGTAATTTTGTAGCAGAGATGGGTTTTACCATGTTGCC 3670

Db 21663 TCACCACACCCAGCT-AGTTTTTGTACCTTAGTAGAGATGGGTTTTGTATGTTGGCC 21605

Qy 3671 AGGCTGGTCTCAAACTCCTGACCTCAAGTGATCGCCTGCCTCAGTCTCCCAAAGTGCTG 3730

Db 21604 AGGCTAGTCTTGAACCTCCTGGCCTCAGTTGATCTG-CTGCCCTAGCCTCCCAAACCTG 21546

Qy 3731 GAATTATAGCGTGAGTCACTGTGCTGCGCCGATTACTGTCTATTTTCTTTATTGCTATA 3790

Db 21545 GGATTACAGSGCATGAGCCACCACACCCAGCC--CTAGAAAAATAAAATTATAAAACAAGAC 21488

Qy 3791 TCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATG 3850

Db 21487 AGGCAATTTAATCTCACTTGTCTAGGTACCTACTATCAAAATGCTGTACTAGGTGCTTAAGA 21428

Qy 3851 CACAGCCTAGATATAAACTTTCTTTTCTTTTAAACAATCTTGACAACTTTGCAGA 3910

Db 21427 ACCACAAATATTTAAAAAGTCACAGGACTTGAAATCCAATGGTTGAAGCAAAACCAAAAT 21368

Qy 3911 ATAAATACAATCTTGCAATCTGCTTTTTCACCTTATCACCTTGTATG-----ACTTTT 3964

Db 21367 ATTACAGAAATTTATCAGCTAGAAATGCAACAAGTCAAAATATTAAAGGAAAAAATTTTCAG 21308

Qy 3965 CATATTGCCCTCAAACTTTATTGTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAA 4024

Db 21307 TTTAGGATTCACACCCAGTAGAAACAATCTTCAAAATGGAGACTTTATCAGACATAGAA 21248

Qy 4025 TAA-----TATGGCTTAATTTGCTTATACATCTCCTGCTCCACTTTAGAAGGCCAAA 4077

Db 21247 AAAGCAGACCTACATAATAAAAAATGTTCAAGCCATTCTCTCAGCCAGAGGAAAAATGAT 21188

Qy 4078 TTTACAAATCTGATGAAGCTATGAACCTCTCCCCAGAGAATAACACACACACACACAC 4137

Db 21187 ACTACATGGAAAGTTGGATCTGTAAAAAGGAAAAGCATTTTGAAGGTAACATTTTGAGT 21128

Qy 4138 ACTCACACACAGTTTTTTTTTAATGTTGCAACTAAGACAAGAAACCTGCATTAGAGGAT 4197

Db 21127 AAATATAAGTGCCTCTTCTCATTTTTTAAATTTTATGCTGTATTTTAAACACACATACCCAT 21068

Qy 4198 GTTTGTTTCATATTAAATAAATAAATACTCAGTTGGCACAGTGACTCAAGCCTGTATAACCAC 4257

Db 21067 GCAAAACAGACATAAAACAGATGACAACAGGCCAGCGCAGTGGCTCATGCTGTAATCCC 21008

Qy 4258 AGTACTTTGGAAGTCCAAGGTGGTGGATCACTTGAGGTGAGAAAGTTTCGAGACCAGCCTG 4317

Db 21007 AGCACTTTGGGAGGCTGAAGTGGTGGATCACTTGAGGTCAGGAGTTTCAAGACCAGCCTG 20948

Qy 4318 GTCAATATGTTGAACCCCTATCTCTACTATAAAATACAAAAATTAGCTGGGTGATGATG 4377

Db 20947 GCCAACAGGTGAAATCCCAGCTCTACTAAAAATACAAAAATTAGCTGGCGTGGTGGCA 20888

Qy 4378 CATGCCTGTAGTCCAGCTACTCGGGAGGCTGAGCAAGAGAAATTGCTTGAACCTGGGAG 4437

Db 20887 CATGCCTGTAATCCAGCTACTGGGAGGCTGAGCAAGAGAAATTGCTTGAACCTGGGAG 20828

Qy 4438 GCAGAGGTTGCAGTGAGCGGAGATCCCACCACCTCCAGCTCCAGCTGGCGACACAGCGAG 4497

Db 20827 GCGGAGGTTGCAGTGAGCCAAGATCATGCCATTGCACCTCCAGTCTAGACGAAGAAGTAAG 20768

Qy 4498 ACTCTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAAA 4550

Db 20767 ACTCCGTCTCAAAAAAAAAGATGACAAACAGTACAAAAGACAAGATGAAAA 20715

RESULT 43

US-09-949-016-16587/c

; Sequence 16587, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 16587

; LENGTH: 55135

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-16587

Query Match 7.8%; Score 389.8; DB 3; Length 55135;

Best Local Similarity 60.4%; Pred. No. 9.1e-79;

Matches 870; Conservative 1; Mismatches 498; Indels 72; Gaps 11;

Qy 3093 GACAGTTTGGGTTTTTTTTTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCAGGC 3152

Db 46243 GTCATTTCAACATAATTATTGTTTCTTTTTAGAGACAGGGTC-TCATCTGTCACCCAGGC 46185

Qy 3153 ATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCTCAACCTCCTGAGCTCAAGGGATC 3212

Db 46184 TGGAGTATAGTGGTGCCATCATAGCCCACTGTAGACTCAAACTCCTGGGCTCAAGTGATC 46125

Qy 3213 TGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGACACCACCGCCTGGCTAA 3272

Db 46124 TTCCCTCTTCCACCTTCCGAGTGGCTAGGACTACAGTGTGTGCCACCATGCCITGGATAA 46065

Qy 3273 TTAACAAAAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACT 3332

Db 46064 TT-----TTTTTTGTAGAAATGGGGTCTCCTATGTGGCCACGCTGGTCTTGAAC 46012

Qy 3333 CTGGCTTCAAGCAATCCTCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGTGAG 3392

Db 26346 AGCTCCCAAAGTGTGGGATGACAGGGGTGAGCCACTGGCGCCAGCCGAGATTGTGCAT 26287

Qy 3062 TTTGCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGG-----GTTTT 3107

Db 26286 TCTTAAAGCTCCAGGGGATGCCAATACTGTCAAGTGGGACCACACATTGTATTTTTTT 26227

Qy 3108 TTTTTGTGTGTTTAGAGACAGGGTCTTGCTGTCTGTCACCCAGGCATGAGCACAGTGGTG 3167

Db 26226 GTTTTTGTGTTTTTTTGAGACAGGGTCTCACTCTGCTTCCAGGCTGGAGTGCAGTGGCA 26167

Qy 3168 CAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGCCT 3227

Db 26166 GGTCTCGGCTCAATGCAACCTCCGCCTCCTGGGTTCAAAGTGATTCTTGTGCCTCAGCCT 26107

Qy 3228 CCCAAGTAGCTGGGACTACGAGCGTGCACCCAGCGCTGCTAAACTCCTGGCTTCAAGCAA 3347

Db 26106 CCCGAGTAGCTGGATTACAGGCTTGAGTTACCATGCCCTGGCTAATTTTTTTTATTATA 26047

Qy 3288 TGAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCAAGCAA 3347

Db 26046 -GTAGAGACGAGGTTTCACCATGTTGCCGAGACTGGTCTCCAACTCCTGGCCTCAATTGA 25988

Qy 3348 TCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGTGAGCCACCATGTGCGGCT 3407

Db 25987 TCCACATACCTCAACTT--CATAGTGTGGGATTACAGGTGAAGCCACTGTGCTTGCT 25930

Qy 3408 ACTTATTTCTTTACATTCCATCTTTCCAAATAGAATGTAAGATCCACAGAACAGGGATTAC 3467

Db 25929 TGTTTTTATTATTTT-----ATTTT 25908

Qy 3468 TGCCTATTTTCTTCTCTTTTGTAGACAGAGTCTCACTTCATCACTCAACCTCCGT 3527

Db 25907 TTATTTTGGATAGGGTCTCACTGTGCCCCAGGCTGGAGTGCAATGGCACAATC----- 25853

Qy 3528 TCAGTCACTGTCAACCTCTGCCTCCCGGTTCAAGYGATTTCTCCTGCCTAAGCCTCCTGA 3587

Db 25852 ATGGCTCCCTGCAGCCTCAAACCTCTGGGATCAAGTGATCTCCACCTCAGCCTTCAA 25793

Qy 3588 GTAGCTGGAATTACAAGCGTGCACCAACCATGCTTGGCTAAATTTT--TGTATTTTAGCA 3645

Db 25792 GTAGCTGGGACTACAGATGGGAACACCAACGCTCCTGTCTAATTTTAAAAAATGTTTGTA 25733

Qy 3646 GAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTG 3705

Db 25732 GAGATGGGTCTCCCTATGTTGCCAGGCTGGTCTTAAACTACTGACCTCAAGTGATCCT 25673

Qy 3706 CCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGCGTGAGTCACTGTGCCCTGGC----- 3760

Db 25672 CTTGCCTTGGCCTCCCAAAGTACTAGGATTTCAGTTGTGAGCCACCATACCCAGCTGGGA 25613

Qy 3761 ---CGATTACTGTCTATTTTCTTTATTGTCTATATCCCCAGATCTAGAGCAGTGTCTGACA 3817

Db 25612 CCACACTGAATAGCAAGGCTCCTGCTAACTCCTTCAGCAGACACATTTCTCCCTCATACCA 25553

Qy 3818 TATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTT 3877

Db 25552 CCTGTTAAGTGATCACTGTAAACTTCTCAATGGCAAGGACAGGCTCTTGTTCATTATGT 25493

Qy 3878 CTTTTTTAAAAACAATCTTGACAACTTTGCAG--AATAAATACAAATCTTGCAATCTGCTT 3935

Db 25492 GCCCTCAACCACTACCTACCACAGTTCCTGGCACACAGTGAGGGCTTAATTAACACCC 25433

Qy 3936 TTTCACTTATCACCTTGTATGACTTTTTTTCATATTGCTCAAACTTTATTGTTACTGTT 3995

Db 25432 ACTGACTTAGGTGGTTTCAGGTTCTAGCAAGTGCCAAACACCTTGAGCAAAAAACTT 25373

Qy 3996 TTTTCATTGTTACTATTTTGTACTGCTGAATAATATGGCTTAATTTGCTTATACATCCTCC 4055

Db 25372 GTTCAAGGTGGGCACAGTAGCTCATGCCTATGATCCAGCACTTTGGAAGGCTGAGGTG 25313

Qy 4056 TGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCTCCCCAG 4115

Db 25312 GGAGGACTGCTTGAGCCCCAGGAGTTTGAGACCTG-----CCTGGGTGA 25270

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Db 25269 CATAGTAAGACTGCATCTCTACAAAAACAAAAACCTTATTCAAAAACATTTCTCGCATGC 25210

Qy 4176 CAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAAATAAATACTCAGTTGGGCAC 4235

Db 25209 TTCCTTTGTGACAGACACTGGAGAAAGCACCTTTTCATAAATGAGTTTGTGGGCCAGATGT 25150

Qy 4236 AGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAACTCCAAAGTGGTGGATCACTTGAGG 4295

Db 25149 GGTGGCTCATGCCCTGTAATCACAGCACTTTTGGAGGCCGAGGCGGATCACTTGAGG 25090

Qy 4296 TGAGAAAGTTCGAGACCAGCCTGGTCAAATATGTTGAAACCCCTATCTCTACTAAAAATACAA 4355

Db 25089 TCAGGAGTTCGAGACCAGCTTGGCCAACATGATAAAAACCCCGTCTCTACTAAAAATAC-A 25031

Qy 4356 AAATTAGCTGGGTAGTGATGATGCATGCCCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAA 4415

Db 25030 AAATTAGCTGGACATGTTGACACACAGCCTGTAATCCAGCTACTCGGAGGCTGAGGCAG 24971

Qy 4416 GAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCAC 4475

Db 24970 GAGAAATGGCTTGAACCTGGGAGGCGGAGGCTACAGTGAGCCAAAGATCATGCCACTGCAC 24911

Qy 4476 CCAGCCTGGCGACACAGCGGAGACTCTATCTCAAAAAATAAATAAATAAA 4531

Db 24910 CCACCCTGGGTGACAGAGTGAGACTGTGTCTCAAAAAATAAATAAATAAATAA 24855

RESULT 46

US-09-949-016-16508/c
; Sequence 16508, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16508
; LENGTH: 30537
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16508

Query Match 7.8%; Score 389.2; DB 3; Length 30537;
Best Local Similarity 53.6%; Pred. No. 9.6e-79;
Matches 1253; Conservative 3; Mismatches 936; Indels 144; Gaps 16;

Qy 2273 ATGTTAAAAATCGCTTCAGGCCAGGCGGCTGCATGCCCTGTAATCCCAGCACTTG 2332

Db 27123 ATTTTAATAGTTACCTGTGGCCAGGCATGGTGGCTGTGCTTATATATCCAGCACTTAG 27064

Qy 2333 GGAGGCCGAGGCGGCGGATCACTTGAGGTCAGAGTTCGAGACCAGCCTGGCCAAACATG 2392

Db 27063 AGAGGCCAAGACAGGCGGATCACCTGAGGTCAGAGTTCGAGACTAGCCTGACCAACATG 27004

Qy 2393 GTGAAACCCCTGTCTCTACTAAAAATAACAAAAATTAGCCGGACATGGTGGCGAGCGCCTG 2452

Db 27003 GAGAAACCCCTCTCTCTACTAAAAA--TACAAAAATTAGCCGGCGTAGTGGCACATGCTTG 26946

Qy 2453 TAACCCCACTACTTTGGGAGACT-----GAGTTGGAGGT 2486

Db 26945 TAATCCTAGCTACTCGGGAGGCTGAGCAGGAGAAATCGCTTTGAACCTGGGAGTCAGAGGT 26886

Qy 2487 TTCAGTGAGCCAAAGGTCGTGTCACTGTGTCCAGCCTGGGTAAC-AGAGCAACTCTGTCT 2545

Db 26885 TGCTGTGAGCCGAGATCAGGCCATTGCACTCCAGCCTGGGCAACAAGAGCAAACTCCGT 26826

Qy 2546 CAAAAAANAATGCTTTCAATAAATATATGATAAAAGGACTATATTTTTCAAGCCA 2605

Db 26825 CTCAAAAAANAAGAAAGAAACACTGATTTAGACCAACTGCCTCGTTTTACAGATAGA 26766

Qy 2606 TAGGATCATTTCTCTGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCTCTGAGAGTGG 2665

Db 26765 GAGGGTGCAGCCTAGAGAAGGTCAGCTCCAGGTCATCCAGGAGGTTAGACTCTTTCCCTCC 26706

Qy 2666 CAGGTGAGSGGTGACCTATTGCTCTGCAGCTTACTCCTATCTCAGCTGTCCCTCCCACTTT 2725

Db 26705 AGCTCAGAGCTTTTCAAACTTTAATGTGCATACAAATCACTTGGCAGTTCTTGTTAAATGT 26646

Qy 2726 CCAGGTGCTGCC-----AGACACATGACAACTGCTAYGACCAGGCCCAAGAGCTGGACA 2779

Db 26645 GCAGATTTCTGATTTGGTAGGTTGCAGGAAGCCTGCGATTTGTATTCTTGTTGTTTCTT 26586

Qy 2780 GCTGTAATTTCTGCTGGACAMMCCGTACACCCACACCTATTTCATACTCGTCTGSGCT 2839

Db 26585 TGTTTGAGATGGAATTTCACTCTTGTGTTGCCAGGCTGGAGTGCAATGGCACTATCTCGGC 26526

Qy 2840 CGGCAATCACCTGTAGCAGTAGGTTTAT-----CCCTTCCTTGACCT 2881

Db 26525 TCACTGCAACCTCTGCCTTCCGGTTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGC 26466

Qy 2882 ATGAATTTAGTTGGTTCTCAGTAGCGCGGGGGGAAATAATAGTAAACAACAGCCATGATT 2941

Db 26465 TGGGATTACAGGCATGTGCCACTATGCTCGGCTAAATTTTGTAATTTTAGTAGAGA-CAGG 26407

Qy 2942 TAGTGTTAATTTCTTGGTTCTGGGCAGTGCTCCTTTAATCCTCAGAACAACACTATGG 3001

Db 26406 GTTCTCCATGTTGGTCAGGCTGGTCTTGAACCTCCTGACCTCAGGTGATCTGCCCACTC 26347

Qy 3002 GATAGGTACAATTATCCTCACTTAACAGATAAGAAAACTGAGSCTCAGAAAGGCTGAGCTA 3061

Db 26346 AGCCTCCCAAGTGTGGGATGACAGGCGTGAGCCACTGCGCCAGCCGAGATTTGTCTAT 26287

Qy 3062 TTTGCCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGG-----GTTTT 3107

Db 26286 TCTTAACAAGCTCCCAGGGATGCCAATACTGTCAAGTTGGGACCACTTGATTTTTTTT 26227

Qy 3108 TTTTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCA CCGAGCATGAGCACAGTGGTG 3167

Db 26226 GTTTTTTGTTTTTTGAGACAGGGTCTCACTCTGTCTTCCAGGCTGGAGTGCAGTGGCA 26167

Qy 3168 CAACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGCCT 3227

Db 26166 GGTTCGCGCTCAATGCAACCTCCGCCTCCTGGGTTCAAGTGATCTTGTGCTCAGCCT 26107

Qy 3228 CCCAAGTAGCTGGGACTACGAGCGTGCACCACCCAGCCTGGCTAAATTAATAAAATTTTTT 3287

Db 26106 CCCGAGTAGCTGGGATTACAGGCTTGAGTTACCATTGCTGGCTGAAATTTTATTATTTTA 26047

Qy 3288 TGTAGAGACTGGGTCTTACTACGTTGSCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAA 3347

Db 26046 -GTAGAGACGAGGTTTCACCATGTTGCGGAGACTGGTCTCCAACTCCTGGCCTCAATTGA 25988

Qy 3348 TCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATTGTGCGGCT 3407

Db 25987 TCCACATACCTCAACTT--CATAGTGTGGGATTACAGGTGTAAGCCACTGTGCTTGTCT 25930

Qy 3408 ACTTATTTCTTTACATTCCATCTTTTCCAATAGAAATGTAAGATCCACAGAACAGGGATTAC 3467

Db 25929 TGTTTTTATTATTTTT-----ATTTT 25908

Qy 3468 TGCCTATTTTCTTCTTTCTTTTGTAGACAGAGTCTCACTTCACTCAACCTCCCGT 3527

Db 25907 TTATTTTGTAGATAGGGTCTCACTGTTGCCCAGGCTGGAGTGAATGGCACATC----- 25853

Qy 3528 TCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTTCTCTGCCTAAGCCTCCTGA 3587

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Qy 3588 GTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTTT--TGTATTTTAGCA 3645

Db 25792 GTAGCTGGGACTACAGATGGGAAACACCACGTCCTGCTAAATTTTTTAAAAAATGTTTGT 25733

Qy 3646 GAGATGGGTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTG 3705

Db 25732 GAGATGGGTTCTCCCTATGTTGCCAGGCTGGTCTTAAACTACTGACCTCAAGTGATCCT 25673

Qy 3705 CCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGCGTGAAGTCACTGTGCCCTGGC----- 3760

Db 25672 CTTGCCCTTGGCCTCCCAAAGTACTAGGATTTTCAGTTGTGAGCCACCATACCCAGCTGGGA 25613

Qy 3761 ---CGATTACTGTCTATTTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACA 3817

Db 25612 CCACACTGAATAGCAAGGCTCCTGCTAACTCCTTCAGCAGACACATTTCTCCCTCATACCA 25553

Qy 3818 TATAGTAGGTGCTCAATAAATAAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTT 3877

Db 25552 CCTGGTAAGTGATCACTGTAAACTTCTCAATGGCAAGGACAGGCTCTTGTTCATTTATGT 25493

Qy 3878 CTTTTTTTAAAAACAATCTTGACAACTTTTGCG--AATAAATACAATCTTGTGATTTCTGCTT 3935

Db 25492 GCCCTCAACCACCTACCTACCACAGTTTCCCGGCACACAGTGAGGGCTTAATTAAACACCC 25433

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Db 25432 ACTGACTCTAGGTGTTTCAGGTTCTCTAGCAAGTGGCAAAACACCTTGAGCAAAAAACTT 25373

Qy 3996 TTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTTATACATCCTCC 4055

Db 25372 GTTCAAGGCTGGGCACAGTAGCTCATGCCTATGATCCCAGCACCTTTTGAAGGCTGAGGTG 25313

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Db 25312 GGAGGACTGCTTGAGCCAGGAGTTTGAGACCTG-----CCTGGGTGA 25270

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Qy 4236 AGTGACTCAAGCCTGTAACCCACAGTACTTTTGGAAAGTCCAAAGGTGGGTGATCACTTGAGG 4295

Db 25149 GGTGGCTCATGCCCTGTAATCACAGCACTTTGGGAGGCCGAGGCGGATCACCTGAGG 25090

Qy 4296 TGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAATACAA 4355

Db 25089 TCAGGAGTTCGAGACCAGCTTGGCCAACATGTATAAAACCCCGTCTCTACTAAAAATAC-A 25031

Qy 4356 AAATTAGCTGGGTGATGATGCATGCCTGATGCCAGCTACTCGGGAGGCTGAGGCCAA 4415

Db 25030 AAATTAGCTGGACATGGTGAACACACGCTGTAATCCAGCTACTCGGAGGCTGAGGCAG 24971

Qy 4416 GAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGAGTGAGCCGAGATCCCCACCTGCACT 4475

Db 24970 GAGAAATGGCTTGAACCTGGGAGGCGGAGGCTACAGTGAGCCAAAGATCATGCCCACCTGCACT 24911

Qy 4476 CCAGCCTGGCGACACAGCGGAGACTCTATCTCAAAAAAATAAATAAATAAATAA 4531

Db 24910 CCACCTGGGTGACAGAGTGAGACTGTGTCTCAAAAAATAAATAAATAAATAA 24855

Db 4655 A C A C T A C C T T G A C T C A C T G C A G C A T C T G C C T C C G G G T T C C A G T G A T T C T C C T G C C T C A G 4714

Qy 3225 C C T C C C A A G T A G T A G C T G G G A C T A C G A G C T G C A C C A C C A C C C T G G C T A A T T A A A A A A T T T 3284

Db 4715 C C T C T C A G G T A G C T G G G A T T A C A G G T A C A T G C C A A T A T G C C C G G C T A A T T T T T A T A - - T T 4772

Qy 3285 T T T T G T A G A G A C T G G G T C T T A C T A C G T T G G C C A G G C T T G T C T T A A A C T C C T G G C T T C A A G 3344

Db 4773 T T T A G T A G A G A C G G G G T T T C A C C A T G T T G G C C A G G C T G G T C T C G A A C T G C T G A C C T C A G G 4832

Qy 3345 C A A T C C T C C T A C C T T G G C A T C C C A A A G T G C T G G A T T A C A G G G T G A G C C A C C A T G T G C G 3404

Db 4833 T G A T C C G C C C A C C T C G G C T T C C C A A A G T G C T A G G A T T A C A G S C G T G A G C C A C C G C G C C C A 4892

Qy 3405 G C T A C T T A T T T C T T T A C A T T C C A T C T T T C C A A T A G A A T G T A A G A T C C A C A G A A C A G G G A T 3464

Db 4893 G C T T C T T C T T C T T C T T C T 4926

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Db 4927 T A T T T G A G G T G G C G A G T T T C A C T C T G T C G C C A G G C T G C A G T G C A G T G C A C A A T C T C 4986

Qy 3525 C G T T C A G C T C A C T G C A A C C T C T G C C T C C C G G G T T C A A G Y G A T T C T C C T G C C T A A G C C T C C 3584

Db 4987 - - - - - A G C T A A C T G C A A C C T C T T C C T C T G A G T T C A A G T G A T T C T T T G C C T G C A C C C C C 5041

Qy 3585 T G A G T A G C T G G A A T T A C A A G C G T G C A C C A C C A T G C T T G G C T A A T T T T T T G T A T T T T T A G C 3644

Db 5042 C G A G C A G C T G G G A T T A C A A G T G C C C A C C A C C A G C C A G A T A A - A T T T T G T A T T T T T A G T 5100

Qy 3645 A G A G A T G G G T T T T A C C A T G T T G C C C A G G C T G G T C T C A A A C T C C T G A C C T C A A G T G A T C T 3704

Db 5101 A G A G A - - G G G T T T T A C C A T G T T G G G C A G G C T G G T C T C A A A C T C T G A C C T C A G G T G A T C C 5158

Qy 3705 G C C T G C C T A G T C T C C C A A A G T G C T G G A A T T A T A G G C G T A G C A C T G T G C C T G G C C G A T 3764

Db 5159 A C C T G C C T C C G C C T C C C A A A G T - C T G G G A T T A C A G G T G T G A G C C A C C G C A C C C G T C G G T T 5217

Qy 3765 T A C T G T C T A T T T T C T T T A T T G C T A T A T C C C C A G - A T C T A G A G C A G T G T C T G A C A T A T A G T 3823

Db 5218 G A T A G G T C T T T T C T A A T A T T A A T A A T T A C G T A G C A T C T C A A C A T G T T A A T G T C A T A A T T T 5277

Qy 3824 A G G T G C T C A A T A A A T A A T T G A T G A A T G C A C A G C C T A G A T A T A A A C T T T C T T T T T C T T T T 3883

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Qy 3884 T T A A A A C A A T C T T G A C A A C T T T T G C A G A A T A A A - T A C A A T C T T G C A T T C T G C T T T T T C A C T 3942

Db 5338 A T A A A C A T G T T T G C T T T A T T T T T A G A T A G G T T T C A C T C T G T C A C C C A G G C T G G A T A C 5397

Qy 3943 T A T C A C C T T G T T A T G A C T T T T T C A T A T T G C C T C A A A C C T T T A T T G T T A C T G T T T T T T C A T 4002

Db 5398 A G T G A C G A G A T C T C G G C T C A C T G C A A C C T C C A C C T T C C C A G C T C A A G G A A T C C T C C A G C C 5457

Qy 4003 T G T T A C T A T T T T A G T C A C T G A A T A A T A T A T G G C T T A A T T T G C T T A T A C - - - - - A T C C T C C T G C 4058

Db 5458 T C A G C C C C T C A G A T A G C C A G G A C T A C A G G C G T A C A G C A T C A C A T C C C G C T A A T T T T T T T T 5517

Qy 4059 T C C A C T T T A G A A G C C A A A T T T A C A A A T C T G A T G A A G C T A T G A A C C C T C T C C C C A G A G A 4118

Db 5518 T T T T T T T T T G T A G T T T T T A T A G A C A C A G G G T T T T G C C A T G T T G C C C A G G C T G T C T C C G A 5577

Qy 4119 A A T A C A C A C A C A C A C A C A C A C A C A G T T T T T T T T T T A T G T T T T G C A A C T A A G A C A A 4178

Db 5578 A C T C C T G G A C T C A A G T A T C C A C C T G G C C T C C C A A A T G G T G G A T T A C A G G C G T 5637

Qy 4179 G A A A C C T G A T T A G A G G A T G T T T T G T C A T A T T A A T T A A A A T A A C T A C A G T T G G G C A G T 4238

Db 5638 G A G C C A T G G C A C C C C A C C T G T T G - - - - - C T T T T A A A A A A G A A A A T G G G G C C A G G C G T G G T 5694

Qy 4239 G A C T C A A G C C T G T A A C C A C A G T A C T T T G G A A G T C C A A G G T G G G T G G A T C A C T T G A G G T G A 4298

Db 5695 G G C T C A C A C C C T G T A A T C C C A G C A C T T T T G G A G G C C G A G G C G G T G G A T C A C - - A A G G T C A 5752

Qy 4299 G A A G T T C G A G A C C A G C C T G G T C A A T A T G T G A A C C C C T A T C T C T A C T A A - - - - - A A A T A C A 4354

Db 5753 G G A G T T C G A G A C C A G C C T G T C C A A C A T G T G A A C C C C A T C T C T A C T A A A A A C A A A A A C A 5812

Qy 4355 A A A A T T A G C T G G G T G T A G T G A T G C A T G C C T G T A G T C C C A G C T A C T C G G G A G S C T G A G G C A 4414

Db 5813 A A A A T T A G C T G G G C G T G G T G G G C A C C T G T A G T T C C A C C T A C T A C C T A C T G G G A G G C T G A G A C A 5872

Qy 4415 A G A G A A T T G C T T G A A C C T G G G A G G C A G A G G T T G C A G T G A G C C G A G A T C C C A C C A C T G C A C 4474

Db 5873 G G A G A A T T G C T T G A A C C T G G G A G G C G G A G G T T G C A G T G A G C C G A A T G C A C C A C T A C A C 5932

Qy 4475 T C C A G C C T G G G C A C A C A G C G A G A C T C T A T C T C A A A A A A A T A A A T A A A A T A A A 4531

Db 5933 T C C A G C C T G G G C A C A G A A T G A G A C T A C A T C T C A A A A A A T A A A A A A A A A A A A G A A A G A 5989

RESULT 50

US-09-949-016-12255/c
; Sequence 12255, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12255
; LENGTH: 54878
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(54878)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12255

Query Match 7.8%; Score 388.6; DB 3; Length 54878;
Best Local Similarity 59.2%; Pred. No. 1.7e-78;
Matches 849; Conservative 1; Mismatches 560; Indels 25; Gaps 10;

Qy 3109 T T T T G T T G T T T T A G A C A G G G T C T T G C T C T G T C A C C C A G G C A T G A G C A C A G T G G T G C 3168

Db 39840 T T T T T T G T T T T T T G A A A G G G T A T C A A T C T G T A A C C C A G G C T A G A G T G C A G T G G T G T 39781

Qy 3169 A A C C A T A G G T C A C T G C A G C C T C A A C C T C C T G A G C T C A A G G G A T C T G C T G A C C T C A G C C T C 3228

Db 39780 G A T C T C G G C T C A C T G T A G C T G C A A C C T C C C A G G C T C A A A A T A T C C A C C T A C T T C A G C C T C 39721

Qy 3229 C C A A G T A G C T G G G A C T A C G A G C G T G C A C C A C C A C C G C T G G C T A A T T A A A A A A T T T T T T 3288

Db 39720 C G A A G T A G C T G G G A C T A C A G G C A C A C C A C T A C A C C T A C A C C T G C C T A A T T - - - - - T T T T A T T T T 39666

Qy 3289 G T A G A G A C T G G G T C T T A C T A C G T T G G C C A G G C T T G T C T T A A A C T C C T G G C T T C A A G C A A T 3348

Db 39665 T C A T A G A G A C G G T T T C A C C A T G T G C C C A - G C T G G T C T C T A A T T T C T G G C T C A A G G G A T 39607

Qy 3349 C C T C C T A C C T T G G C A T C C C A A A G T G C T G G G A T T A C A G G G G T G A G C C A C C A T G T G C G G C T A 3408

Db 39606 C T G C C T A T C T C A G T C T T C C A A A G T G C T G G G A C T A T T G G T A T G A G C C A C C A C C G C C T G G C T T 39547

Qy 3409 C T T A T T T C T T T A C A T T C C A T C T T T C C A A T A G A A T G T A A G A T C C A G A A C A G G G A T T A C T 3468

Db 39546 GACAGCTTTCATGATGTAATTATTTAAATTAGCCCTTACAGTGAACCTGTGAAGGCTAAATT 39487

Qy 3469 GCCTATTTCTCCTTTCT-----TTTTGAGACAGAGTCTCACTTCATCACCTCAACC 3522

Db 39486 TTTTTTTTTTTTTTTTGTAGACGGAGTCTGTCTTTGTGCGCAGGCTGGAGTACAGTGGCG 39427

Qy 3523 TCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCCTGCCTAAGCCT 3582

Db 39426 CGATCTTGGCTCACTGCAACCTCCAACCTCCCTGGTTCAAGCGATTTTCTGCCTCAGCCT 39367

Qy 3583 CCTGAGTAGCTGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTTGTATTTTA 3642

Db 39366 CCCAAGTAGCTGGGATTACAGGCACGTGCCACCACACCCAGCTAA-TTTTGTATTTTA 39308

Qy 3643 GCAGAGATGGGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGAT 3702

Db 39307 GTAGAGTTGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACGCCCTGACCT--GGTGAT 39250

Qy 3703 CTGCCTGCCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCG 3762

Db 39249 CTGCCTGCCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCAACGCCCGCCT 39190

Qy 3763 ATTACTGTCTAATTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAG 3822

Db 39189 GGTAGTCTTTATTACATACCCCTTAGCTTCTCTCATTTGAG---TTAATATAATTTT 39134

Qy 3823 TAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTCTTTTCTTTT 3882

Db 39133 TCCAAGTCCCAGTGCCTAGCCCCACAAGCACCATCTTTGTTCTTTCCATGTATGTCTCCATG 39074

Qy 3883 TTTAAAAACAATCTTGACAACTTTTGCAGATAAATAACAATCTTGCATTCTGTTTTTCACT 3942

Db 39073 AAGAGAACACTACCTTCTCAAAAGAACAAAGGAATACATATTTGTGCTGTGAAGATTCCAC 39014

Qy 3943 TATCACCTTGTATGACTTTTTTCATATTTGCCTCAAACCTTTATTTGTTACTGTTTTTCAT 4002

Db 39013 AATGAGGTTCTGTTAAAGTACACTTTTGTACAGAACAGATCTGTGGTAGGACCTTGTATG 38954

Qy 4003 TGTTACTATTTTAGTCACTGAAATAATATGGCTTAATTTGCTTATACATCCTCCTGTCCA 4062

Db 38953 ACTAGC---TTCAATTCAGTTAAACATTTACTGAATCTCCACCATGTAGGCACCTGTGCCT 38897

Qy 4063 CTTTAGAAGGCCAAATTTTACAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAAATA 4122

Db 38896 CCTTACAGAGATATAAGATATTAAGAGAGAGTTTCTGTCTTCAAGGACATTTATACATT 38837

Qy 4123 CACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAA 4182

Db 38836 TAGAAAGGGATACAAATGTAAAATAAACACAATACAGTTTAATATGTGCAACAGTGGGA 38777

Qy 4183 CCTGCATTAGAGGATGTTTGTTCATAT-TAATTAATAATAACTCAGTTGGGCACAGTGAC 4241

Db 38776 GTGTTTCATATCACAGAAGAGTACAGAGTCAAGAGTGATATCTAGCCCGGTGCGGTGGC 38717

Qy 4242 TCAAGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAA 4301

Db 38716 TCACACCTGTAATCCTAGCACTTTGGGAGGCCAAGGCAGGCAGATCATTTGAGGTCAGGA 38657

Qy 4302 GTTCGAGACCAGCCTGGTCAATATGTGAAACCCTTATCTCTACTAAAAATACAAAAATTA 4361

Db 38656 GTTTGAAACCAGCGGGACCAACCGTGTGAAACCCTGTCACTACTAAAAATACAAAAACGA 38597

Qy 4362 GCTGGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAT 4421

Db 38596 CCCAGGCGTGTGATGGCGCCTGTATCCCAGCTACTTTGGGAGGCTGAGGCAGGAGAAT 38537

Qy 4422 TGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAG-CCGAGATCCCACTGCACCTCCAGC 4480

Db 38536 CGCTTGAATCTGGGAGGTGGAAATTGCAGTGAGCCCGAGATCGTGCCATTGCACCTCCAGC 38477

Qy 4481 CTGGGCGAC-ACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAAGGA 4534

Db 38476 CTGGGTGACAAGAGTGAAACTCCATCTCAAAAAAATAAAAAATAAAGTAAAAATGTA 38422

RESULT 51

US-09-949-016-15316
; Sequence 15316, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15316
; LENGTH: 144322
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(144322)
; OTHER INFORMATION: n = A,T,C or G

Query Match 7.8%; Score 388; DB 3; Length 144322;
Best Local Similarity 58.6%; Pred. No. 3.6e-78;
Matches 893; Conservative 1; Mismatches 536; Indels 94; Gaps 9;

Qy 3094 ACAGTTTGGGTTTTTTTTTGTGTGTGTGTAGAGACAGGGTCTTGTCTGTCAACCCAGGCA 3153

Db 37596 ACAAACTTTTTTTTTTTTTTTTTTTTTTTTGTGAGCGGAGTCTTGTCTGTGCGCCAGGCT 37655

Qy 3154 TGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCT 3213

Db 37656 GGAGTGCAGTGGTACAACTCTTGGCTCACTGCAACTCCGCCCTCCCAGGTTCTCACCATT 37715

Qy 3214 GCTGACCTCAGCCTCCAAAGTAGCTGGGACTACGAGCGTGCACCACCGCTGGCTAAT 3273

Db 37716 TCCTGCCTCAGCCTCCGAGTAGCTGGGACTACAGCGCCTGCCACCAACACCTGGCTAAT 37775

Qy 3274 TAAAAAAATTTTTTGTAGAGACTGGGTCTTACTACTGTTGGCCAGGCTTGTCTTAAACTC 3333

Db 37776 TTTTACAA-TTTTGTAGAGAGATGGGGTTTCACTGTGTAGCCAGGATGGTCTCGATCTC 37834

Qy 3334 CTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGTCTGGGATTACAGGGTGAGC 3393

Db 37835 CTGACCTC--GTGATCCACCTGCCTCGGCCTCCCAAAGTGTCTGGGATTACAGGCGTGAGC 37892

Qy 3394 CACCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTCCAAATAGAATGTAAGATCCAC 3453

Db 37893 CACCACGCCCGCCCTGAACCTCAATAAACTTTTATCCAAGCACCTGGATAAAGGATATCCT 37952

Qy 3454 AGAACAGGGATTACTGCGCTATTTTCTTCCTTTCTTTTGTGAGACAGAGTCTCATTTCATC 3513

Db 37953 GAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTGTGAGATGGAGTCTCATTCTTGT 38012

Qy 3514 ACCTCAACCT-----CCGTTTCACTCACTGCAACCTCTGCCTCCCGGGTT 3558

Db 38013 TGCCAGGCTGGAGTGCAGTGGCACTATGTGGTCACTGTAACTCTGCCTTCTGGGTT 38072

Qy 3559 CAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGTGGGAATTACAAGCGTGCACCAACCATG 3618

Db 38073 CAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGTGGGATTACAGGTGCCTACCACCATA 38132

Qy 3619 CTGGCTAAATTTTTTGTATTTTGTAGCAGAGA-TGGGGTGTTTTACCATGTTGCCCAGGCTGG 3677

Db 38133 CCCAGCTAAATTTTGTATTTTTTAGTGAGACGGGGGTTTACCATGTTGGCCAGGCTGG 38192

Qy 3678 TCTCAAACCTCTGACCTCAAGTGAATCTGCCTGCCTCAGTCTCCAAAGTCTGGAAATTAT 3737

Db 38193 TCTCAAACCTCTGACCTCAGGTGATCCACCCGCTTGGCCTCTACAGTCTGGGATTAC 38252

Qy 3738 AGCGGTGAGTCACTGTGCTCGCCGATTACTGTCTATTTTCTTATTGCTATATCCCCAG 3797

Db 38253 AGACATGAGCCACTGTGCCCGCCTCCTGAATTTTCACATTAATAATCTGCAAAAGGAAAAG 38312

Qy 3798 ----ATCTAGAGCAGTGTCTGCACATATAGTAGTGCTCAATAATAATAATTGATGAATGCAC 3853

Db 38313 CAGATTTAATGTGAAGATGACAGGAATTTTCTGGGCACITTTCAAGGTCCTAAGGTTGGTA 38372

Qy 3854 AGCCTAGATATAAACTTTTCTTTTCTTTTAAACAATCTTGACAACTTTGCAGAAATA 3913

Db 38373 GCCCTAGTTTTTTCACCTTCAGACCTTAGCTTTTATCTGAAGGAAAAACACCAGAAACAGAA 38432

Qy 3914 AATACAAATCTTGCAATCTGCTTTTTCACCTTATCACCTTGTTATGACTTTTTCATATGCC 3973

Db 38433 GATACCTTAGGGAGTGGAAATGGGGTAGAGGGGTGAGAAITTCCTTTTACTTAATACT 38492

Qy 3974 TCAAACCTTATTTACTGTTTCTTTTCTTTTCTTTTAAACAATCTTGACAACTTTGAATGCC 4033

Db 38493 GTACTATATATTTAAATGCTTTTACAGTGATAATTTTATAATAAGGAAAAGAGGGA 38552

Qy 4034 TTAATTTGCTTATACATCCTCTGCTCCACTTT-----AGAAGGCCAAATTTAC 4082

Db 38553 TTAAGTAAAAGGAAAACACTGTGTATATAATTTTAGATATAATACAAATTCAGATTTT 38612

Qy 4083 AAATCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAAATACACACACACACACTCA 4142

Db 38613 AAGTTACTACACAGATGTTCCCTCGATTTAGGAGGGGTTATATCCCAATATTGTAAGTCA 38672

Qy 4143 CA-----CA 4146

Db 38673 AAATGCATTTAATACACCTAACCTACTGAGTATCATAGCCAGTCCACCTTAATTGIGCT 38732

Qy 4147 CAGTTTTTTTAAATGTTTGCAACTAAGACAAGAAAACCTGCATTAGAGGATGTTTGTTC 4206

Db 38733 GAGAACTACTGATGTTAGCTTACAGTTGGACAAAATATCTAGCACAAAAGCCTATATTACA 38792

Qy 4207 TATTAATTAATAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTG 4266

Db 38793 ATAAAGTATTAAGTATCTTGGCTGGCGCGGTGGCTCACACCTGTAATCTCAGCACITTTG 38852

Qy 4267 GAAGTCCAAGGTGGTGGATCACITTGAGGTGAGAAAGTTTCGAGACCAGCCTGGTCAATATG 4326

Db 38853 GGAGGCCAAGGCAGGTGGATCACTTGATGCCAGGAGTTCGAGACTAGCCTGGCCAAACATG 38912

Qy 4327 GTGAAACCCCTATCTCTACTAAAAATAACAAA---ATTAGCTGGGTGATGATGCATGCC 4383

Db 38913 GTGAAACCTCATCTGTACTAAAAATAACAAAACATTAGTTGGGTATGGTGGCGTGIGCT 38972

Qy 4384 TGAGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAAACCTGGGAGGCAGAG 4443

Db 38973 TGTAAATCCAGCTACTCTGGAAGCTGAGGCACAAGAAATCACTGGAA-CTGGGAGGTGGAG 39031

Qy 4444 GTTGCAGTGAGCCGAGATCCCACCCTGCACTCCAGCCTGGGGACACACGAGACTCTA 4503

Db 39032 GTTGCAGTGAGCTGAGATCACGCCACTGTACTGCAGCCTGGGTGATAGAACCAGACATTTG 39091

Qy 4504 TCTCAAAAAATAAATAAATAAAA 4527

Db 39092 TCTCAAAAAATAAATAAATAAATAAAA 39115

RESULT 52
US-09-949-016-16115
; Sequence 16115, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16115
; LENGTH: 59319
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16115

Query Match 7.7%; Score 385.6; DB 3; Length 59319;
Best Local Similarity 59.1%; Pred. No. 8.6e-78;
Matches 848; Conservative 1; Mismatches 510; Indels 77; Gaps 8;

Qy 3104 TTTTTTTGTGTTGTAGAGACAGGGTCTTGTCTGTCTGTCACCCAGGCATGAGCACAGT 3163

Db 19809 TGTTTTGTGTTTTTGAGAGGGAGTCTCACTGTGTGCCCAGGCTGGAGTGCAAT 19868

Qy 3164 GGTGCAACCATAGGTCACTGCAGCCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 3223

Db 19869 AGCGTGATCTCGGCTCACTGCAACCTCTGCCTCCCGGATTCAAGCAATTTCTCCTGCCCTCA 19928

Qy 3224 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACACGCCTGGCTAATTTAAAAAAFT 3283

Db 19929 GCCTCCCAAGTAGCTGGGATTACAGGCACCTGCCACCGCTGCCAGCTAATT---TTTGTA 19985

Qy 3284 TTTTGTAGAGACTGGGTCTTACTACTAGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAA 3343

Db 19986 TTTTAGTAGAAACGGTTTTTTTACCGTGTGGCAGGCTGGTCTTGAACCTCCTGACCTCAA 20045

Qy 3344 GCAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGC 3403

Db 20046 GTGATCCACCCGCTCGGCTCCCAAAGTCTGGGATTATAGGCATGAGCCACTGTAAAC 20105

Qy 3404 GGCTACTTATTTCTTTACATTCATCTTTTCCAATAGAAATGTAAGATCCACAGAACAGGA 3463

Db 20106 TGCCTTTTTTTTTTTTTTTT----- 20126

Qy 3464 TTAATGCTCTATTTTCTTCTTTTCTTTTGTAGACAGAGTCTCACTTCAATCACCTCAACCT 3523

Db 20127 -----TTTTTTTTTTTTTTTTTTTGTAGACAGTCTTGTCTGTGCCCCAGGCTG 20176

Qy 3524 CCGTTCAAGCTCACTGCAACCTCT-----GCCTCCCGGGTTCAAGYGATTTCTCCTGCCT 3576

Db 20177 GAGTGCAGTGGTGTGATACGGCTCACTGCATCCTCCAGGTTCAAGCGATTCTCCTGCCT 20236

Qy 3577 AAGCCTCCTGAGTAGCTGSAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTGTGTA 3636

Db 20237 CAGCCTCCTGAGTAGCTGGGATTACAGGTGTCCAGTACCAACACCTGGCTAATTTTGTAT 20296

Qy 3637 TTTTAGCAGAGATGGGTTTTTACCATGTTGCCCCAGGCTGGTCTCAAACCTCCTGACCTCA 3696

Db 20297 TTTTAGTAGAGACAGGGTTTCTCCCTGTTGGCCAGGCTGATCTCCAACCCCTGAGTTCA 20356

Qy 3697 AGTGATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGGGTGAGTCACTGTGCC 3756

Db 20357 GCGAATCTGCCACCTTGGCCTCCCAAAGTGTGGATTACAGGCGTGATCCAC----- 20410

Qy 3757 TGGCCGATTACTGTCTATTTTCTTTATTTGCTATATCCCCAGATCTAGAGCAGTGTCTGAC 3816

Db 20411 --CACAGTGACCATGGAAAGTCTTTAAAGTCAGTTGGTGAGGAGGATTAGAATAT----- 20463

Qy 3817 ATATAGTAGGTGCTCAATAAATAAATTTGATGAATGCACAGCCTAGATATAAACTTTCTTTT 3876

Db 20464 -TAATTTGCTTTCACATTACTTACATGGATATTTTGTAGTGTAAACCAAGCCTCTATT 20522

Qy 3877 TCCTTTTAAACAATCTTGACAACTTTGCAGATAAATAACAATCTTGCATTTCTGCTTT 3936

Db 20523 AAATCTAGAATAACATCACCTTCTGCTGCCTGCTAAATATTATTGAATATTTAGGGCTT 20582

Qy 3937 TTCACCTATCACCTTGTTATGACTTTTTCATATTGCCCTCAAACCTTTATTGTTACTGTT 3996

Db 20583 CTTGAGGAAGTCACATTCTTAAACAATTACTACTTGAATGATGACTGCTAACTTCTTTT 20642

Qy 3997 TTTCAATTGTACTATTTTAGTCACCTGAATAATATGGCTTAATTGCTTATACATCCTCCT 4056

Db 20643 TCCATATAACAGTATAATAAAGAAATAGAGCCCTATCGCACATCAGACACAAAAATC 20702

Qy 4057 GCTCCACTTTAGAAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCCCAGA 4116

Db 20703 AATCCTGGACAGATTGAAGAACTAAGTACAAAGAGCAAACTTTAAAGTTAGAAAAATA 20762

Qy 4117 GAAATACACACACACACACACTCACACACAGTTTTTTTTTTAATGTTTGCAACTAAGAC 4176

Db 20763 CAGGAGAAACCATGCAACCTCAGAGTAGAGAAGGAATTTTTTCCCAGTCTTTAAATAC 20822

Qy 4177 AAGAAACCTGCAATAGAGGATGTTTGTTCATATTAAATTAATAAATAACTCAGTTGGGCACA 4236

Db 20823 TTG-ACTGTATTCAGGGCATTTCTTTACAAAACTACAGTACAAATTATCAGGCTGGGCACA 20881

Qy 4237 GTGACTCAAGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAAGGTGGGTGGATCACTTGAGT 4296

Db 20882 GTGGCTCACACCTGTAATCCCAGCACTTCGGGAGGCCAAAGGTGGCGGATCAC--GAGGT 20939

Qy 4297 GAGAAAGTCGAGACCAAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATAC-AA 4355

Db 20940 CAGGAGATCAAGACCATCTCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAATACAAA 20999

Qy 4356 AAATTAGCTGGGTGTAGTGATGCTGCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAA 4415

Db 21000 AAATTAGCGGGCGTGGTGGTGCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAG 21059

Qy 4416 GAGAAATGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACCTGCACT 4475

Db 21060 GAGAAATGGCATGAACCCGGGAGGCAGAGCTTGCAAGTGGCCAAAGATCGCACCACCTGCACT 21119

Qy 4476 CCAGCCTGGCGCACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAA 4531

Db 21120 CCAGCCTGGCGCAGCAGAGTGAGACTCTGTCTCAAAAAATAAATAAATAAATAA 21175

RESULT 53

US-09-949-016-14878/c

; Sequence 14878, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14878

; LENGTH: 17704

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(17704)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14878

Query Match 7.7%; Score 384.8; DB 3; Length 17704;

Best Local Similarity 59.7%; Pred. No. 7.7e-78;

Matches 888; Conservative 1; Mismatches 538; Indels 61; Gaps 12;

Qy 3099 TTGGGTTTTTTTTTTGTTGTTTGTAGACAGGGTCTTGCTC-TGTCAACCAGGATGAG 3157

Db 4293 TTTTTTTAAATTTTTTTTTTTTGTGAGACCAAGTTTGTCTTGTCAACCAGGCTGGAG 4234

Qy 3158 CACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGGATCTGCTG 3217

Db 4233 TGCAATTACACGATCTTGGCTCACTGCAACCTCCACCTCCAGGTTCAACCCGATTCTCCT 4174

Qy 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACCACCGCTGGCTAAATAAA 3277

Db 4173 GCCTCAGCCTCCCGAGTAGTTGGGACTACAGGCCACCCACCATCATGCCCGGCTAAATTTT 4114

Qy 3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGG 3337

Db 4113 GTA--TTTTTAGTAGACAGAGGTTTTCACCATGTTGCCAGGCTGGT-TTGAACCTCCTGA 4057

Qy 3338 CTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGTCTGGGATTACAGGGGTGAGCCACC 3397

Db 4056 CCTCAAGTGATCCACCCGCTCAGCCTTCCAAAGTGTGGGATTACAGGCATGAGCCACT 3997

Qy 3398 ATGTGCGGCTACTTATTCTTTTACATTCCATCTTCCAAATAGAATGTAAGATCCACAGAA 3457

Db 3996 GCGTTCGGCCTGAGTCACTGAATTTCTATAAAGGTGATTGCATTATGCCCTGTT 3937

Qy 3458 CAGGGATTACTGCTTATTTCTTCCCTTTCTTTTGTAGACAGAGTCTCACTTCAACACC- 3516

Db 3936 TAAAGATCTCTAAAAAGACTATTCTCTTTTTTTTTTTGGACAGAGTCTCACTCTGTCCCCA 3877

Qy 3517 -----TCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCCTCCCGGTTCAAGYG 3564

Db 3876 GGCTGGAGTGCAGGGGCACAATCTCAGCTCACTGCAGCCCCCGCCTCCTGGGTTCAAGCG 3817

Qy 3565 ATTCTCCTGCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGC 3624

Db 3816 ATTCTTCTGCCCTCAGCCTCTCGAGTAGCTCGGAGTACGGGCACAAGCCACCACGCCAGC 3757

Qy 3625 TAATTTTTTGTATTTTAGCAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAA 3684

Db 3756 TAATT-TTTGTATTTTAGTAAAGACAGGGTTTACCATATTGGCCAGGCTGGTCTCGAA 3698

Qy 3685 CTCCTGACCTCAAGTGATCTGCCCTGCCCTCAGTCTCCAAAGTGTGGAATTATAGCGCTG 3744

Db 3697 CTCCTGACCTC--GTGATCTGCCCGCCTCAGCCTCCCAAGTGTGGAATTACAGGCATA 3640

Qy 3745 AGTCACCTGTGCCCTGGCCGATTAAGTGTCTATTTTCTTTTATGCTATATCCCCAGATCTAGA 3804

Db 3639 AGCCACCGCGCCCGCAAGTGTAAACTTTTAAAGATGACATACAAAGCCCTGCAATGACCT 3580

Qy 3805 G-----CAGTGTCTGACATATAGTAGGTGCTCAATAAATAAATTGA 3844

Db 3579 GGCCCTTCTCTCTCTAGCCTTACTGTGAGATTGACTGTACCACATTTCTAGCATTGA 3520

Qy 3845 TGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTCTTTTAAAC-AACTTTGACAAC 3903

Db 3519 AGTATTGGGCAAGTTTTTTTAACTGTCAAGTGAAGGATACTAATGCTAATCAGGGGGAGA 3460

Qy 3904 TTGCAGAAATAAATACAACTTTGCAATCTCTGCTT--TTTCACTTATCACCTTTGTTATGACTT 3961

Db 3459 TAACAGCATATAAAGTGCCCAAGCATACTGCTGCTTAGCGTTAACAATAAATATTGGCT 3400

Qy 3962 TTTTCATATTGCCCTCAAACTTTATTGTTACTGTTTCTTTTCTTTTCTTTTACTATTTTAGTCACT 4021

Db 3399 ATTGTGGAAGAAGCAACAATATTGTCATGTTATTTTTTTCAGTCTCTACTGCTCTCAAGA 3340

Qy 4022 GAATAAATATGGCTTAATTTTGCTTATACATCCTCCTGCTCCACTTTAGAAAGGCCAAATTTA 4081

Db 3339 GGATGCTTTGAACTGTTGATTGGGTAATGTTTTTAACATAAACGGAACCTCTCCACTCCACC 3280
Qy 4082 CAAATCTGATGAAAGCTATGAACCC-----TCTCCCCAGAGAAATAACACACACACAC 4137
Db 3279 GAAAAAGAAAGAGAGGAAGAACAGATTATCTGAACAGACTGAGAAGAAAATTGGAGG 3220
Qy 4138 ACTCACACACAGTTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCAATTAGAGGAT 4197
Db 3219 TGAAGAAGTTGAGTGACTGGGAGGATTAAAGAGAGGCCCATCGAGTTGTTTGTGCGGAG 3160
Qy 4198 GTTTGTTCATATTAAATTAATAACTCA-----GTTGGGCACAGTGACTCA 4244
Db 3159 ATGAGTTAGCAGTAGTATAAACTTTAAGAAAGAGAGATCTGGCCGGCGCAGTGGCTCA 3100
Qy 4245 AGCCTGTAACCCACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTT 4304
Db 3099 TGCCTGTAATCCCAGCACCTTTGGAGGCTGAGGCTGGCGGATCAC-TGAGGTCAGGGGTT 3041
Qy 4305 CGAGACCAGCCTGGTCAATATGTTGAAACCCCTATCTCTACTAAAAATAACAAAAATTAGCT 4364
Db 3040 CAAGACAGCCTGGCCAAACACGGTGAACCCCGTCTCTACTAAAAATAACAACAATTAGCT 2981
Qy 4365 GGGTGPAGTGATGCATGCCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAFTGC 4424
Db 2980 TGGTGTGGTGGCGCAGGCCCTATAATCCAGCTACTCTGGAGGCTGAGGCAGGAGATCGC 2921
Qy 4425 TTGAACTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCAACCACTGCACCTCCAGCCTGG 4484
Db 2920 TTGGACTGGGAGGTGGAGGTGCGAGTGAGCCGAGATTGCACCACTGCACCTAGCCTGG 2861
Qy 4485 GCGACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAAAG 4532
Db 2860 ACTACAGAGACTCTGTCAAAAAACAATAAACAATAAAGAGAG 2813

RESULT 54
US-09-949-016-13010
; Sequence 13010, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13010
; LENGTH: 18620
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13010

Query Match 7.7%; Score 383.8; DB 3; Length 18620;
Best Local Similarity 59.0%; Pred. No. 1.3e-77;
Matches 855; Conservative 1; Mismatches 553; Indels 40; Gaps 10;

Qy 3104 TTTTTTTTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCACAGT 3163
Db 8642 TATTTATTATTATTTTTTTGAGACAAAGTCTTGCTCTGTCAACCCAGGCTGGAGCGCAAT 8701
Qy 3164 GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 3223
Db 8702 GGTGCTATCTCGGCTCACTGGAACTCCGCCCTACCAAGTTCAAAGCGATTCTCTTGCTCA 8761
Qy 3224 GCCTCCCAAGTAGCTGGGACTACGAGCGGTGCACCAACCGCCTGGCTAATTTAAAAAAATT 3283

Db 8762 GCCTCCTGAGTAACCTGGGACTACAGGCGCGTGCCTCATGCCCCGCTAATTTTTGTGTA--T 8819
Qy 3284 TTTTGTAGAGACTGGGTCTTTACTACGTTGGCCAGGCTTGTCTTAAACCTCCTGGCTTCAA 3343
Db 8820 TTTTAGTAGAGACGGGTTTTCACCGTGTACCAGG-TTATCTCAATCTCCTGACTT--T 8876
Qy 3344 GCAATCCTCCTACCTTGGCATCCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGC 3403
Db 8877 GTGATCTGCCTGCCTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCATGCCT 8936
Qy 3404 GGCTACTTATTTCTTACATTTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGA 3463
Db 8937 GGCCTAACTTGCCTTATTATTATTTTTTTTTTTTATTGAATTT----- 8982
Qy 3464 TTACTGCCTATTTTCTCCTTTTCTTTTTTTGAGACAGAGTCTCACTTTCATCACCTCAACCT 3523
Db 8983 TTTTTTTTTTTTGGAGATGGAGTTTCACTCTCCTTGTCCAGGCTGGAATGCAATGGTGC 9042
Qy 3524 CCGTTCAGCTCACTGCAACCTCTGCCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCTC 3583
Db 9043 GATCTCTGCTCATTTGACCCCTCTGCCCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTC 9102
Qy 3584 CTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTTGTATTTTAG 3643
Db 9103 CCAAGTAGCCGAGATTACAGGTGCCCCGCCAGCAGCCTGGCTAATTTTT--GTATTTAG 9160
Qy 3644 CAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC 3703
Db 9161 TAGAGACGGGGTTTCACTATGTTGTCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATC 9220
Qy 3704 TGCCTGCCTCAGTCTCCCAAAGTCTGGAAATTATAGGCGTGAGTCACTGTGCCTGGCCGA 3763
Db 9221 CACCTGCCCTCGGCTCCCAAAGTTCTCGGAATTACAGGCTTGAGCCACTGCGCCGCGCTA 9280
Qy 3764 TTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGT 3823
Db 9281 TTTATTTATTTTGGACAGGATCTTGCTCTGTCAACCAGGCTGGAGTGCAGTGGTGTA 9340
Qy 3824 AGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAATTTCTTTTCTTTT 3883
Db 9341 TCCTGGCTCACTGACGCTCCACCTTCCGGGCTCAAGTGATCCTCCCACCTCAGCTCCC 9400
Qy 3884 TTAAACAATCTTGACAACTTTGCAGAATAAATACAATCTTGCAATTTCTGCTTTTCACTT 3943
Db 9401 AAGTAACTGGGACCATAGGCTTGTGTCAACCATAGCCTGGCTAATTTTTTGCATTTTAGTA 9460
Qy 3944 ATCACCTTGTATGACTTTTTTCATATTGC-----CTCAAACTTTATTGTTACTGTTTT 3997
Db 9461 GAGACAGGGTCTCACTGTGTGCCAGGCTGGTCTCGAACTCCTGAGCTCAAGCCATCTG 9520
Qy 3998 TTCATTGTTACTATTTTAGTCACTGAATAATATGCTTAATTTGCTTATACATCCTCCTG 4057
Db 9521 CCCACCTCGGCTCCCAAAGTCTGGGATTACAGACATAGCCACCATGCTGCTCTCATA 9580
Qy 4058 CTCACCTTTAGAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCTCCAG-- 4115
Db 9581 ACTTGCTTTAGAGCATACCAAGTGGCTGTAGTTTGCTTTTTTCCAACTTATCAATAGGA 9640
Qy 4116 -----AGAAATACACACACACACACTCACACAGTTTTTTTTTTTAAATGTTTGAAC 4170
Db 9641 TGGAAAGCATGTATAAAAATGGGACTAATTTTATCAGAACTTTTTTATTGATTGGACACAAC 9700
Qy 4171 TAAGACAAGAAACCTGCATTAGAGGATGTTTG--TTCATATTAAATTAATAAATAACTCAGT 4228
Db 9701 TAGAGAAATGGACCTTATATCCACCAGACTGGAAGTGGGTTCAAGAGATTAAAGCTCAGC 9760
Qy 4229 TGGGCACAGTGACTCAAGCCTGTAACCAACAGTACTTTTGGAAAGTCCAAGTGGTGGATCA 4288
Db 9761 CAGGCACGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGCGAGATCA 9820
Qy 4289 CTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAA 4348

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Db 9821 C--AAGGTCAGGAGATCCAGACCATCCTGGCTAACACAGTGAAACCCCGTCTCTACTAAA 9878
Qy 4349 AATAC--AAAAATTAGCTGGGTAGTGATGCCTGTAGTCCAGCTACTCGGGAGG 4406
Db 9879 AATACGAAAAAATTAGCTGGCGTGGTGGCGGTGCCTGTAGTCCAGCTACTCGGGAGG 9938
Qy 4407 CTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCAC 4466
Db 9939 CTGAGGCAGAGAAATGGCGTGAACCCGGGAGGCAGAGCTTGCAGTGAGCCGAGATTGCGC 9998
Qy 4467 CACTGCACTCCAGCCTGGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAATAA 4526
Db 9999 CACTGCCCTCCAGCCTGGGTGACAGAACGATACTCCGTCTCAAAAAAATAAATAAATAA 10058
Qy 4527 ATAAAGGAT 4535
Db 10059 AAAAGAGAT 10067

RESULT 55
US-09-949-016-14172/c
; Sequence 14172, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14172
; LENGTH: 194933
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(194933)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14172

Query Match 7.7%; Score 383.4; DB 3; Length 194933;
Best Local Similarity 59.6%; Pred. No. 4.7e-77;
Matches 859; Conservative 1; Mismatches 487; Indels 94; Gaps 9;

Qy 3098 TTTGGGTTTTTTTTTGTGTTTAGACAGGGTCTTGCTCTGTCACCCAGGCATGAG 3157
Db 4948 TTTTGTGTTTTTTTTTTTTTTTGTGAGACAGAGTCTCGCTCTGTCACCCAGGCTGGAG 4889
Qy 3158 CACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTG 3217
Db 4888 TGCAGTGGCACAATCTCAGCTCACTGCAACGTCTGCCTCCCGGTTTAAGGGATTCTCCT 4829
Qy 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGGCTAATTAAA 3277
Db 4828 GCCTCAGCCTCCCAATAGCTGGGACTACAGGTGCCCCCACCACCGCCTGCCTAAATTTT 4769
Qy 3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTCTAAACTCCCTG 3337
Db 4768 TTGTATATTTAGTAGAGATGGGGTTTTCAACCATGTTGGCCAGGCTGGTCTCAAAC- 4715
Qy 3338 CTTCAAGCAATCTCCTACCTTGGCATCCCAAAAGTGTGGGATTACAGGGGTGAGCCACC 3397
Db 4714 --TCAGGCAATTGGCCCACTCAGCCTCCCAAAAGTGTGGGATTACAGGCATGAGCCACT 4657
Qy 3398 ATGTGGGGCTACTTATTTCTTTTACATTCCATCTTTTCCAATAGAAATGTAAGATCCACAGAA 3457
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Db 4656 GTGCCTGGCCAAAACCCACCTTTTCTTTCTTCCTTC------ 4621
Qy 3458 CAGGGATTACTGCCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTCACTACACT 3517
Db 4620 -----TTTATCTTTGGGACAGGATCTCACTCTATCAACC 4587
Qy 3518 CAACCTCCGTTCA-----GCTCACTGCAACCTCTGCCTCCCGGTTTCAAGYGATCTTCC 3571
Db 4586 AGGCTGGAGTACAATCAAGGCTCACTGCAGCCTCTACCTCCCATGCTCAAGTGATCCTCC 4527
Qy 3572 TGCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCACCATGCTTGGCTAATTTT 3631
Db 4526 CACCTCAGCCTCCCAAGTAGCTGGGACTACACATGTGCTTCAACAAGCCTGGCTAATTTCT 4467
Qy 3632 TTGTATTTTGTAGCAGAGA-TGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTG 3690
Db 4466 TTGATTTTTTTGTAGACAGGGGTCTTACTATGTGTGCCCAGGCTAGTCTTTGAACCTCTG 4407
Qy 3691 ACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGGCGTGAGTCAC 3750
Db 4406 GGCTCAAGTGATCTCCACCCCTGGCCTCCCAAGGTGTGGGACTACAGGCAGGAGCCAC 4347
Qy 3751 TGTGCCCTGGCCGATTACTGTCTATTTTCTTTTATGCTATATCCCCAGATCTAGAGCAGTG 3810
Db 4346 CCTGCCCAGCCAAAACCCACCTTTCTATCAACAATGATTAAT-----GTTTTATAACATG 4293
Qy 3811 TCTGACATATAGTAGTGTCTCAATAAATAAATTGATGAATGCACAGCCTAGATATAAACTT 3870
Db 4292 TATTAATAAAATTAACCTGATATCAATATATCTGCTCACCCAAAAGACAGAGATAAAAC-- 4235
Qy 3871 TCTTTTCTTTTTTAAAAACAATCTTGACAACCTTTGCAGAAATAAATAACAATCTTGCAATC 3930
Db 4234 -----CCCAAACTAGACATGAACATATAAATAAATCTTCTGCTGCTACTT 4189
Qy 3931 TGCTTTTTCACCTTATCACCTTGTATGACITTTTTCATATTTGCCTCAAAACCTTTATTGTTA 3990
Db 4188 TGTGTTTAGTTTGGGAAGTAATAACTGTAGCTTTGAAAACAAGACAAATCTTTACTCAACC 4129
Qy 3991 CTGTTTTTTTCATTGTACTATTTTAGTCACCTGAATAATATGGCTTAATTTTGCITTATACAT 4050
Db 4128 AAAAACTTAAAGTGTAGCAGTAATGTAA--GGAGAAATCTGCCATATATTTATAAATAC 4071
Qy 4051 CCTCCTGCTCCACTTTTAGAAGGCCAAAATTTTACAAATCTGTGAAAGCTATGAACCTCTC 4110
Db 4070 TATAGAAATAACATAAAGGCCCAAGAAATCAGAGTATTTTAAAAAGATACTGTATGAGACA 4011
Qy 4111 CCCAGAGAAATACACACACACACACACTCAACACTCACACAGTTTTTTTTTAATGTTTGAAC 4170
Db 4010 AAATAAACATTTCACTTACAACACACAGAGAAGTGGACAATAAAAAATGACITTTTATTGAAA 3951
Qy 4171 TAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAATAAATAAATCACTGATG 4230
Db 3950 TGAGGGATTTAGGTGACGTATTAAAAATAACTTCTTACATGCATAGATTA---TCAGCCA 3895
Qy 4231 GGCAAGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACT 4290
Db 3894 GGCATGGTGTCTCACGCTGTAAATCCCAACACTTTGGGAGACCAAAGCGGGTGGATCACC 3835
Qy 4291 TGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAA 4350
Db 3834 TGAAGTCAGGAGTTCGAGACTAGCCCGCCAAACATGGTGAAACCTGGTCTCTACTAAAAA 3775
Qy 4351 TACAAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGTACTCGGGAGGCTGA 4410
Db 3774 TACAAAAAATTAGCTGGGCATGGTGGCATGTGCCTGTAAATCCCAGTACTAGGTAGGCTGA 3715
Qy 4411 GCGAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACTACT 4470
Db 3714 GGCAGAAGAATCACTTTGAACCCCGGAGGCAGAGGTTGCAGTGAGCCGAGATTGTGCCACT 3655
Qy 4471 GCACTCCAGCCTGGCGAC-ACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAATA 4529
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Db 3654 GCACTCCAGCTGGGCAACAAGAGCAAACTCCATCTCAAAAAAAAAAGCATAGATTATC 3595

Qy 4530 A 4530

Db 3594 A 3594

RESULT 56

US-09-949-016-13025

; Sequence 13025, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13025

; LENGTH: 102053

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(102053)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13025

Query Match 7.7%; Score 382.6; DB 3; Length 102053;

Best Local Similarity 57.3%; Pred. No. 5.3e-77;

Matches 858; Conservative 1; Mismatches 530; Indels 108; Gaps 5;

Qy 3104 TTTTTTTTGTGTTTGTAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCAGT 3163

Db 40691 TTTTTTTTGTGTTTGTAGACAGAGTCTCGCTCTGTCAACCCAGGCTGGAGTGCA 40750

Qy 3164 GGTGCAACCATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 3223

Db 40751 GCGCAATCCAGCTCAGTGCACCTCGCCTCCAGGTTCAAGAGATTCTCTTGCCTCA 40810

Qy 3224 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCCACCGCTGGCTAATTAAAAAATT 3283

Db 40811 GCCTCCCGAGTAGCTGGGATTACAGGTGCCCCGCCACCATGCCAGCTAAGTTTTTGTAT 40870

Qy 3284 TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCAA 3343

Db 40871 TTTTAATAGAGACGGGGCTTCACCAGGTTACCCAGGCTGGTCTCGAACCCCTGACCTCAG 40930

Qy 3344 GCAATCCTCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGC 3403

Db 40931 GTGATCCACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCATGCC 40990

Qy 3404 GGCTACTATTCTTTTACATTCCATCTTTTCCAATAGAAATGAAGATCCACAGAACAGGGA 3463

Db 40991 GGCCTTCCAAAACATATTTGAATCACTTCTTTTGTGTGTAATTTAAGAAATCAATTG 41050

Qy 3464 TTACTGCTATTCTTCTCTCTTTCTTTTGTAGACAGAGTCTCATTTCATCACCTCAACCT 3523

Db 41051 ATACAGTACAGTCAATTTATGTGTGTTGTTTTCAGTTTTTGGGTCTCTTTTCCCATCTGT 41110

Qy 3524 CCGT-----TCAGCTCACTGCAACCT 3544

Db 41111 TGATTATTTTATATGCCCAGGCTGGAGTGCAGTGGTGCAATCTCAGTTGACTGCAACCT 41170

Qy 3545 CTGCCTCCCGGTTTCAAGYGATTCTCCTCGCTTAAGCCTCCTGAGTAGCTGGAATTACAAG 3604

Db 41171 CTGCCTCTGGGTTACGTGATTCTCTCGCTTAGCTCCCAAGTAGCTGGTACTACAGG 41230

Qy 3605 CGTGCAACCATGCTTGGCTAAATTTTGTATTTTAGCAGAGATGGGGTTTACCATG 3664

Db 41231 CAGGTGCTGCCACGCCAGGCTAA-TTTTGTATTTTAGTAGAGATGGGGTTTACCATG 41289

Qy 3665 TTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCAAA 3724

Db 41290 TTGGTCAGGCTGGTCTCGAACTTCTGAGCTCAGGCAATCCGCCTGCCTGGGCCCTTCCAAA 41349

Qy 3725 GTGCTGGAATTATAGCCTGAGTCACTGTGCCCTGGCCGATTACTGTCTATTTTCTTTATT 3784

Db 41350 GTGCTGAAATTACAGGCGTGAGCCACTACACCCAGCC--TCCATCCTTGTGTGATTTAATT 41407

Qy 3785 GCTATATCCCAGATCTAGAGCAGTGTCTGACAFATAGTAGGTGCTCAATAAATAATTGA 3844

Db 41408 ACTAATATCCGTAATAGTCAATGTTTTTTGAAACACATTAGAAGAGGAAGATGGGCCGGA 41467

Qy 3845 TGAATGCACAGCCTAGATATAAACTTCTTTTCTTTTAAACAACATCTTGACAACTT 3904

Db 41468 CG-----TGGTGGCTCATG 41481

Qy 3905 TGCAGAAATAATACAATCTTGCAATCTGCTTTTTCACCTTATCACCTTGTATGACTTTT 3964

Db 41482 CCTATAATCCCAGCACTTTGGGAGGCTGAGGTGGGAGGATCACTTGAGCTCAGGAGTTG 41541

Qy 3965 CATATTGCCTCAACCTTTATTGTTACTGTGTTTTTTCATTTGTTACTATTTTAGTCACTGAA 4024

Db 41542 AGACCAGCTTAGGCAATATAGTGAGACCCTGTCTCTATTACTGAAAAAACAGTTTTTAAA 41601

Qy 4025 TAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTACAA 4084

Db 41602 TTTAAAAAATGAAGAAAAAATGTGATAC-----CATGGTCCC 41641

Qy 4085 ATCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAAATACACACACACACACTCACA 4144

Db 41642 TTATAGTGGAAAAGAAAGAGGTGAATGAGCTTTTAATGATTGAGGGAAGCCCCAAACTAGTT 41701

Qy 4145 CACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTGTT 4204

Db 41702 TGTTTCTGTTTTCAAACCAGTTTTTTAAATTTCTGTTCCATTCTGAAACCTAGCCTTTTA 41761

Qy 4205 CATATTAATTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTT 4264

Db 41762 ACATTTAAGATAGAAATGTTGGGCTGGGTTTCGATGGCTCACACCTGTAATCCCAGCACTT 41821

Qy 4265 TGGAAAGTCCAAGTGGTGGATCACTTGAGGTGAGAAAGTTTCGAGACCAGCCTGGTCAATA 4324

Db 41822 TGGGATGCCAAGTGGTGGATCACTTGAGGTGAGGAGTTTCGAGACCCCGCTGACCAACA 41881

Qy 4325 TGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAGTGGGTGTAGTGTATGATGCTCCT 4384

Db 41882 TGGTGAGACCCCTGTCTCTACTAAAAATACGAAAAATTAGCTGTGCGTGGTGGGCTTCT 41941

Qy 4385 GTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGG 4444

Db 41942 GTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGG 42001

Qy 4445 TTGCAGTGAGCCGAGATCCCACCACTGCATCCAGCCTGGCGGACACAGCGGAGCTCTAT 4504

Db 42002 TTGCAGTGAGCTGACATTGGGCCATTGCACTCCAGCCTGGGTAACGAGCGAACTACATCT 42061

Qy 4505 CTCAAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAAAACAACTAATAAGATT 4561

Db 42062 CAAAAAATAAATAAATAAATAAAGGATGTTGGAACTAGAAGGATTCTTAAAAATTCTT 42118


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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12153
; LENGTH: 23569
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(23569)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12153

Query Match          7.6%; Score 381; DB 3; Length 23569;
Best Local Similarity 60.3%; Pred. No. 6.5e-77;
Matches 902; Conservative 1; Mismatches 476; Indels 116; Gaps 12;

Qy 3096 AGTTGGGTTTTTTTTTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATG 3155
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7032 ATTTTAAATTTTAAATTTGTTTATTTAGAGACAGGGTCTTGCTCTGTTGCCAGGCAGG 7091

Qy 3156 AGCAGTGGTG--CAACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCT 3213
    || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7092 AGTGAGTGGTGCACAATCATAGTTCACTGCAGCCTTGAACTCCTGGACTCAGGCAGTCT 7151

Qy 3214 GCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCAACCCCTGGCTAAT 3273
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7152 CCCTGCCCTCAGCCTCCCAAGTAGCTGGGACTACAGGTGCTCACCACCATGCCCTGGCTAAT 7211

Qy 3274 TAAAAAAA-----TTTTTTTGTAGAGAC-TGGGTCTTACTACGTTGGCCAGGCTTGCT 3326
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7212 TAAAAAAAATTTTTTTTTTTTGTAGAGACAGGGTCTTGCTGTTGCCAAGGCTGCTCT 7271

Qy 3327 TAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGTCTGGGATTACAGG 3386
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7272 CAAATTCCTGGGCTCAAGCAA---TCCTACCTCTGTCTCCCAAAAGTTTGAGATGACAGG 7328

Qy 3387 GGTGACCACCATGTGCGGCTACTTATTTCTTTTACATTCATCTTTCCAATAGAATGTAA 3446
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7329 TATGAGCCACCATGCCCTGGCCAGGCATCAGTATTTTTTTTGAAGCTCCAGGTGAATCAA 7388

Qy 3447 GATCCAGAAACAGGGATTACTGCGCTA----- 3473
    || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 7389 TGTGAGACAACTTTGGGTACTGCTGACATAGGCATTTTTTAAAAAAACTCCCTGATTTT 7448

Qy 3474 -----TTTTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTTCATCACCTCAAC 3521
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7449 ATTTTATTTAAATTAATTAATTTTATTTTGTGACGCGAATCTTGCTCTGTCGCCAGGC 7508

Qy 3522 CTCCTG-----TCAGTCACTGCAACCTCTGCTCCCGGTTCAAGYGATT 3567
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7509 TGGGGTGCAGTGGCGCGATCTCGGCTCACTGCAAGCTCCACCTCCCGGTTTCATGCCATT 7568

Qy 3568 CTCCTGCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAA 3627
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7569 CTCCTGCTTCAGCCTCCCAAGTAGCTGGGACTACAGGCGCCCGCCACCCAGCTAA 7628

Qy 3628 TTTTGTGATTTTGTAGCAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTC 3687
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7629 TTTTGTGATTTTGTAGTAGACGCGAGTTTACCCTGTTAGCGGGATGGTCTCGATCTC 7688

Qy 3688 CTGACCTCAAGTGATCTGCCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGCGCTGAGT 3747
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7689 CTGACCTC--GTGATCCACCGCCTCGGCCTCCCAAAGTGTAGGATTACAGGCGAGAC 7746

Qy 3748 CACTGTGCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCA 3807
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7747 CACTGCGTCCAGCCAACTCCCTGATTT-----AATGTGCAGGC 7786

Qy 3808 GTGCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAA 3867
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Db 7787 AGGATTGAGACTAACTACTCTAGTCTAATGGTTCTGAAACCTTGAGCAGGCTTCAAAATCA 7846

Qy 3868 CTTTCTTTTCTTTTAAAAACAATCTTGACAACCTTTGCAGAAATAAATACTTTGCA 3927
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Db 7847 C-TTGGAGGCTTGTGAAACTCAAGTTTCAAGTGTGGCTGCATTTCCAGAGTTTCTGA 7905
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3928 TTCTGCTTTTTCACCTTATCACCTTGTGTTATGACTTTTTCATATTGCTCAAAACCTTTATTG 3987
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7906 TTCAG---TAGGCTTGGGAGCGGAGCTGTGAATTTGCATTTCTAGCTAGTCTCTAAAG 7962
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 3988 TTACTGTTTTTTTCATTGTTACTATTTTGTAGTCACTGAATAATATGGCTTAATTGCTTATA 4047
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7963 GTTGCTGATGCACCTGGTCTGGGGACCACACTGGGGTTCCTCTGATCTCAATGGGAAGAA 8022
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4048 CATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCCT 4107
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8023 TGGAAATCAGGAGTGGTAGAGGCTGGATACCTTATTAAACAGAGATG----- 8067
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4108 CTCCCAGAGAAATACACACACACACACACTCATCACACAGTTTTTTTTTTAATGTTTGC 4167
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8068 ---GGGTGAGCACAAATATCTCAAGAAGCCACAGGGCTAGAGTGGTAACACAGAGTGT 8124
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4168 AACTAAGACAAAGAACTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATAAATCAG 4227
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8125 GACTGGCAGGAACCTGTGGGTATAATCATGGSAGTCCCTGGAATTAATAATGTTGGGG 8184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4228 TTGGGCACAGTGACTCAAGCCTGTAACCCACAGTACTTTTGAAGTCCAAGGTGGGTGGATC 4287
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8185 CCAGGCACGGTGGCTCATGCCTATAATCCACAGCACTTTGGGAGGCCAAGCCAGTGGGTC 8244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4288 ACTTGAGGTGAGAAGTTCGAGACCAGCCCTGGTCAATATGGTGAAAACCTTATCTACTATA 4347
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8245 ACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAAACATGGCGAAACCCCATCTACTATA 8304
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4348 AAATACAAAAATTAGCTGGGTGTAGTGTATGATGATGCTGTAGTCCCAGCTACTCGGAGGC 4407
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8305 AAATACAAAAATTAGCCAGGCGTGGTGGTGCTGCTATAATCCAGCTACTCGGAGGC 8364
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4408 TGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACC 4467
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Db 8365 TGAGGCAGGAGAAATTGTTGAACCCGAGAGCGGAGGTTGCAGTGAGCCGAGACACACC 8424
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 4468 ACTGCACTCCAGCCTGGCGCACACAGCGAGACTCTATCTCAAAAAATAAATAAA 4522
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8425 ACTGCACTCCAGCCT--GGTGACAGAGCGAGACTCCGCTCTCAAAAAAGAAAAAAA 8478
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RESULT 59
US-09-949-016-15351
; Sequence 15351, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15351
; LENGTH: 23574
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(23574)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15351
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Query Match		7.6%;	Score 381;	DB 3;	Length 23574;
Best Local Similarity		60.3%;	Pred. No. 6.5e-77;		
Matches 902;		Conservative	1;	Mismatches 476;	Indels 116; Gaps 12;
QY	3096	AGTTTGGGTTTTTTTTTGTGTTGTTAGACAGGGTCTTGCTGTCTGTCACCCAGGCATG	3155		
Db	7032	ATTTTTTAATTTTTTAATTTGTTTTTAGACAGAGGGTCTTGCTCTGTTGCCAGGCAGG	7091		
QY	3156	AGCACAGTGGTG--CAACCATAGGTCACTGCAGGCCTCAACCTCTGAGCTCAAGGGATCT	3213		
Db	7092	AGTGCAGTGGTGACAATCATAGTTCACCTGCAGGCCTTGAACCTCTGGACTCAGGCAGTCT	7151		
QY	3214	GCTGACCTCAGCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACGCGCTGGCTAAT	3273		
Db	7152	CCCTGCCTCAGCTCCCAAGTAGCTGGGACTACAGGTGCTCACCAACATGCCTGGCTAAT	7211		
QY	3274	TAAAAAAA-----TTTTTTGTAGAGC-TGGGTCTTACTACGTTGGCCAGGCTTGCT	3326		
Db	7212	TAAAAAAAATTTTTTTTTTTGTAGACAGGGGTCTTGCTGTGTGTGCCAAGGCTGGTCT	7271		
QY	3327	TAAACTCCTGGCTTAAGCAATCCTCTACCTTGGCATCCCAAAAGTCTGGGATTACAGG	3386		
Db	7272	CAAAATCCTGGGTCAAGCAA--TCCTACCTCTGTCTCCCAAAGTGTGAGATGACAGG	7328		
QY	3387	GGTGAGCCACCATGTGCGGCTACTTTATTTTACATTCCATCTTTCCAATAGAATGTAA	3446		
Db	7329	TATGAGCCACCATGCCTGGCCAGGCATCAGTATTTTTTTGAAGCTCCAGGTGAATCCAA	7388		
QY	3447	GATCCACAGAACAGGGGATTACTGCCTA-----	3473		
Db	7389	TGTGCAGACAACTTTGGGTACTGTCTGACATAGGCATTTTTTTAAAAAACTCCCTGATTTT	7448		
QY	3474	-----TTTTCTTCTCTTTCTTTTTTGAGACAGAGTCTCACTTTCATCACCTCAAC	3521		
Db	7449	ATTTTATTTAAATTAATTAATTTTATTTTTTTTGAGACGGAATCTTGCTCTGCGCCAGGC	7508		
QY	3522	CTCCGT-----TCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATT	3567		
Db	7509	TGGGGTGACGTGGCGCGATCTCGGCTCACTGCAAGCTCCACCTCCCGGGTTCATGCCATT	7568		
QY	3568	CTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAA	3627		
Db	7569	CTCCTGCTTCAGCCTCCCAAGTAGCTGGGACTACAGGCGCCCGCCACCAACGCCCCAGCTAA	7628		
QY	3628	TTTTTTTGATTTTAGCAGAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACCTC	3687		
Db	7629	TTTTTTTGATTTTAGTAGAGACGGAGTTTACCCGTGTTAGCCGGATGGTCTCGATCTC	7688		
QY	3688	CTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGAGT	3747		
Db	7689	CTGACCTC--GTGATCCACCCCGCTCGGCCTCCCAAAGTGTAGGATTACAGGCGAGAGC	7746		
QY	3748	CACGTGCGTGGCCGATTACTGTCTATTTTCTTTATTTGCTATATATCCAGATCTAGAGCA	3807		
Db	7747	CACGTGCGTCCAGCCAACTCCCTGATTTT-----AATGTGCAGGC	7786		
QY	3808	GTGCTGCACATATAGTAGGTGCTCAATAAAAATAATTGATGAATGCACAGCCTAGATATAAA	3867		
Db	7787	AGGATTGAGACTAACTACTCTAGTCTAATGTTCTGAAACTTGAGCAGGCTTCAAATCA	7846		
QY	3868	CTTTCTTTTTTCTTTTTTAAACAATCTTGACAACCTTTGCAGATAAAATACAATCTTGCA	3927		
Db	7847	C-TTGGAGGCGCTTGTGAAACTCAAGTTTCAAGTGTGGGCTGCATTCACAGAGTTTCTGA	7905		
QY	3928	TTCTGCTTTTTCACCTTATCACCTTGTATGACTTTTTTCATATGCTTCCCTCAAACTTTATTG	3987		
Db	7906	TTCAG---TAGGTCTTGGGGAGCGGAGCTGTGAATTTTGCAATTTCTAGCTAGTCTCTAAAG	7962		
QY	3988	TTACTGTTTTTTTCATTGTTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATA	4047		
Db	7963	GTTGCTGATGCACCTGGTCTGGGGACCAACACTGGGGTTCCCTCTGATCTCAATGGGAAGAA	8022		
QY	4048	CATCCTCCTGCTCCACTTTTAGAAGGCCAAAATTTACAAATCTGATGAAAGCTATGAACCCCT	4107		

Db	8023	TGGAATCAGGAGTGGTAGAGGCTGGATACTTTATTAACAGAGATG-----	8067
QY	4108	CTCCCCAGAGAAAATACACACACACACACACTTCACTCACACAGTTTTTTTTTAATGTTTGC	4167
Db	8068	--GGGTGAGCACAAATTATCTCAAGAACCCACAGGGCTAGAGTGGTAACCCAGAGTGTTTT	8124
QY	4168	AACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATAACTCAG	4227
Db	8125	GACTGGCAGGAACCTGTGGTATAATCATGGGAGTCCCTGGAATTAATAATGTTGGGG	8184
QY	4228	TTGGGCACAGTGACTCAAGCCTGTAACCCACAGTACTTTTGGAAGTCCAAGGTGGGTGATC	4287
Db	8185	CCAGGCACGGTGGCTCATGCTATAATCCCAGCACTTTGGGAGGCCAAGCGAGTGGTTC	8244
QY	4288	ACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAAACCTATCTCTACTAA	4347
Db	8245	ACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAAACATGGCGAAAACCCCATCTCTACTAA	8304
QY	4348	AAATACAAAAATTAGCTGGGTGTAGTGATGATGCTGCTGTAGTCCCAGCTACTCGGAGGC	4407
Db	8305	AAATACAAAAATTAGCCAGGCGTGGTGGTGCTATAATCCCAGTACTCGGAGGC	8364
QY	4408	TGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACC	4467
Db	8365	TGAGGCAGGAGAAATTGTTGAACCCGAGAGCGGAGGTTGCAGTGAGCCGAGACACACC	8424
QY	4468	ACTGCACTCCAGCCTGGCGCACACAGCGAGACTCTATCTCAAAAAATAATAATAA	4522
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RESULT 60

US-09-949-016-12068
; Sequence 12068, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12068
; LENGTH: 51671
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12068

Query Match		7.6%;	Score 380.2;	DB 3;	Length 51671;
Best Local Similarity		59.2%;	Pred. No. 1.4e-76;		
Matches 880;		Conservative	0;	Mismatches 518;	Indels 89; Gaps 10;
QY	3105	TTTTTTTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCCAGGCATGAGCACAGTG	3164		
Db	45852	TTCTTTTTTTTTTTTTTCTGAGACAGGGTCTTGCTCTGTGGTACAGGCTGGAGTCAGTG	45911		
QY	3165	GTGCAACCATAGTGCACCTGCAGCCTCAACCTCCTGA-GCTCAAGGGATCTGCTGACCTCA	3223		
Db	45912	GCAAATCATGGCTCACCGCAGCCTCAACCTCCCCAGGCTCAAGCAATCCCCCAACTCA	45971		
QY	3224	GCCTCCCAAGTAGCTGGGACTACGAGCGTGCAGCCACCCACCGCTGGCTAATTAATAAAAT	3283		
Db	45972	TCCTCTTGAGTAGCTGGGACTACAGGCGCACACACCAGGTCCTGCTAATTTTGTGTA--T	46029		

QY	3284	TTTTTGTAGAGACTGGGTCTTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTCAA	3343
Db	46030	TTTTTGTAGAGATGGGTTTACCACATGTTGCCAGGCTGGTCTCAAACCTCCTGAGCTCAA	46089
QY	3344	GCAATCCTCCTACCTTGGCATCCCAAAGTGTCTGGATTACAGGGGTGAGCCACCATGTGC	3403
Db	46090	GTGATCCTCCCGCCTTGGCCTCCCAAAGTGTCTGGGATTACAGGCGTGAGCCACCGCACCC	46149
QY	3404	GGCTACTTATTT-----CTTTACATTCCATCTTTCCAATAGAAATGTAAGAT	3449
Db	46150	AGAAAAGAAATCTTACAGAGAGAAAAACATATTCTAGACCCCTGAAGATATACAGTTAACT	46209
QY	3450	CCACAGAACAGGGATTACTGCCTATT-----TTC	3478
Db	46210	CTCGAACATGGGGTTATGGGGTGCTGACCCCTTAAAAGTCAAATATTCCCATATAAACTT	46269
QY	3479	TTCTCTTTCTTTTGTGAGACAGAGTCTCATCTTCATCACCTCAAACCTCCGT-----	3527
Db	46270	CTTTTCTTTTGTGAGACAGAGTCTCACTCTGTTGCCAGGCTGGAGTGCAGAGGTGCG	46329
QY	3528	---TCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCCTGCCTAAGCCTCC	3584
Db	46330	ATCTCAGCTCACTGCAGCCTCCATCTCCTAGGTTTAAAGTATTCTCCTGCCTCAGCCTCC	46389
QY	3585	TGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGCTGGCTAAATTTTGTATTTTAGC	3644
Db	46390	TGAGTAGCTAGGATTACAGGTGTATGCCGCCACGCCCTAGCT-ACTTTTGTATTTTAGT	46448
QY	3645	AGAGATGGGGTTTACCATTGTTGCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTGATCT	3704
Db	46449	AGAGATGGGGTTTACCATTGTTGCCAGGCTGGTCTCGAACTCCTGACTTCAAGTAAATCC	46508
QY	3705	GCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGACTCACTGTGCCTGGCCGAT	3764
Db	46509	ACCTGCCTTGGCCTCCCAAAGTGTGGGATTACAGGCATAAGCCACTGTGCCCGGCC--	46565
QY	3765	TACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTA	3824
Db	46566	----TCATATAAGTTTGTACGCCCCCTCACCCCAAATTTAACTACTGATAGCCTACCAT	46621
QY	3825	GGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAAACTTCTTTTCTTTT	3884
Db	46622	GACCAAAGCCTTACTGTATAAACAGTTGATTACATATATTGTGTATATATACTGTAT	46681
QY	3885	TAAACAATCTTGACAACTTTGCAGATAAATAACAATCTTGCAATCTGCTTTTTCACCTTA	3944
Db	46682	TCTTACAGTAAGGTATGGTAGAGAAAGGAAATATTAAGRAAATCAGGCCAGATGCAGTG	46741
QY	3945	TCACCTTGTTATGACTTTTTTCATATTGCCTCAAACCTTTTATTGTTACTGTTTTTTCATTG	4004
Db	46742	GCTCATGCCGTAAATCCTAGCACTTTGGGAAGTTGAGGAGGGGGATCACTTGAGCTCAG	46801
QY	4005	TTACTATTTTAGTCACTGAATAATATGGCTTAATTGCTTATACATCCTCCTGCTCCACT	4064
Db	46802	GAATTCAGACCAGCCTGGCAACATGGCAAAACTCCATTGCTACAAAAAATAAAAAA	46861
QY	4065	TTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAAATACA	4124
Db	46862	AAAAATAGAAAAAATTAGCAGGAGGCTGAGGTGGGAGGATCACTTGAGCCTGGGAGGTA--	46919
QY	4125	CACACACACACACTCACACACAGTTTTTTTAAATGTTTGAACAATAAGACAAGAAACC	4184
Db	46920	-----AAAGCTGCAGTCAGCTGTGACTGTACCACCTGCAGCTCCAGTCTGGGAGAC	46968
QY	4185	TGCATTAGAGGATGTTTGTTCATATTAATAAATAAATAAATAAATAAATAAATAAATAA	4244
Db	46969	AGAGCAAGACTGTGTCTCTAAAAAAT-----AAAATTTAAGCCTGGGTGTAGTGGCTCA	47023
QY	4245	AGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTT	4304
Db	47024	TCCCTGTAAATCCAGCACCTTTGGGAGGCAAAAGGTGGGCGGATCACCTGAGGCCAGGAGTT	47083
QY	4305	CGAGACCCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAAATACAAAAATTAGCT	4364

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Maximum Match 100%
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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB ID	Description
		Match	Length		
1	4997.4	100.0	12174	8	US-10-607-806-1
C 2	474.8	9.5	333811	8	US-10-741-600-17681
C 3	456.6	9.1	42360	7	US-10-322-281-618
C 4	444.4	8.9	126990	7	US-10-717-597-68
C 5	438	8.8	58448	6	US-10-017-161-1659
6	434.2	8.7	93544	7	US-10-322-281-676
C 7	434.2	8.7	160482	5	US-10-087-192-100
C 8	433.2	8.7	91760	5	US-10-087-192-844
9	429.8	8.6	92500	9	US-10-723-681-1
C 10	425.4	8.5	38538	7	US-10-322-281-448
11	416	8.3	139257	3	US-09-920-671-11
C 12	414.6	8.3	187844	8	US-10-719-993-6883
C 13	414.2	8.3	196686	5	US-10-087-192-484
C 14	413.6	8.3	86001	7	US-10-317-500-4
15	412.4	8.3	45367	6	US-10-085-117-328
C 16	405.8	8.1	227246	7	US-10-322-281-314
C 17	403.6	8.1	23639	3	US-09-740-043-3
C 18	402	8.0	171843	9	US-10-981-277-44
C 19	401.8	8.0	103574	9	US-10-756-149-2307
C 20	400.4	8.0	14176	3	US-09-764-864-1644
C 21	400.4	8.0	177531	8	US-10-484-577-660
C 22	400	8.0	46878	8	US-10-741-600-17664
- 23	399	8.0	87687	5	US-10-087-192-1978

24	398.6	8.0	174448	5	US-10-087-192-148	Sequence 148, App
C 25	398.4	8.0	167343	3	US-09-962-436-281	Sequence 281, App
C 26	398.4	8.0	167343	3	US-09-964-824A-273	Sequence 273, App
C 27	398.4	8.0	167343	9	US-10-843-641A-2740	Sequence 2740, Ap
C 28	398.4	8.0	167343	9	US-10-843-641A-5576	Sequence 5576, Ap
29	398.4	8.0	201143	7	US-10-240-425-1099	Sequence 1099, Ap
30	396	7.9	76798	3	US-09-880-107-3949	Sequence 3949, Ap
31	394.6	7.9	19300	7	US-10-317-271A-4	Sequence 4, Appli
32	391.4	7.8	1980090	8	US-10-719-993-6815	Sequence 6815, Ap
33	391.4	7.8	1980090	8	US-10-741-600-17676	Sequence 17676, A
34	390.8	7.8	15000	3	US-09-954-531-175	Sequence 175, App
35	390.8	7.8	15000	9	US-10-843-641A-1242	Sequence 1242, Ap
C 36	390	7.8	13224	3	US-09-764-853-897	Sequence 897, App
C 37	389.6	7.8	23456	7	US-10-322-281-64	Sequence 64, Appl
38	389.6	7.8	60057	5	US-10-087-192-700	Sequence 700, App
39	389	7.8	62555	8	US-10-741-600-17630	Sequence 17630, A
C 40	389	7.8	120955	9	US-10-756-149-4579	Sequence 4579, Ap
C 41	388.8	7.8	150275	9	US-10-981-277-55	Sequence 55, Appl
42	388	7.8	75252	5	US-10-087-192-904	Sequence 904, App
43	387.8	7.8	48001	7	US-10-304-107-4	Sequence 4, Appli
44	387.8	7.8	300000	6	US-10-262-552-33	Sequence 33, Appl
45	387.8	7.8	300000	7	US-10-703-210-33	Sequence 33, Appl
46	386.4	7.7	304905	7	US-10-271-416-1	Sequence 1, Appli
47	385.2	7.7	61103	5	US-10-087-192-58	Sequence 58, Appl
48	385	7.7	13104	8	US-10-482-065-22	Sequence 22, Appl
C 49	384.8	7.7	114411	8	US-10-723-860-3910	Sequence 3910, Ap
C 50	384.2	7.7	73237	7	US-10-741-601-5712	Sequence 5712, Ap
C 51	383.4	7.7	96594	3	US-09-997-722-22	Sequence 22, Appl
52	383.4	7.7	227246	7	US-10-322-281-314	Sequence 314, App
C 53	382.2	7.6	6892	3	US-09-764-877-3770	Sequence 3770, Ap
C 54	382.2	7.6	6892	6	US-10-242-515-3770	Sequence 3770, Ap
55	382	7.6	47219	7	US-10-699-941-10	Sequence 10, Appl
56	382	7.6	59884	7	US-10-699-941-11	Sequence 11, Appl
57	381	7.6	57759	9	US-10-783-271-108	Sequence 108, App
58	380.8	7.6	32193	3	US-09-764-877-2623	Sequence 2623, Ap
59	380.8	7.6	32193	6	US-10-216-464-37	Sequence 37, Appl
60	380.8	7.6	32193	6	US-10-242-515-2623	Sequence 2623, Ap
C 61	380.4	7.6	183610	8	US-10-484-577-664	Sequence 664, App
C 62	380	7.6	75252	5	US-10-087-192-904	Sequence 904, App
63	379.8	7.6	72604	6	US-10-162-497-7	Sequence 7, Appli
64	379.8	7.6	72604	8	US-10-629-313-7	Sequence 7, Appli
65	379.8	7.6	150275	9	US-10-981-277-55	Sequence 55, Appl
66	379.6	7.6	256493	5	US-10-087-192-1000	Sequence 1000, Ap
67	379.4	7.6	3239	5	US-10-027-632-114978	Sequence 114978,
68	379.4	7.6	3239	6	US-10-027-632-114978	Sequence 114978,
69	379	7.6	276276	5	US-10-087-192-754	Sequence 754, App
C 70	378.4	7.6	32204	3	US-09-764-855-327	Sequence 327, App
C 71	378.4	7.6	32204	3	US-09-764-872-517	Sequence 517, App
C 72	378.4	7.6	32204	5	US-10-072-349-327	Sequence 327, App
73	377.6	7.6	48509	7	US-10-322-281-510	Sequence 510, App
C 74	376.8	7.5	72691	8	US-10-741-600-17712	Sequence 17712, A
75	376.6	7.5	48069	8	US-10-719-993-6756	Sequence 6756, Ap
76	375.6	7.5	221600	9	US-10-840-590-1	Sequence 1, Appli
77	375.4	7.5	103574	9	US-10-756-149-2307	Sequence 2307, Ap
78	374.2	7.5	12683	6	US-10-242-355-703	Sequence 703, App
C 79	374.2	7.5	58845	5	US-10-087-192-40	Sequence 40, Appl
80	374	7.5	96592	3	US-09-997-722-88	Sequence 88, Appl
C 81	374	7.5	160552	8	US-10-697-828-11	Sequence 11, Appl
82	373.4	7.5	42794	8	US-10-741-600-17670	Sequence 17670, A
83	372.8	7.5	52677	5	US-10-087-192-130	Sequence 130, App
C 84	372.2	7.4	32152	3	US-09-764-853-328	Sequence 328, App
85	372.2	7.4	32152	3	US-09-764-872-518	Sequence 518, App
C 86	372.2	7.4	32152	5	US-10-072-349-328	Sequence 328, App
87	371	7.4	13224	3	US-09-764-853-897	Sequence 897, App
C 88	370.8	7.4	149671	6	US-10-236-031B-53	Sequence 53, Appl
C 89	369.8	7.4	96592	3	US-09-997-722-88	Sequence 88, Appl
C 90	369.6	7.4	87001	8	US-10-741-600-17792	Sequence 17792, A
C 91	368.6	7.4	108111	8	US-10-719-993-6843	Sequence 6843, Ap
92	368.6	7.4	202814	8	US-10-719-993-6812	Sequence 6812, Ap
93	368.2	7.4	35770	8	US-10-741-600-17693	Sequence 17693, A
C 94	368.2	7.4	67697	8	US-10-719-993-6997	Sequence 6997, Ap
C 95	368.2	7.4	67697	8	US-10-741-600-17928	Sequence 17928, A
C 96	367.8	7.4	29921	8	US-10-719-993-6848	Sequence 6848, Ap

Db	4620		AGATCTCACTCCTCTGGAATGGGGCCACAGGCCACAGCAACAGGGATGGCCAGCCCCG	4679
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Db	4680		CAGTCTCAAWTCGAGGTTCCCACTGGGGCTTAAGGGCTCCTCTATTGGGTTCCCTCAAG	4739
Qy	241		GCTGGCACTTTTCAACCTGCAAGTCTGAACTCAGATTGCCCTGAGCTAAGAAAGCTTGCC	300
Db	4740		GCTGGCACTTTTCAACCTGCAAGTCTGAACTCAGATTGCCCTGAGCTAAGAAAGCTTGCC	4799
Qy	301		TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA	360
Db	4800		TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGGCA	4859
Qy	361		TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCACCTTACTCA	420
Db	4860		TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCACCTTACTCA	4919
Qy	421		ACTAAGTAGTTAGGCCAATCTCCCATTTATTTATTTATTTAAATTTTATTTTATTT	480
Db	4920		ACTAAGTAGTTAGGCCAATCTCCCATTTATTTATTTATTTAAATTTTATTTTATTT	4979
Qy	481		TACTTTATTTATTTTGGACGGGGCTCACTCTGTGCCCCAGGCTGGAGTGGGGTGGG	540
Db	4980		TACTTTATTTATTTTGGACGGGGCTCACTCTGTGCCCCAGGCTGGAGTGGGGTGGG	5039
Qy	541		TGATCTCAGATCACTACAACTCCATCTCCTGGGTTCAAATAAATCTCTTGCCCTCAGCCT	600
Db	5040		TGATCTCAGATCACTACAACTCCATCTCCTGGGTTCAAATAAATCTCTTGCCCTCAGCCT	5099
Qy	601		CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACCATGCCCAGCTAA	660
Db	5100		CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACCATGCCCAGCTAA	5159
Qy	661		TTTTTTGTGTGTTTTTTTGGTAGAGACAGGTTTTTCACCATGTTGGCCAGGCTGGGTGAC	720
Db	5160		TTTTTTGTGTGTTTTTTTGGTAGAGACAGGTTTTTCACCATGTTGGCCAGGCTGGGTGAC	5219
Qy	721		CTCCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCTTTCTAATGCAGTATCCAGT	780
Db	5220		CTCCCTTTTAGATTCTCCTCATCCTGCTCTATTCTTCCCTTTCTAATGCAGTATCCAGT	5279
Qy	781		TTCCCTTACTTATCACATTTATTTATTTCTTATTTATTTAGACACAGAGTCTTGCTTTGT	840
Db	5280		TTCCCTTACTTATCACATTTATTTATTTCTTATTTATTTAGACACAGAGTCTTGCTTTGT	5339
Qy	841		CGCCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT	900
Db	5340		CGCCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT	5399
Qy	901		CACGCCAATTCTCCGCCTCAGCCTCCCCAGTAGCTGGGACTAAGGGCGCCTGCCACCAG	960
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Db	5460		CCCCGCTAAATTTTGTATTTTAAATAAAGACGGGGTTTCATCGTGTAGCCAGGATGG	5519
Qy	1021		TCTCGATCTCATGACCTTGTGATCCGCCTGCCTCGGCCCTCCAAAGTCTGGGATTACAG	1080
Db	5520		TCTCGATCTCATGACCTTGTGATCCGCCTGCCTCGGCCCTCCAAAGTCTGGGATTACAG	5579
Qy	1081		GCATAGCCACCGTGCCCGGCTTATCACATTTATTTATTTATTTATTTCTCTCCCACTA	1140
Db	5580		GCATAGCCACCGTGCCCGGCTTATCACATTTATTTATTTATTTATTTCTCTCCCACTA	5639
Qy	1141		GGTTGTAAGCTCCATGAGGTTAGAGATTATTTATTTATTTATTTATTTATTTATTTAT	1200
Db	5640		GGTTGTAAGCTCCATGAGGTTAGAGATTATTTATTTATTTATTTATTTATTTATTTAT	5699
Qy	1201		TATTTATTTATTTATTTTCACTGCTGTATCTCTAGCTCCTAGGACAGAGCCTGGCACAT	1260

Db	5700		TATTATTATTATATCTGTTCACCTGCTGTATCTCTAGCTCCTAGGACAGAGCCTGGCACAT	5759
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Db	5760		AGTAAAGTGTCTCAATAAATATTCACTGGATAAAACAGTGCAGATAGTTTTAAAACTATCTGAC	5819
Qy	1321		CTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCCGGAAGCAGAGTTTGCAGTGAAGTG	1380
Db	5820		CTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCCGGAAGCAGAGTTTGCAGTGAAGTG	5879
Qy	1381		AAATCGTGTCACTGCACCTCAAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAA	1440
Db	5880		AAATCGTGTCACTGCACCTCAAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAA	5939
Qy	1441		AAAAAACTATCAGGCCTAGCTGGGTGGCACATGCCTGTAAATCCTAGCTGAGGCGGTAGGG	1500
Db	5940		AAAAAACTATCAGGCCTAGCTGGGTGGCACATGCCTGTAAATCCTAGCTGAGGCGGTAGGG	5999
Qy	1501		TCCCAGAAGAAAGAAAGAAAAAGAAAGATATATATATATATATATATACACACACAA	1560
Db	6000		TCCCAGAAGAAAGAAAGAAAAAGAAAGATATATATATATATATATATACACACACAA	6059
Qy	1561		GATATAAACTTTATATATATAAAGTTTTTCATTAATAAAAAAACCCTCTACCCACTT	1620
Db	6060		GATATAAACTTTATATATATAAAGTTTTTCATTAATAAAAAAACCCTCTACCCACTT	6119
Qy	1621		TCACCTTTACCAGGTTCCCTGGGTCCAACGGTCTTCAGAGGAGGCAGCTGGCAGGGTCAAG	1680
Db	6120		TCACCTTTACCAGGTTCCCTGGGTCCAACGGTCTTCAGAGGAGGCAGCTGGCAGGGTCAAG	6179
Qy	1681		GAGGCAGCGTGGGACCCGAGGGAGCAGGAAGGCAGTGTGTCCCCGGGTGCTGGCAGACC	1740
Db	6180		GAGGCAGCGTGGGACCCGAGGGAGCAGGAAGGCAGTGTGTCCCCGGGTGCTGGCAGACC	6239
Qy	1741		GATTTGAACTCTGGCTATGTCTTCTTGACGTGGCCGCCCGCMCAGCGGCATCAGCCCTC	1800
Db	6240		GATTTGAACTCTGGCTATGTCTTCTTGACGTGGCCGCCCGCMCAGCGGCATCAGCCCTC	6299
Qy	1801		GGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCAGGGAGTGACCCCTT	1860
Db	6300		GGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCCTGATCCCAGGGAGTGACCCCTT	6359
Qy	1861		TGGAATACAACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGTGGATG	1920
Db	6360		TGGAATACAACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGTGGATG	6419
Qy	1921		AACCTGGACAAGTAAGTATCGCCCTGCAGGAAATTTGGAGTGCCTGCCGGGGCGGGGTG	1980
Db	6420		AACCTGGACAAGTAAGTATCGCCCTGCAGGAAATTTGGAGTGCCTGCCGGGGCGGGGTG	6479
Qy	1981		GGGCACACGCCAAGGATCTCAGAGGCATACAAAGGGGACTTGATATCTGCTAAGGATA	2040
Db	6480		GGGCACACGCCAAGGATCTCAGAGGCATACAAAGGGGACTTGATATCTGCTAAGGATA	6539
Qy	2041		ACATATTTTCACTCTTGTCAAATAAAACAAATATGTTCCAAGAGGACCCCTGTAGCGAACG	2100
Db	6540		ACATATTTTCACTCTTGTCAAATAAAACAAATATGTTCCAAGAGGACCCCTGTAGCGAACG	6599
Qy	2101		CACCCCGTTAGAGATGGAACAAATGACCCGACGTGCAAAAAACAGTGGCGATGTCCTCC	2160
Db	6600		CACCCCGTTAGAGATGGAACAAATGACCCGACGTGCAAAAAACAGTGGCGATGTCCTCC	6659
Qy	2161		AGTGGCAGAAATGTAGCAACAGTAAACATCACAGCAACTATCCACGTGTCATTTCTAGCA	2220
Db	6660		AGTGGCAGAAATGTAGCAACAGTAAACATCACAGCAACTATCCACGTGTCATTTCTAGCA	6719
Qy	2221		GTGGTTGTCACTGCACCTTCTGAATACAGGATTTTACTGTATTCTTGCAACCATGTTAAA	2280
Db	6720		GTGGTTGTCACTGCACCTTCTGAATACAGGATTTTACTGTATTCTTGCAACCATGTTAAA	6779
Qy	2281		AATCGCTTTTACGGCCAGCGCGGTGGCTCATGCCTGTAAATCCCAGCATTTTGGAGGCCG	2340
Db	6780		AATCGCTTTTACGGCCAGCGCGGTGGCTCATGCCTGTAAATCCCAGCATTTTGGAGGCCG	6839

Qy	2341	AGCGGGCGGATCAC	TTGAGGTCAGGAGTT	CGAGACCAGCCTGGCCAA	CATGGTGAAC	2400
Db	6840	AGCGGGCGGATCAC	TTGAGGTCAGGAGTT	CGAGACCAGCCTGGCCAA	CATGGTGAAC	6899
Qy	2401	CTGCTCTACTAAAA	ATACAAAAATAGCCG	GACATGGTGGGAGCG	CCTGTAAACCCA	2460
Db	6900	CTGCTCTACTAAAA	ATACAAAAATAGCCG	GACATGGTGGGAGCG	CCTGTAAACCCA	6959
Qy	2461	GCTACTTGGGAGAC	TGAGTTGGAGGTTT	CAGTGAGCCAAAGT	CGTGCTCACTGCTGCCAG	2520
Db	6960	GCTACTTGGGAGAC	TGAGTTGGAGGTTT	CAGTGAGCCAAAGT	CGTGCTCACTGCTGCCAG	7019
Qy	2521	CCTGGGTAAAGAG	CAACTCTGTCTCAAAAA	AAAAAATGCTTTCA	ATAAATATATGATA	2580
Db	7020	CCTGGGTAAAGAG	CAACTCTGTCTCAAAAA	AAAAAATGCTTTCA	ATAAATATATGATA	7079
Qy	2581	AAAGGACTTATAT	TTTTTCAAGCCATAG	GATCATTTCTCCTGA	AGCATCTTGGCGAAGTC	2640
Db	7080	AAAGGACTTATAT	TTTTTCAAGCCATAG	GATCATTTCTCCTGA	AGCATCTTGGCGAAGTC	7139
Qy	2641	ATCCCCACCTGTT	CCTGAGAGTGGCAG	GTGAGGCTGACCTAT	TGCTCTGCACTTACTC	2700
Db	7140	ATCCCCACCTGTT	CCTGAGAGTGGCAG	GTGAGGCTGACCTAT	TGCTCTGCACTTACTC	7199
Qy	2701	CTATCTCAGCTGTC	CCCTCCCACTTTCAG	AGTGCTGCCAGACAT	GACAACTGCTAYGAC	2760
Db	7200	CTATCTCAGCTGTC	CCCTCCCACTTTCAG	AGTGCTGCCAGACAT	GACAACTGCTAYGAC	7259
Qy	2761	CAGGCCAAGAAGCT	GGACAGCTGTAAAT	TTCTGCTGGACAMM	CGGTACACCCACACCTAT	2820
Db	7260	CAGGCCAAGAAGCT	GGACAGCTGTAAAT	TTCTGCTGGACAMM	CGGTACACCCACACCTAT	7319
Qy	2821	TCATACTCGTCTCT	GGCTCGGCAATCAC	CTGTAGCAGTAGGTT	TATCCCTTCCTTGACC	2880
Db	7320	TCATACTCGTCTCT	GGCTCGGCAATCAC	CTGTAGCAGTAGGTT	TATCCCTTCCTTGACC	7379
Qy	2881	TATGAATTCAGTT	GGTTCTCAGTAGCG	CGGGGAAATAATAG	TAAACAACAGCCATGAT	2940
Db	7380	TATGAATTCAGTT	GGTTCTCAGTAGCG	CGGGGAAATAATAG	TAAACAACAGCCATGAT	7439
Qy	2941	TTAGTGTTAAATTT	CTTGGTTCTGGG	CAGTGTCTCCTTTA	ATCCTCAGAAACAACATATG	3000
Db	7440	TTAGTGTTAAATTT	CTTGGTTCTGGG	CAGTGTCTCCTTTA	ATCCTCAGAAACAACATATG	7499
Qy	3001	GGATAGGTACAAT	TATCCTCACCTTA	CAGATAAAGAAAA	CTGAGGCTCAGAAGGCTGAGCT	3060
Db	7500	GGATAGGTACAAT	TATCCTCACCTTA	CAGATAAAGAAAA	CTGAGGCTCAGAAGGCTGAGCT	7559
Qy	3061	ATTTGCCCAAGAT	CACACAGCTTGTAG	TGGTGACAGTTTGG	GTTTTTTTGTGTTGT	3120
Db	7560	ATTTGCCCAAGAT	CACACAGCTTGTAG	TGGTGACAGTTTGG	GTTTTTTTGTGTTGT	7619
Qy	3121	TTAGAGACAGGGT	CTTGCTCTGTCA	CCAGGCATGAGCAC	AGTGGTGCACCATAGGTCA	3180
Db	7620	TTAGAGACAGGGT	CTTGCTCTGTCA	CCAGGCATGAGCAC	AGTGGTGCACCATAGGTCA	7679
Qy	3181	CTGCAGCCTCAA	CCTCCTGAGCTCA	AGGGATCTGCTGA	CCCTCAGCCTCCCAAGTAGCTGG	3240
Db	7680	CTGCAGCCTCAA	CCTCCTGAGCTCA	AGGGATCTGCTGA	CCCTCAGCCTCCCAAGTAGCTGG	7739
Qy	3241	GACTACGAGCGT	GCACCCACCGCT	GCTAAATTA	AAAAAATTTTGTAGAGACTGGG	3300
Db	7740	GACTACGAGCGT	GCACCCACCGCT	GCTAAATTA	AAAAAATTTTGTAGAGACTGGG	7799
Qy	3301	TCTTACTACGTT	GGCCAGGCTTGT	CTTAAACTCCTG	GCTTCAAGCAATCCTCCTACCTTG	3360
Db	7800	TCTTACTACGTT	GGCCAGGCTTGT	CTTAAACTCCTG	GCTTCAAGCAATCCTCCTACCTTG	7859
Qy	3361	GCATCCCAAAGT	GTGGGATACAGG	GGTGAGCCACCAT	TGTGCGGCTACTTATTTCTTTA	3420
Db	7860	GCATCCCAAAGT	GTGGGATACAGG	GGTGAGCCACCAT	TGTGCGGCTACTTATTTCTTTA	7919

Qy	3421	CATTCCATCTTTCC	AATAGATCCACA	GAACAGGGATT	TACTGCCTATTTCTT	3480
Db	7920	CATTCCATCTTTCC	AATAGATCCACA	GAACAGGGATT	TACTGCCTATTTCTT	7979
Qy	3481	CCTTTCTTTT	TGAGACAGAGTCT	CACCTT	CATCACCTCCGTT	CAGCTCACTGCA 3540
Db	7980	CCTTTCTTTT	TGAGACAGAGTCT	CACCTT	CATCACCTCCGTT	CAGCTCACTGCA 8039
Qy	3541	ACCTCTGCCTCC	CGGTTCAAGYGAT	TTCTCCTG	CTTAAGCCTCCTG	AGTAGCTGGAATTA 3600
Db	8040	ACCTCTGCCTCC	CGGTTCAAGYGAT	TTCTCCTG	CTTAAGCCTCCTG	AGTAGCTGGAATTA 8099
Qy	3601	CAAGCGTGCA	CCACCATGCTTGG	CTAATTTTTT	TGTATTTTAG	CAGAGATGGGTTTTAC 3660
Db	8100	CAAGCGTGCA	CCACCATGCTTGG	CTAATTTTTT	TGTATTTTAG	CAGAGATGGGTTTTAC 8159
Qy	3661	CATGTTGCC	AGGCTGCTCAAA	CTCCTGAC	CTCAAGTGATCTGC	CTGCCTCAGTCTCC 3720
Db	8160	CATGTTGCC	AGGCTGCTCAAA	CTCCTGAC	CTCAAGTGATCTGC	CTGCCTCAGTCTCC 8219
Qy	3721	CAAAGTGCTG	GAATATATAGG	CGTGAGT	CACTGCGCTG	CGCGATTACTGTCTATTTCTT 3780
Db	8220	CAAAGTGCTG	GAATATATAGG	CGTGAGT	CACTGCGCTG	CGCGATTACTGTCTATTTCTT 8279
Qy	3781	TATTGCTATAT	CCCCAGATCTAG	AGCAGTGTCTG	ACATATAGT	AGTGTCTCAATAATAA 3840
Db	8280	TATTGCTATAT	CCCCAGATCTAG	AGCAGTGTCTG	ACATATAGT	AGTGTCTCAATAATAA 8339
Qy	3841	TTGATGAATG	CACAGCCTAGAT	ATAAACTTTCT	TTTTTAA	AAACAATCTTGACA 3900
Db	8340	TTGATGAATG	CACAGCCTAGAT	ATAAACTTTCT	TTTTTAA	AAACAATCTTGACA 8399
Qy	3901	ACTTTCAGAA	TAAATAACAAT	CTTGCA	TTCTGCTTTT	CACCTTATCACCTTGTATGACT 3960
Db	8400	ACTTTCAGAA	TAAATAACAAT	CTTGCA	TTCTGCTTTT	CACCTTATCACCTTGTATGACT 8459
Qy	3961	TTTTCATAT	TGCCTCAA	ACCTTATTT	TGTTACTGTTT	TTTTCATTTTAGTCAC 4020
Db	8460	TTTTCATAT	TGCCTCAA	ACCTTATTT	TGTTACTGTTT	TTTTCATTTTAGTCAC 8519
Qy	4021	TGAATAATAT	TGGCTTAAT	TGCTTATAC	ATCCTCCTGCT	CCACTTTAGAAGGCCAAATTT 4080
Db	8520	TGAATAATAT	TGGCTTAAT	TGCTTATAC	ATCCTCCTGCT	CCACTTTAGAAGGCCAAATTT 8579
Qy	4081	ACAAATCTG	ATGAAAGCTAT	GAACCTCTC	CCCCAGAAAA	TACACACACACACACT 4140
Db	8580	ACAAATCTG	ATGAAAGCTAT	GAACCTCTC	CCCCAGAAAA	TACACACACACACACT 8639
Qy	4141	CACACACAGT	TTTTTTTAA	TGTTTGCA	ACTAAGACA	AGAAACCTGCAATTAGAGGATGTT 4200
Db	8640	CACACACAGT	TTTTTTTAA	TGTTTGCA	ACTAAGACA	AGAAACCTGCAATTAGAGGATGTT 8699
Qy	4201	TGTTCATAT	TAAATAAA	TAAC	TCAGTTGGG	CACAGTCAAGCCTGTAAACCACAGT 4260
Db	8700	TGTTCATAT	TAAATAAA	TAAC	TCAGTTGGG	CACAGTCAAGCCTGTAAACCACAGT 8759
Qy	4261	ACTTTGGA	AGTCCAA	GGTGGTGAT	CAC	TTGAGGTGAGAAAGTTCGAGACCAGCCTGGTC 4320
Db	8760	ACTTTGGA	AGTCCAA	GGTGGTGAT	CAC	TTGAGGTGAGAAAGTTCGAGACCAGCCTGGTC 8819
Qy	4321	AATATGGT	GAAACCC	TATCTCTA	CTAAAAA	TACAAAAATTAGCTGGGTGTAGTGATGCAT 4380
Db	8820	AATATGGT	GAAACCC	TATCTCTA	CTAAAAA	TACAAAAATTAGCTGGGTGTAGTGATGCAT 8879
Qy	4381	GCCTGTAGT	CCCAGCTACT	CGGAGGCTG	AGGCAAG	AGAATTGCTTGAACCTGGGAGGCA 4440
Db	8880	GCCTGTAGT	CCCAGCTACT	CGGAGGCTG	AGGCAAG	AGAATTGCTTGAACCTGGGAGGCA 8939
Qy	4441	GAGGTTGC	AGTGAGCC	GAGATCC	CACTGCA	CTCCAGCCTGGCGCACACAGCGAGACT 4500
Db	8940	GAGGTTGC	AGTGAGCC	GAGATCC	CACTGCA	CTCCAGCCTGGCGCACACAGCGAGACT 8999
Qy	4501	CTATCTCA	AAAAAATA	ATAATAA	TAAATAA	AGGATCGGAGAGAAACAAACTAATAAGAT 4560

Db	9000	CTATCTCAAAAAATAAAATAAAATAAAGGATCGAGAGAAACAAAACTAATAAGAT	9059
Qy	4561	TCCTGAAGGTAACGAGAGATACGTAAATTTATATGTAATAAAGTTTAAATGCATTTAACT	4620
Db	9060	TCCTGAAGGTAACGAGAGATACGTAAATTTATGTAATAAAGTTTAAATGCATTTAACT	9119
Qy	4621	GTAATCTTATTGTTTATTTTGGTTATAAAAGTAACAAGCCAAAAGTAATGCAACTTCAA	4680
Db	9120	GTAATCTTATTGTTTATTTTGGTTATAAAAGTAACAAGCCAAAAGTAATGCAACTTCAA	9179
Qy	4681	ACKCTACATAAATAATCTATTATGAAAGTGGAAGGCATCTATAATCCTACTACCCAAAAGA	4740
Db	9180	ACKCTACATAAATAATCTATTATGAAAGTGGAAGGCATCTATAATCCTACTACCCAAAAGA	9239
Qy	4741	TAACCAGTTACATAATTCCTCCAGATTTTGGGGCATACACTAGCTTTTTTATTTTGGGAA	4800
Db	9240	TAACCAGTTACATAATTCCTCCAGATTTTGGGGCATACACTAGCTTTTTTATTTTGGGAA	9299
Qy	4801	AATTTCCATGTGCAGGCATACCTAATTTTCTAAATGTCTATGTAGTATCCATTTAAGG	4860
Db	9300	AATTTCCATGTGCAGGCATACCTAATTTTCTAAATGTCTATGTAGTATCCATTTAAGG	9359
Qy	4861	ATGTTCCATAAATTTTAAAAATACATGCTTTAAAGTAGAGAAACTAGTTGGGCATGTTG	4920
Db	9360	ATGTTCCATAAATTTTAAAAATACATGCTTTTAAAGTAGAGAAACTAGTTGGGCATGTTG	9419
Qy	4921	CTCAGCCCTGTATCCAGCACTTTTGGGAGGCCGAGGCAAAATGGATCACTTGAGGTCCGGA	4980
Db	9420	CTCAGCCCTGTATCCAGCACTTTTGGGAGGCCGAGGCAAAATGGATCACTTGAGGTCCGGA	9479
Qy	4981	GTTTGAGACCGCCTGGACAA	5001
Db	9480	GTTTGAGACCGCCTGGACAA	9500

RESULT 2

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US-10-741-600-17681/c
; Sequence 17681, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17681
; LENGTH: 333811
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(333811)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Table
US-10-741-600-17681

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Query Match 9.5%; Score 474.8; DB 8; Length 333811;
Best Local Similarity 50.9%; Pred. No. 1.8e-97;
Matches 1926; Conservative 3; Mismatches 1650; Indels 203; Gaps 26;

Qy	794	ACATTATATATTCTTATTTATTTATTTAGACACAGAGTCTTGCTTTGTGCGCAAGGCTGGA	853
Db	10492	AAAACTTTTTGTGTTGTTGTTTGAGATGGAGTCTCACTGTGTACCCAGGCTGGA	10433
Qy	854	GTACAGTGGTGGCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGTTACGCGCAATCTCC	913
Db	10432	GTACAGTGGTGGCAATCTCGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGTGAATCTCC	10373
Qy	914	CGCCTCAGCCTCCCCAGTAGCTGGGACTAAAGGCGCCTGCCACCACGCCCGCTAATTTT	973

Db 7220 CTTTATAATGTAAAAACTCAAGGTGGTTTAAAGTGAATATTTTAAAAATGGTGAAT 7161
Qy 4224 TCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAGGTGGTG 4283
Db 7160 TCAGCCAGGCACGGTGGCTCAGATCTGTAAATCCAGCAGCTTTGGAAGGCCGAGGYGGTG 7101
Qy 4284 GATCACTTGAGGTGAGAAAGTTTCGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTTA 4343
Db 7100 GATCAC--AAGGTCAAGAGACTGGGACCGTTCTGGCTAACACGATGAAACCCCACTCTA 7043
Qy 4344 CTAAAAATAC---AAAAATTAGTGGGTGTAGTGATGCATGCCTGTAGTCCCAGTACTC 4400
Db 7042 TGAATAATACAAAAAATAATTAGCCAGCCGTGGTGGTGGATGCCTGTAGTCCCAGTACTC 6983
Qy 4401 GGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCAGA 4460
Db 6982 GGGAGGCTGAGGCAGGAGAAATGGCGTGAACCCGGGAGGCAGAGCTTGCAGTGAGCCAAGA 6923
Qy 4461 TCCCACCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAATA 4520
Db 6922 TGGCACCACTGCACCTCCAGCCTGGGCGACAGAGTGAGACTCTGTCTCAAAAAAATAATA 6863
Qy 4521 AA 4522
Db 6862 AA 6861
RESULT 3
US-10-322-281-618/c
; Sequence 618, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 618
; LENGTH: 42360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-281-618
Query Match 9.1%; Score 456.6; DB 7; Length 42360;
Best Local Similarity 99.8%; Pred. No. 8.7e-94;
Matches 456; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4545 ACAAACTAATAAGATTCTCTGAAGTAAGCAGAGATACGTAAATATATATGTAATAAGTT 4604
Db 42360 ACAAACTAATAAGATTCTCTGAAGTAAGCAGAGATACGTAAATATATATGTAATAAGTT 42301
Qy 4605 TAAATGCATTTTAACTGTAATCTTATTGTTTATTTTGGTTATAAAAGTAAACAGCCAAA 4664
Db 42300 TAAATGCATTTTAACTGTAATCTTATTGTTTATTTTGGTTATAAAAGTAAACAGCCAAA 42241
Qy 4665 AGTAATGCAACTTCAAACKCTACATAAATATCTATTATGGAAGTGAAGGCATCTATAA 4724
Db 42240 AGTAATGCAACTTCAAACCTCTACATAAATATCTATTATGGAAGTGAAGGCATCTATAA 42181
Qy 4725 TCCTACTACCCAAAGATAACCAAGTTACATATTCCTCCAGATTTTGGGCATACACTAGC 4784
Db 42180 TCCTACTACCCAAAGATAACCAAGTTACATATTCCTCCAGATTTTGGGCATACACTAGC 42121
Qy 4785 TTTTTTATTTGGGAAAAATTTCCATGTGCAGGCATACCTAAATTTTCTAAATGTCTATGT 4844
Db 42120 TTTTTTATTTGGGAAAAATTTCCATGTGCAGGCATACCTAAATTTTCTAAATGTCTATGT 42061
Qy 4845 AGTATTCATTTAAGGATGTTCCATAATTTTAAAAATACATGCTTTAAAGTAGAGAACT 4904

Db 42060 AGTATTCCATTAAAGGATGTTCCATAATTTTAAAAATACATGCTTTTAAAGTAGAGAACT 42001
Qy 4905 AGTTGGGCATGTGGCTCACGCCTGTATCCAGCACTTTTGGAGGCCGAGCAAATGGA 4964
Db 42000 AGTTGGGCATGTGGCTCACGCCTGTATCCAGCACTTTTGGAGGCCGAGCAAATGGA 41941
Qy 4965 TCACTTGAGGTCGGAGTTTGAGACCAGCCTGGACAA 5001
Db 41940 TCACTTGAGGTCGGAGTTTGAGACCAGCCTGGACAA 41904
RESULT 4
US-10-717-597-68/c
; Sequence 68, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 126990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-68
Query Match 8.9%; Score 444.4; DB 7; Length 126990;
Best Local Similarity 54.1%; Pred. No. 1.1e-90;
Matches 1225; Conservative 3; Mismatches 987; Indels 51; Gaps 14;
Qy 2291 AGCCAGGCGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGCGG 2350
Db 28169 AGCCAGGCGGTGATGGCTCATGCCTGTGATCCAGCACTTTGGGAGGCCAAGGTGGTGG 28110
Qy 2351 ATCACTTGAGGTCAAGATTCGAGACCAGCCTGGCCAAACATGGTGAAACCCCTGTCTCTAC 2410
Db 28109 ATCACGTGAGGTCAAGATTTAGTGGCGTGGTGCGAGACACCTATAGTCTAGTCTAGCTAC 28050
Qy 2411 TAAAAATACAAAAATTAGCCGACATGGTGGGAGCGCC----TGTAACCCAGCTAC 2465
Db 28049 T-AAAAAATACAAAAATTAGTGGCGTGGTGCGAGACACCTATAGTCTAGTCTAGCTAC 27991
Qy 2466 TTGGGAGACTGAGTTGGAGGTTTCAGTGAGCCCAAGGTCGTGTCACTGCTGCCAGCCTGG 2525
Db 27990 TTGGGAGGCTGAGGCGGGGAATCGTTTGAACCCGGGAGGTAGAGGCTGAAGTGAGCTGAG 27931
Qy 2526 GTAACAGAGCAACTCTGTCTCAAA----AAAAAAAATGCTTTCAATAAATATATGATAA 2581
Db 27930 ATCACACCACCTGCACTCCAGCCTAGGTGACAGCAAGGCCTCATCTCAAAAAACAATG 27871
Qy 2582 AAGGACTTATATTTTTCGAAGCCATAGGATCATTTCTCCTGAAGCATCTTGGCGAAGTCA 2641
Db 27870 GTGGCCAGGCACGGTGGCTCACGTCAAGTAATCCCAGCACTTTGGGAGGCCAAGCGCGGC 27811
Qy 2642 TCCCCACCTGTTCTGAGAGTGGCAGGTGAGGCTGACCTATTGCTCTGCACTTACTCC 2701
Db 27810 AGATCATGAGGTCAAGGATCAAGACCATCCTGGCTAAACACGGTGAACCCCGTCTCTAC 27751
Qy 2702 TATCTCAGCTGTCCCTCCCACTTTTCCAGGTGCTGCCAGACACATGACAACCTGCTAYGACC 2761

Db 27750 TAAAAATACAAAAAAATTAGCCGGGCATCGTGGTGGCGCCTGTAATCCAGCTACTTTGGG 27691
QY 2762 AGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCACACCTATT 2821
Db 27690 AGGCTGAGCGGGAGAAATGGCGTGAACCCGGGAGCGGAGCTTGCAGGGAGCGGAGATCG 27631
QY 2822 CATACTCGTCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCTTGACCT 2881
Db 27630 CACTGCTGCGTCCATTCCAGCCTGGGAGACAGAGTGAGACTCCATCTCAAAACAAAACA 27571
QY 2882 ATGAATTTAGTTGGTTCTCAGTAGGCCGGGGGAAATAATAGTAAC-----AACAG 2933
Db 27570 AAACAAAACAAAACAAAGTGGTGGGCATGCCTCTAATCCTAGTACTTGGGAAGGCTGAG 27511
QY 2934 CCATGATTTAGTGTAAATTTCTTGTTCTGGGCAGTGTCTCCTTTAATCCTCAGAACAA 2993
Db 27510 GCAGGAGAATCGCTTGAACCCCGGAAGCAGAGGCTGCAGTGAGCCAAAGATCACACCACTG 27451
QY 2994 CACTATGGGATAGGT-ACAATTATCCTCACTTAACAGATAAGAAAAACTGAGGCTCAGAAG 3052
Db 27450 TACTCCAGCCTGGGTGACAGAACGAGACTCTCCATAAGTTCACATGAAATAACCAACAT 27391
QY 3053 GCTGAGCTATTTGCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTT 3112
Db 27390 TCTAATCCGACACCGCAAGATTTTACTTAGCCTTCACCATGTCCATATCTTTAACTCCTT 27331
QY 3113 GTTGTGTTTAGAGACAGGGTCTTGCTCTGTCACCCCAGGCATGAGCACAGTGGTGCAACC 3172
Db 27330 TCTCTAATGCTGAGATGGAGTCTCACTGTCACCCCAGGCTGGAGTGCAGTGTGATC 27271
QY 3173 ATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCAA 3232
Db 27270 TCA-----CCTCCACCTCCCAGGTTCAAGCGATTCTCTGCTCAGCCTCC-TG 27223
QY 3233 GTAGCTGGGACTACGAGCGTGCACCAACAGCCTGGCTAATTAACAAAAATTTTGTGTAG 3292
Db 27222 GTAGCTGGGAATACAGGCGTGCACCAACCATGCCGGCTAATTTTATA--TTTTCAGTAG 27165
QY 3293 AGACTGGGTCTTACTACGTTGGCCAGGCTGTCTTAAACTCCTGGCTTCAAGCAATCCTC 3352
Db 27164 AGTCGCAGTTTCACCATGTTTCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCCAC 27105
QY 3353 CTACCTTGCGATCCCAAAGTGTGGGATPACAGGGGTGAGCCACCATGTGCGGCTACTTA 3412
Db 27104 CCGCCGCAGCTCCCAACGTCGCTGGGATAATAGGGGTGAGCCACTGCACCTGGCCTTTCT 27045
QY 3413 TTTCTTTTACATCCATCTTTTCCAAATAGAATGTAAGATCCACAGAACAGGGATTACTGCT 3472
Db 27044 GTACTCTTTATTCTATTTCACTGGTCTGTTTCTTTTGGTTTCAGTATCATAGTACTTTG 26985
QY 3473 ATTTTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACTCAACCTCCGTTTCAG 3532
Db 26984 TTTCTGTAGCTTAAAAATAT--ATATATTTAAAGACTGGAATGCAGTGGCATGATCTCAGC 26927
QY 3533 TCACTGCAACCTCTGCCCTCCCGGTTCAAGYGATTCTCCTGCCCTAAGCCTCCTGAGTAGC 3592
Db 26926 TCACTGCAACCTCCACCTCCCAGGCTCAAATATTCTTGTGACTCAGCCTCCTGAGTAGC 26867
QY 3593 TGGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTTTGTATTTTGTAGCAGAGATGG 3652
Db 26866 TGGGATTACAGCAGGCAGCACCAACCATGCCCACTAA-TTTTTGTATTTTCAGTAGAGTGGA 26808
QY 3653 GGTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTGCC 3712
Db 26807 AGTTTCACCATGTTTCTTAGGCTGATCTTAAACTCCTGACCTCAGTGATCCGCCCGCGT 26748
QY 3713 CAGTCTCCCAAGTGTCTGGAATTATAGGCGTGAGTCACTGTGCTGGCCGATTACTGTCT 3772
Db 26747 CAGCCTCCCAAGTGTCTGGGATAACAGGCATAAGCTGCTGCGTGCAGCCTTTCTGTATTC 26688
QY 3773 ATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCA 3832
Db 26687 TTTATTCTGTTTCATTGATCTGTTCCCTTTTGGTTTTCAGTATCATACTATTTTGTGTTGTT

QY 3833 ATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTCTTTTAAAAACAA 3892
Db 26627 TTCTATAGCTTAAAAAATATGTATTTT---TTTGGAGATAGGCTCTCACTGTGTACCCAG 26571
QY 3893 TCTTGACAACTTTTGACAGAAATAATACAATCTTGCAATCTGCTTTTTCACTTATCACCCTTG 3952
Db 26570 GCTGGAGTGTACTGGTGTGATCATGGCTCACTGCATCCTCAACCTCCTATACTCA-ATTG 26512
QY 3953 TTATGACTTTTTTCATPATTCCTCAAAACCTTTATTTGTACTGTTTTTTCATTGTTACTATT 4012
Db 26511 ATCCTCCCACTCAGCCTCCCAAGTAGCTGCACCACCATGTTTGGCTAATTTTAAATTT 26452
QY 4013 TTAGTCACTGAATAATATATGGCTTAATTTTGCTTATACATCCTCCTGCTCCACTTTAGAAAG 4072
Db 26451 TTTGTAGAAAACAGAGTCTTGCCATGTCACCCCAGGCTGGTCTTTGAACCTCCTGGGCTGAAG- 26393
QY 4073 CCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAAATACACACACACA 4132
Db 26392 --AGATCCGCTGACCTCATCTCCCAAAGTCTGGAATTACAGGTGTGCACCACCTTGCC 26335
QY 4133 CACACACTCACACACAGTTTTTTTTTTTAAATGTTTGCAACTAAGACAAGAA-----ACC 4184
Db 26334 CAGCCAAAAATATGTTTTTGGCAGATCACCTGAGCTGGGAGTTCAAGACCAGCCTTGCC 26275
QY 4185 TGCATTAGAGGATGTTTGTTCATATTAAATTAATAAAATAACTCAGTTGGGCACAGTGACTCA 4244
Db 26274 AACATGGCAAAACCTTGTCTCTACTAAAGAATACAAAAATTTATCTGGGCGCAGTGGCTCA 26215
QY 4245 AGCCTGTAACCCACAGTACTTTTGGAAAGTCCAAGTGGGTGGATCACTTGAGGTGAGAAGTT 4304
Db 26214 TGTCTGTAATCCAGTACTCTGGAAGGCCAAGGCAGGTGGATCACCTGAGGTGAGGAGTT 26155
QY 4305 CGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCT 4364
Db 26154 TAAGACCAGCCTGGCCAAACCTGGTGAAACCCCTGTCTCTACTAAAAATACAAAAATTAGCT 26095
QY 4365 GGGTGTAGTGATGCATGCCTCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGC 4424
Db 26094 GGGCGTGGTGACCGGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAAGAGATCAC 26035
QY 4425 TTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCACCTCCAGCCTGG 4484
Db 26034 TTGAACCTGGGAGGTAGAGGTTGCAGTGAGCCGAGATCATGCCATTGCACCTTAGCCTGG 25975
QY 4485 GCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAAATAAA 4530
Db 25974 GTGACAGAGCGAGATTCTGTCTCAAAAAAGAAAAAGAAAAA 25929

RESULT 5
US-10-017-161-1659/c
; Sequence 1659, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1659
; LENGTH: 58448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source

;
; LOCATION: (1) .. (58448)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201) .. (225)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9878) .. (9957)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11015) .. (11151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11245) .. (11963)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12136) .. (12283)
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; NAME/KEY: CDS
; LOCATION: (16345) .. (16400)
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; NAME/KEY: CDS
; LOCATION: (16922) .. (17048)
; FEATURE:
; NAME/KEY: CDS
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17532) .. (17609)
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; NAME/KEY: CDS
; LOCATION: (17717) .. (17816)
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; NAME/KEY: CDS
; LOCATION: (19089) .. (19652)
; FEATURE:
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; LOCATION: (30262) .. (30402)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32047) .. (32232)
; FEATURE:
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; LOCATION: (38643) .. (38797)
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; NAME/KEY: CDS
; LOCATION: (50745) .. (51037)

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57674) .. (58248)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (14021) .. (14120)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (25450) .. (25549)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (32482) .. (32581)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (41206) .. (41305)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (50772) .. (50871)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-1659

Query Match 8.8%; Score 438; DB 6; Length 58448;
Best Local Similarity 50.3%; Pred. No. 2.le-89;
Matches 1980; Conservative 3; Mismatches 1653; Indels 302; Gaps 31;

Qy 799 TATTATTATTCTTATTATTATTGAGACAGAGTCTTGCTTTGTCGCCAAGGCTGGAGTACA 858
Db 36200 TTTTGTGTTTTTTTTTTTTTTTGAGACGGAGTCTCGCTCTGTGCCCCAGGTGGAGTGCA 36141
Qy 859 GTGGTGGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGTTACGCCATTCTCCGGCT 918
Db 36140 GTGGCGCAATCTTGGCTCACTGCAAGCTCCGGCTCCGGGTTACGCCATTCTCTGGCT 36081
Qy 919 CAGCCTCCCCAGTAGCTGGGACTAAAGCGCCTGCCACCACGCCCGCTA-ATTTTTTTG 977
Db 36080 CAGCCTCCCGCTAGCTGGGACTACAGGCGCCTGCCATCAGCCCCAGCTATTTTTTTTG 36021
Qy 978 TATTTTAAATAAGACGGGGTTTCATCGTGTAGCCAGGATGGTCTCGATCTCATGACCT 1037
Db 36020 TATTTTGTAGAGACGGGGTTTACCGTGTAGCCAGGATGGTCTCGATCTCTGACCT 35961
Qy 1038 TGTGATCCGCCTGCCTCGGCTCCCAAAGTGTCTGGGATTACAGGCATGAGCCACCGTGCC 1097
Db 35960 CGTGATCCACCCACCTTGGCCTCCCAAAGTGTCTGGGATTACAGGCGTGAGCCACCGTGCC 35901
Qy 1098 CGGCCCTTATCACATTATTATTATTGTTTTTCTCTCCCACTAGGTTGTAAGTCCATGA 1157
Db 35900 CGGCCGAAACTCAGTT-----TTTTAAAAAAGAGAGGCTGGGCT 35858
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Db 35564 -----AAAAAGAAAA 35555
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RESULT 8
US-10-087-192-844/c
; Sequence 844, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 844
; LENGTH: 91760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(91760)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-844

Query Match 8.7%; Score 433.2; DB 5; Length 91760;
Best Local Similarity 61.6%; Pred. No. 3.5e-88;
Matches 906; Conservative 1; Mismatches 474; Indels 89; Gaps 10;
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QY 4172 AAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATAACTCAGTTGG 4231

Db 18851 AAAACCAAACTAAGCTATTCCCGAGAAGAAATCTGTAATCAAAGATAAGCTCTGCCGG 18910

QY 4232 GCACAGTGACTCAAGCCTGTAAACCACAGTACTTTGGAAGTCAAGGTGGGTGGATCACTT 4291

Db 18911 GCACAGTGGCTCACGC-----CTTTTGGAGGCCAAGCGGGCGGATCACCT 18956

QY 4292 GAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAAT 4351

Db 18957 GAGGTCAGGAGTCTAGACCTGCCAGGCCAACAATGGTAAACCTCATCTCTACTAAAAAT 19016

QY 4352 ACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCAGCTACTCGGGAGGCTGAG 4411

Db 19017 ACAAAAATTAGTAGATGTGGTGGGTACCTGTAGTCTCAGTACCTGGGAGGCTGAG 19076

QY 4412 GCAAGAGAAATTGCTTGAAACCTGGGAGGCAGAGGTTGCAGTGNAGCCGAGATCCCACCACTG 4471

Db 19077 GCAAGAGAAATGCTTGAAACCTGGGAAGTAGAGGTTGCAGTGNAGCCGAGATTGCACCACTG 19136

QY 4472 CACTCCAGCTGGCGCACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAA 4531

Db 19137 CACTCCAGCCTGGGCGACGGAGTGAGACGACCTCACAAAAAATTACATAAATAAATAATGAA 19196

QY 4532 GGATCGGAGAGAAACAAA 4550

Db 19197 AAGTAAAAATAAAAAATACAA 19215

RESULT 10

US-10-322-281-448/c

; Sequence 448, Application US/10322281

; Publication No. US20040126762A1

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc S. Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001000

; CURRENT APPLICATION NUMBER: US/10/322,281

; CURRENT FILING DATE: 2002-12-17

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 448

; LENGTH: 38538

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(38538)

; OTHER INFORMATION: n = A,T,C or G

US-10-322-281-448

Query Match 8.5%; Score 425.4; DB 7; Length 38538;

Best Local Similarity 60.0%; Pred. No. 1.4e-86;

Matches 879; Conservative 1; Mismatches 552; Indels 33; Gaps 9;

QY 3067 CCAAGATCACACAGCTTGTAAGTGGTGACAGTTTGGGTTTTTTTTTTGTTGTTTAGAG 3126

Db 35304 CAAAAAATAAAAAATAAATAATTTTGTTCCTAGATTATAGTTAAGGGGCTTTTGTAG 35245

QY 3127 ACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAGTGGTGCAACCATAGTCACTGCA 3185

Db 35244 ATGAAGTTTGTCTTGTGGCCAGGCTGGAGTGCATGGTGATCTTGGCTCACAGCA 35185

QY 3186 GCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTA 3245

Db 35184 ACCTCCACCTCCAGGTTCAAGCGATTCTCCTCTCAGCCTCCTGAGTAGCTGGGATTA 35125

QY 3246 CGAGCGTGCAACCACGCTGGCTAATTAATAAAAAATTTTTTTGTAGAGACTGGGTCTTA 3305

Db 35124 CAGGCATGCGCCACCACACCCAGCTAATTTTGTGTA---TTTTTAGTAGAGATGGGTTTCT 35068

QY 3306 CTACGTTGGCCAGGCTTGTCTTAAACCTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATC 3365

Db 35067 CCATGTTGGTCAGGCTGGTCTTGAACCTCCTGACCTCAGGTGATCCACCCCTCCTTGGCTTC 35008

QY 3366 CCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTC 3425

Db 35007 CCGAAGTGTGGGATTACAGGCATGAGCCACTGCGCCTGGC-----CTCAGTTAAGGGA 34954

QY 3426 CATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGATTACTGCCCTATTTTCTTCCTTT 3485

Db 34953 CTTTTTACATATTTATTTATTTATTTATTTATTTATTTATTTGAGACGAAGTCTCGCTGTT 34894

QY 3486 CTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTC 3545

Db 34893 GTTCTCCAGGCTGGAGTGCAATGGCAGACC-----TTGGCTCACTGCAACCTC 34845

QY 3546 TGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGC 3605

Db 34844 CGCCTCCCGGTTCAAGCGATTCTCCTGTCTTGGCCTCCCAAGTAGCTGGGATTACAGGC 34785

QY 3606 GTGCACCACCATGCTTGGCTAAATTTTTTGTATTTTAGCAGAGATGGGGTTTTACCATGT 3665

Db 34784 GCCTGCCATCATGCCTGGCTAA-TTTTGTATTTTAGTAGACGCGGTTTCACCATTA 34726

QY 3666 TGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAG 3725

Db 34725 TGGCCAGGCTGGTCTTGAAGTCTGACTTCAGGTGATCTGCCTGCCTCGGCTCCCAAAG 34666

QY 3726 TGCTGGAATTATAGGCGTGAGTCACTGTGCCTGSCCGATTACTGTCTATTTTCTTTATTG 3785

Db 34665 TGCTGGGATGACAGGTGTGAGCCACCACACTCGGCTTTATTTATTTATTTTCGAGACAGG 34606

QY 3786 CTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGAT 3845

Db 34605 GTATCTC-----TCTGTTGCCAGGCTGGAGTGCAGTGGTGCAGTCAAGGCTGGTGTGCA 34552

QY 3846 GAATGCACAGCCTAGATATAAACTTTCTTTTTTCTTTTTTTTAAACAATCTTGACAACTTT 3905

Db 34551 GCCTCAAACTCCTGGGCTCCAGCA--ATTCTCCTGCCTCAGCCTCCTGGGTAGCTGGAAC 34494

QY 3906 GCAGAATAAATACAAATCTTGCAATTCCTGCTTTTTTCACTTATCACCTTGTATGACTTTTTTC 3965

Db 34493 TACAGGTGCAAAATTATCATGCTGCCTGGCTAATTTTTTAAATTTTTTGTCAAGATGGGGTCTCT 34434

QY	3966	ATATTGCTCAAAACCTTTATTGTTACTGTTTTTTTCATTGTTACTATATTTTAGTCACTGAAT	4025
Db	34433	CTATATTGCCAGGCTGGTCTCAAACCTCTGGCCTCAAGTGATCTCCCTTCTGGGCTTCA	34374
QY	4026	AATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACITTTAGAAGGCCAAATTTACAAA	4085
Db	34373	AAAAGTGCTGGGATTATAAGTATGAGCCACCACCTCCGGCCTTCCCTCCTTCCTTCCTTC	34314
QY	4086	TCTGATGAAAGCTATGAACCTCTCTCCCGAGAGAAATACACACACACACACACTCACAC	4145
Db	34313	CTTTCTGCCTTCTCTCCTTCTCAAAAAAATAAAAAAAGAGTCAGTGTTGCTGA	34254
QY	4146	ACAGTTTTTTTTTAATGTTTGCACTAAGACAAGAAACCTGCAATTAGAGGATGTTTGTTT	4205
Db	34253	CTGGTATGTCTGATTACCTGCAATATATGATATATTTATTCCAATAAAGATGCTTGCTTT	34194
QY	4206	ATA--TTAATTAATAAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACT	4263
Db	34193	TTCTTTTGTTAAAAAGTATCCGGCCAGGCGGATGGCTCAAGCTGTAAACCCAGTACT	34134
QY	4264	TTGGAAGTCCAAAGGTGGGTGGATCACTTGAGGTGAGAAGTTTCGAGACCAGCCTGGTCAAT	4323
Db	34133	TTGGGAGGCTGTGGTGGGCGGATCACCTGAGATCAGGAGTACGAGACCAGCCTGGCCAAC	34074
QY	4324	ATGGTGAACCCCTATCTCTACTAAAAATACAAAAAATTAGCTGGGTGTAGTGATGATGCC	4383
Db	34073	ATGGTAAAAACCCCATCTCTACTAGAAATACAAAAATTTAGCTGAGTGTAGTGGCAGCACC	34014
QY	4384	TGTAGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAG	4443
Db	34013	TGTAATCCAGCTACTTGGGAGGCAAGGAGAGAAATTGTTGAACCCGGGAGGCAGAG	33954
QY	4444	GTTGCAGTGAGCCGAGATCCCAACCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTA	4503
Db	33953	GTTGCAGTGAGCCAAGATCACACCAATTGCACCTCCAGCCAGGGGGACA-AGAGAGACTCTG	33895
QY	4504	TCTCAAAAAAATAAAATAAAAT	4528
Db	33894	TCTCAAAAAAATAAAATAAAAT	33870

RESULT 11
US-09-920-671-11
; Sequence 11, Application US/09920671
; Publication No. US20030083283A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF COREST EXPRESSION
; FILE REFERENCE: RTS-0297
; CURRENT APPLICATION NUMBER: US/09/920,671
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 91

	Query Match	8.3%;	Score 416;	DB 3;	Length 139257;
	Best Local Similarity	54.0%;	Pred. No. 4.2e-84;		
	Matches 1222;	Conservative	3;	Mismatches 948;	Indels 89; Gaps 15;
QY	2291	AGGCCAGGCGCGTGGCTCATGCGCTGTAATCCCAGCACCTTTGGGAGGCCGAGGGCGCGG			2350
Db	63398	AGGCTGAGCATAGTGGTCTACACCTGTAATCCTAGCACCTTTGGGAGGCTGAGGCGAGCGCA			63457

Qy	2351	ATCACTTGAGGTCAGGAGTTCGAGACCAAGCCCTGGCCAAACATGGTGAAACCCCTGTCTCTAC	2410
Db	63458	ATTGCCCTGAGGTCAGGAGTTAAAGACCAAGCCCTGGCCAAACATGGTGAAACCCCGTCTCTAC	63517
Qy	2411	TAAAAAATACAAAAATTAGCCGGACATGGTGGGAGCGCCTGTAAACCCAGTACTATTGGG	2470
Db	63518	T-AAAAATACAAAAATTAGCCGGGTGTGGTCACAGGCGTCTGTATCCAGCTACTCAGG	63576
Qy	2471	AGACTGA-GTTGGAGGTTTCAGTGAGCCAAAGGTCGTGTCACTGCTGTCCAGCCTGGGTAA	2529
Db	63577	AGGCTGAGGCAAGAGAAATTCCTTGAACCTGGGAGGTGGAGGTTGCGGTCACTCGAGATCG	63636
Qy	2530	CAGAGCAACTCTGTCTCAAAAAAATAAATGCTTTTCAATAAAATATATGATAAAAGGACTT	2589
Db	63637	CGCCACTGCACCTCCAGCCTGGGCAACAGAGTGAGACTTTTGTGCACACACACACACAC	63696
Qy	2590	ATATTTTTTCAAGCCATAGGATCATTTCTCCTGAAGCATCTTGGCGAAGTCATCCCCACC	2649
Db	63697	ACACACACACACACACGCGTAAATAAACCTATGAACC--AACTAATGCAGTGGATTTC	63754
Qy	2650	TGTTCTCTGAGAGTGGGAGGTGAGGGCTGACCTATTTGCTCTGCACCTTACTCTCTATCTCAG	2709
Db	63755	CAAAATTAAGATTAAAGCTTGTGTAAAGTTGTAATGTTCTTGATGTACCCATTTATTTGAG	63814
Qy	2710	CTGTCCCTCCCACCTTCCAGGTGCTGCCA-GACACATGACAACTGCTAYGACCAGGCCAA	2768
Db	63815	TGGAACACAGATTCTTTTCAATCTTTTGAATCACTTTGCTGAGATTTTTTTTATTTTATA	63874
Qy	2769	GAACTGGAACAGCTGTAATTTCTGCTGGACAMMCGGTACACCCACACACCTATTCATACTC	2828
Db	63875	TTTTTTTTTTGGAGACAGAGTCTCGCTGTGTGCGCCAGACTGGAGTGCAGTGGTGTGATC	63934
Qy	2829	GTGCTCTGGCTCGGCAATCACCTGTAGCAGT-AGGTTTATCCCTTCCTTGACCTATGAAT	2887
Db	63935	TAGGCTCACTGCAACCTCCACCTCCCGGTTCAAGCGATTCTCCTGCCTCAGCTCCTGA	63994
Qy	2888	TCTAGTTGGTTCTCAGTAGGCCGGGGGAAATAATAGTAAACAACAGCCATGATTTAGTGT	2947
Db	63995	GTAGCTAGGATTATAGGCATGTGCCACCACACTCAGCTAATTTTGTATTTTCAGTAGAGG	64054
Qy	2948	TAAATTTTCTTGTTCTGGCAGTGTCTCCTTTAATCTCAGAACAACACTATGGGATAGG	3007
Db	64055	TAGGGTTTCACCATGTAGGCCAGGCTGGTCTCAAACTCCTGACCTCAAGCGATCCGCCTG	64114
Qy	3008	TACAAATTATCCTCACTTAAACAGATAAGAAAACTCAGGCTCAGAAAGGCTGAGCTATTTGCC	3067
Db	64115	CTCAGCCTCCCTGAGTATTGGGATTATAGGTGTGAGCCAC-----GGTGTCCCGC	64164
Qy	3068	CAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTTTAGAGA	3127
Db	64165	CAAGCTGAGACATTTTAAAGAAAATGTTTCTGTTTTTTTGTGTTATTTGTTGTTGTTGAGA	64224
Qy	3128	CAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGC	3187
Db	64225	TGGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCA-----TCACTGCAAC	64277
Qy	3188	CTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCCAAGTAGCTGGGACTACG	3247
Db	64278	CTCTGCCTCCTGGGTTCAAGCAATTCTCCTGTCTCCAGCCTCCTAGGTAACGGGACTGCA	64337
Qy	3248	AGCGTGCAACCACCGCTGGCTAATTAAAAAAATTTTTTTGTAGAGACTGGGTCTTACT	3307
Db	64338	GGCTTGCCACCATATACCTGGCTGATTTTTTTGTATTTTATA-GTAGAGATGGGTTTTTACC	64396

QY	3428	TCTTTCCATAGAAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCCTTTCT	3487
Dd	64516	TTTTTTGAGATCAGGTCTCACTCTGTGCGCCAGGGTGAGTGCAGTCGCGCAATC-----	64570
QY	3488	TTTTTTGAGACAGAGTCTCACATTTCATCACCTCAACCCTCCGTTTCAGCTCACTGCAACCTCTG	3547
Dd	64571	-----TCAGCTCACTGCAACCTCCG	64590
QY	3548	CCTCCCCGGTTCAAAGYATTCTCCTGCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGT	3607
Dd	64591	CCTTCCAGGTTCAAGTGATTCTCTTGCCTCAGCCTCCCACAGCAGGTGGGATTTTCAGGCAT	64650
QY	3608	GCACCACCATGCTTGGCTAAATTTTTTGTATTTTTTAGCAGAGATGGGGTTTTTACCATGTTG	3667
Dd	64651	ACACCACCATGCATGGCTCA-TTTTTTGTATTTTTTAGTAGAGA-GGGGTTTTTCAACATGTTG	64708
QY	3668	CCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTGATCTGCTGCCTCAGTCTCCCAAAGTG	3727
Dd	64709	GCCAGGATGGTGCAGAACTCCTGACCTCATGTGATCCACCGCATCAGCCTCCCAAAGTG	64768
QY	3728	CTGGAATTAFAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTCTTTATTTGCT	3787
Dd	64769	CTGGGATTATAAGCGTGAATCACTGCACCTGGCTAGAAAACATCTTCTAAAGCCTAATCTT	64828
QY	3788	ATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGTGCTCAATAAATAATTGATGA	3847
Dd	64829	TTTTTTTTTTTCCCTTATATAATTTAGGTTGACTATGTAAACCCAAAAACACATAGGGTAGAA	64888
QY	3848	A----TGCACAGCCTAGATATAAACTTTCTTTTCTTTTAAACAAATCTTGACAACT	3903
Dd	64889	ACTCGTGAAAAATATTTTGGAGGATATCTTTTGCAAAGTGTGTGCCTCACGGTGCTGGAT	64948
QY	3904	TTGCAGAAATAAATACAAATCTTTGCAATCTCTGCTTTTTCATTATCACCTTGTATTAGCTTTT	3963
Dd	64949	ATGGATGTGTGCTTAGTGTCAAGTGCAATTTAGGATTTCCACCTGTATGTATGCTTT	65008
QY	3964	TCATATTGCTCAAAACCTTTATTGTACTGTCTTTTTCATTATGTTA--CTATTTTAGTCAC	4020
Dd	65009	TGGTGAGTCCCTTTAGGCGATATGCTCCTCATGTTTCAAGGAGTAATGGCATACTGTTTCAT	65068
QY	4021	TGAATAATATGGCTTAATTTGCTTATACATCTCTGCTCCACTTTAGAAAGGCCAAATTT	4080
Dd	65069	TTAAACCCCATGTTTAAATCCTAAATTAAGACCGATTACITCTTCTTGGAGCTAATTTCT	65128
QY	4081	ACAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAAATACACACACACACACACT	4140
Dd	65129	TAACTTTTCTGATGATGTTTTTTGTGTCTTAAGTTAAGACTAATAATACACAGAACTTAA	65188
QY	4141	CACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTT	4200
Dd	65189	CTCATCCCTTTTGATATTAGAGATTTTGGTTTTATTATCTAGTGGAAATTTTAAATATCAT	65248
QY	4201	TGTTTCATATTAAATTAATAAATACTCA-----GTTGGGCACAGTGACTCAAGCTG	4250
Dd	65249	TTTACATGTTTACTCTCAAGATCTGATGATTGACTGCTGGGTGCAGTGGATCACACCTG	65308
QY	4251	TAAACCACAGTACTTTGGAAGTCCAAGTGGGTGGATCACTTCAGAGTGAGAAGTTCCGAGAC	4310
Dd	65309	TAAATCTCAGCACTTTGGGAGGCCAAGGCGGGCAGATCACTTCAGGTTCAGGATTCGAGAC	65368
QY	4311	CAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGT	4370
Dd	65369	CAGCCTGGCTAACATGGTGAAACCCCTGTCTGTAGTAAAAATACAAAAATTAGCCCGACTT	65428
QY	4371	AGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAAC	4430
Dd	65429	GGTGGTGGCTGCTGTAAATCCAGCTACTGGGGAGACAGAGGTGAGAGAAATCACTTGAAC	65488
QY	4431	CTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCATCCAGCCTGGGGCACA	4490
Dd	65489	CCCAGAGGCGGAGGTTGCAGTGAGCCTAGATCACTCCATTGCACTCCAGCCTGGGGCACA	65548
QY	4491	CAGCGAGACTCTATCTCAAAAAAAAAATAATAAATAAATAAAG	4532

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Db      65549 GAGTGAGACTCCGTCCTCAAAAAAAAAAAAAAAAAAAAAAGAG 65590
|||||
RESULT 12
US-10-719-993-6883/c
; Sequence 6883, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6883
; LENGTH: 187844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(187844)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-3)
US-10-719-993-6883

Query Match      8.3%; Score 414.6; DB 8; Length 187844;
Best Local Similarity 60.7%; Pred. No. 1.1e-83;
Matches 868; Conservative 3; Mismatches 462; Indels 98; Gaps 8;

QY      3105 TTTT...TTTGTGTTAGAGACAGGGTCTTGCTCTGTACCCAGGCGATGAGCACAGTG 3164
Db      94170 TTCATTCA...TTTCGAGATGGGGTCTTGCTCTGTGTCCAGGCTGGAGTGAATG 94111

QY      3165 GTGCAACCATAGGTCACGAGCGCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAG 3224
Db      94110 GTGCAATCTCGGCTCACTGCAACCTCCACCTCCAGGATTCAGTGATCTCTCTGCTCAG 94051

QY      3225 CCTCCCAAGTAGCTGGGACTACGAGCGTGCACCCACGCGCTGGCTTAATTA...AAATTT 3284
Db      94050 CCTCTGAGTAACTGGGATTACAGACMCCTGCCACCCACACCGGCTAATTTTGTGTA--TT 93993

QY      3285 TTTTGTAGAGACTGGGCTTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCAAG 3344
Db      93992 TTAGTAGAGATGGAGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAAA 93933

QY      3345 CAATCCTCTACCTTGGATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCG 3404
Db      93932 GGATCCACCCACCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCGCCCA 93873

QY      3405 GCTACTTATTTCTTTACATTCATCTTTCCAAATAGAATGTAAGATCCACAGAACAGGGAT 3464
Db      93872 GCCATGTACATTTATAATGTACTATATCTCCTTTGGT-----CACCATCTTGCTCT 93822

QY      3465 TACTGCCCTATTTTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCTC 3524
Db      93821 TTTT...TTTTTTTTTTTTTTTTTTTGTGAGACAGAGTCTTGCTCTGTCGCCCGAGGCTGG 93762

QY      3525 CGT-----TCAGCTCACTGCAACCTCTGCTCTCCCGGTTTCAAGYATTTCTC 3570
Db      93761 AGTGCAGTGGCGGATCTCGGCTCACTGCAAGCTCCGCTCCTTGCTCAAGCCATTTCTC 93702

QY      3571 CTGCGCTAAGCCTCTCTGAGTAGCTGGAATTACAAGCTGTCACCACTGCTGGCTAATTT 3630
Db      93701 CTGCTCAGCCTCCAGAGTAGCTGGGACTACATGTGCCACCAACCCAGCCCGGAGAAATTT 93642

QY      3631 TTTGTATTTT...TAGCAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTG 3690
Db      93641 TTTGTATTTT...TAATGGAGACGGGGTTTTTACCCGTTGTAGCCAGGATGGTCTCGATCTCCTG 93582

QY      3691 ACCTCAAGTGATCTGCCTGCCTCAGTCTCTCCCAAAGTGTGGAATTATAGGCGTGAGTCAC 3750
|||||

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Db 93581 ACCTC--GTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGAGTGAGCCAC 93524
Qy 3751 TGTGCTGGCCGATTACTGCTATTTTCTTTATTGCTATATFCCCCAGATCTAGAGCAGTG 3810
Db 93523 TGGGCCCGCCACACACCTCGTCTCTGATGCTTTTTTTTTTCACTTCTGGAGAG----- 93469
Qy 3811 TCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTT 3870
Db 93468 -----AGGAAATC 93461
Qy 3871 TCCTTTTCTTTTAAACAATCTTGACAACTTTGCAGAAATAAATACAATCTTGCAATC 3930
Db 93460 TATATGTTCTTCAACATATCTCTAATACCTTCTTTACCTTCTCTCTAATATCTAATACTA 93401
Qy 3931 TGCTTTTCACTTATCACCTTGTATGACTTTTTTCATATTTGCCCTCAAACCTTTATGTTA 3990
Db 93400 TATATACATACATATAGTGTGTATATATATATGCAATGTATATATAGTATTATATGTATAT 93341
Qy 3991 CTGTTTTCATTTGTTACTATTATTTAGTCACTGAATAATATGCTTAATTTGCTTATACAT 4050
Db 93340 ATATAATAACAGGTTCTTATTATGTTATCCATTGCTTGAATTAACAATGTTTTTTTCA- 93282
Qy 4051 CCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTC 4110
Db 93281 -----AAACCTATAAAAGACCTTAAACAAGRTAAGGATGAGAGGAACCTTGAGTTGC 93229
Qy 4111 CCCAGAGAAATACACACACACACACACTCACACACAGTTTTTTTTTTTAAATGTTGCAAC 4170
Db 93228 CCAAGATAAAATTTTGTCTCAAAGTCTCTCACTTTTGTTCATGTTGTTTAAATCTCTCAATA 93169
Qy 4171 TAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATAAATAAA-----CTCA 4226
Db 93168 TATTTAATCTATTGGCAATTACAATAATTTTGTTTTGGTCACAAAAAATAAGCTCCTGG 93109
Qy 4227 GTTGGGCAAGTGACTCAAGCCTGTAAACCAAGTACTTTTGGAAAGTCCAAGGTGGGTGGAT 4286
Db 93108 GCTGGACAGGTGGCTCACGCCCTGTAATCCCAGCACTTTTGGAGGCCGAGAGGGTGGAT 93049
Qy 4287 CACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGTTGAAACCTTATCTCTACTA 4346
Db 93048 CAC--CAGGTCAAGAGATGGAGACCATCCTGGCCAACATGGTAAAACTCTGTCTCTACTA 92991
Qy 4347 AAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGGAGG 4406
Db 92990 CAAATACAAAAATTAGCTGGCGTGTGGCATGCGCCTGTAGTCCCAGCTACTCRGGAGG 92931
Qy 4407 CTGAGGCAAGAAATTTGCTTGAACTTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCAC 4466
Db 92930 CTGAGGCAGAGAACTGCTTGAACTTGGAGGCAGACGTTTGACGGAGCTGAGATCACGC 92871
Qy 4467 CACTGCCTCAGCCTGGCGACACAGCGAGACTCTATCTCAAAAAATAA 4517
Db 92870 CACTGCCTCCAGCCTGGGTGACAGAGCGAGACTCTATCTCAAAAAATAA 92820

RESULT 13

US-10-087-192-484/c
; Sequence 484, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 484
; LENGTH: 196686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(196686)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-484

Query Match 8.3%; Score 414.2; DB 5; Length 196686;
Best Local Similarity 60.7%; Pred. No. 1.3e-83;
Matches 869; Conservative 1; Mismatches 464; Indels 97; Gaps 8;

Qy 3105 TTTT TTTT TTTT TTTT TAGAGACAGGGTCTTGCTCTGTCACCCAGGCAATGAGCACAGTG 3164
Db 98993 TTCATTCA TTTTATTTCATTCGAGATGGGGTCTTGCTCTGTGTCAGGCTGGAGTGAATG 98934
Qy 3165 GTGCAACCATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAG 3224
Db 98933 GTGCAATCTCGGCTCACTGCAACCTCCACCTCCAGGATTCAGTGATTCTCCTGCCTCAG 98874
Qy 3225 CCTCCCAAGTAGTGGGACTACGAGCGTGCACACCCACGCCCTGGCTAATTAATAAAATTT 3284
Db 98873 CCTCCTGAGTAACCTGGATTACAGACACCTGCCACCAACCCGGCTAATTTTGTATA--TT 98816
Qy 3285 TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAG 3344
Db 98815 TTTAGTAAAGATGGAGTTTCAACCATGTTGGCCAGCCTGGTCTCAAACCTCCTGACCTCAA 98756
Qy 3345 CAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCG 3404
Db 98755 GGATCCACCCACCTTGGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGCCCCCA 98696
Qy 3405 GCTACTTATTTCTTTTACATTCCATCTTTTCCAATAGAATGTAAGATCCACAGAACAGGGAT 3464
Db 98695 GCCATGTACATTTATAAATTGTAATAATACTCCTTTGGT-----CACCATCTTGTCTT 98644
Qy 3465 TACTGCCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTCATCACTCAACCTC 3524
Db 98643 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TGAGACAGAGTCTTGCTCTGTGCCAGGCTGG 98584
Qy 3525 CGT-----TCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAAGYGAATCTC 3570
Db 98583 AGTGCAGTGGCGGATCTCGGCTCACTGCAAGCTCCGCCTCCCTGGTCAACGCCATCTC 98524
Qy 3571 CTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTT 3630
Db 98523 CTGCCTCAGCCTCCAGAGTAGCTGGGACTACATGTGCCACCAACCAACCGCCGGGAGAAATTT 98464
Qy 3631 TTTGTATTTT TAGCAGAGATGGGGTTTTTACCATTGTTGCCAGGCTGGTCTCAAACTCCTG 3690
Db 98463 TTTGTATTTT TAATGGAGACGGGGTTTACCCGTGTAGCCAGGATGGTCTCGATCTCCTG 98404
Qy 3691 ACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGGCGTGAGTCAC 3750
Db 98403 ACCTC--GTGATCCACCCACCTCAGCCTCCCAAAGTCTGGGATTACAGGAGTGAGCCAC 98346
Qy 3751 TGTGCTTGGCCGATTAATGCTATTTTCTTTATTGCTATATCCCAGATCTAGAGCAGTG 3810
Db 98345 TGGCCCCGGCCACCACCTCGTCTTCTGATTGCTTTTTTTTTCACCTTCTTGAGAG----- 98291
Qy 3811 TCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTT 3870
Db 98290 -----AGGAAATC 98283
Qy 3871 TCCTTTTCTTTTAAACAATCTTGACAACCTTTGCAGAAATAAATACAATCTTGCAATC 3930
Db 98282 TATATGTTCTTCAACCATATCTCTAATACCTTCTTTACCTTCTCTCTAATATCTAATACTA 98223
Qy 3931 TGCTTTTTCACCTTATCCTTGTATGACTTTTTTCATATTGCCTCAAACCTTTTATGTTA 3990
Db 98222 TATATACATACATATAGTGTATATATATATATGCAATGATATATATATATATATATATAT 98163

QY	3991	CTGTTTTTTCATTGTTACTATTATTTAGTCACCTGAATAATATGGCTTAATTTGCTTATACAT	4050
Db	98162	ATATAATAAACCAAGGTTCTTATTATTATGTATCCATTGCTTGAATAACAATGTTTTTTCATCA-	98104
QY	4051	CCTCCTGCTCCACTTTAGAAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCCTCTC	4110
Db	98103	-----AAACCTATAAAAAGACCTTAAACAAGGTAAGGATGAGAGGAACCTTGAGTTGC	98051
QY	4111	CCAGAGAAATACACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGC AAC	4170
Db	98050	CCAAGATAAAATTTTGTCTCAAAGTCTCTCACTTTGTGTTTCATGTGTTTAAATCTCTCAATA	97991
QY	4171	TAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAATAA---CTCA	4226
Db	97990	TATTTTAACTATTGGCAATTACAATAAATTTTGTGTTTGGTCACAAAAAATAAGCTCCTGG	97931
QY	4227	GTTGGGCACAGTGACTCAAGCCTGTAACCAACACAGTACTTTTGGAAAGTCCAAGGTGGGTGGAT	4286
Db	97930	GCTGGACACGGTGGCTCACGCCCTGTAATCCCAGCACCTTTTGGAGGCCGAGGAGGTTGGAT	97871
QY	4287	CACTTGAGGTGAGAAATTTCGAGACCAGCCCTGGTCAATATGGTGAAACCCCTATCTCTACTA	4346
Db	97870	CAC--CAGGTCAGGAGATGGAGACCATCTCTGGCCAAACATGGTAAAACTCTGTCTCTACTA	97813
QY	4347	AAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCCTGAGTCCCAGCTACTCGGAGG	4406
Db	97812	CAAATACAAAAAATTAGCTGGGCGTGGTGGCATGCGCCTGTAGTCCAGCTACTCGGAGG	97753
QY	4407	CTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCAC	4466
Db	97752	CTGAGGCAGGAGAACTGCTTGAACCTGGGAGGCAGACGTTGTCAGCGAGCTGAGATCAGC	97693
QY	4467	CAC TGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAA	4517
Db	97692	CAC TGCACTCCAGCCTGGGTGACAGCGAGACTCTATCTCAAAAAATAA	97642

RESULT 14

US-10-317-500-4/c

; Sequence 4, Application US/10317500

Publication No. US20040115637A1

GENERAL INFORMATION:

; APPLICANT: Robert McKay

APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: MODULATION OF PPAR-ALPHA EXPRESSION

; FILE REFERENCE: RTS-0380

; CURRENT APPLICATION NUMBER: US/11

; CURRENT FILING DATE: 200

; NUMBER OF

; SEQ ID NO 4

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; LENGTH: 8

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TYPE: DNA

; ORGANISM

FEATURE:

Query Match	8.3%;	Score 413.6;	DB 7;	Length 86001;
Best Local Similarity	61.0%;	Pred. No. 1.2e-83;		
Matches 878; Conservative	1;	Mismatches 490;	Indels 71;	Gaps 10;

Qy	3105	TTTTTTTGTGTTGTTT	TAGACAGGGTCTT	GTCTGTCA	CCAGGCATGAG	CAGTG	3164
Db	69229	TTTTTTTTTCTTTTTT	TGACGGAGTGC	ACTCTGTG	CCCGAGGCTGGAGTGC	CAGTG	69170
Qy	3165	GTGCAACCATAGGT	CAC	TGCAGCCTCA	ACCTCCTGAGCTCA	AGGGATCTGCTGACCTCAG	3224
Db	69169	GTGCGATCTCAGCT	CAC	TGCAACCTCCG	CCTCCCGGGTTCAAGCTATTTCTCCTGTCTCAT		69110
Qy	3225	CCTCCCAAGTAGCT	TGGGACTACGAGCGTGC	ACCA	CCACGCTGGCTAATTA	AAAAAATTT	3284
Db	69109	CCTCCCAAGTAGCT	TGGGATTACAGGTGTGC	ACTACCATGCC	CAGCTAATTTTGTGA--TT		69052

Db 68040 GGGCATGGTGATGTAAGTCTGTAGTCCAGCTACTCAGGAGGCTGAGGTAGGACAATCAC 67981
Qy 4425 TTGAACCTGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCAACCACTGCACCTCCAGCCTGG 4484
Db 67980 TTGAACCCAGAGCGGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACCTCCAGCCTGC 67921
Qy 4485 GCGACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAA 4544
Db 67920 GCGACAGAGTGAGACTCCATCTCAAAAAATAAATAAATAAATAAAGAAAGAAAGAAA 67861

RESULT 15
US-10-085-117-328
; Sequence 328, Application US/10085117
; Publication No. US2003023234A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 45367
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-328

Query Match 8.3%; Score 412.4; DB 6; Length 45367;
Best Local Similarity 54.4%; Pred. No. 1.5e-83;
Matches 1322; Conservative 2; Mismatches 918; Indels 190; Gaps 17;

Qy 2279 AAAATCGCTTTCAGGCCAGGCGGGTGGCTCATGCTGTAATCCAGCACCTTTGGGAGGC 2338
Db 38718 AAAATGAAGTCAAGGCCGGGTGCGGTGGCTCAGCCTGTAATCCAGCACCTTTGGGAGGC 38777
Qy 2339 CGAGCGGGCGGATCACTTTAGGTCAGGAGTTTCGAGACCAGCCTGGCCAAACATGGTGAAA 2398
Db 38778 TGAGGTGGGCAGATAACCTGAGTCAGAAAGTTCAAGACCAGCCTGGCCAAACATGGCGAAA 38837
Qy 2399 CCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTAACCC 2458
Db 38838 CCCTGTCTCTAC-CAAAAAATACAAAACTTAACTGGGCATGGTGGCCCCATGCCTGTAACCC 38896
Qy 2459 CAGTACTTTGGGAGACTGAG-----TTGAGGTTTCAGT 2492
Db 38897 CAGTACTCGGCGGGCTGAGGCAGGAGAAATCACTTGAACCCAGGATGTGGAGGTTGCAGA 38956
Qy 2493 GAGCCAAGGTCGTGTCACTGCTGTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAA 2552
Db 38957 GAGCGGAGCTTGTGCCACTGCACTTCAGCCTGGGTGACAGAGCAAGACTCTGTCTCAAAA 39016
Qy 2553 AAAAAATGCTTTCAATAAATATATGATAAAAGGACTTATATTTTCAAGCCATAGGATC 2612
Db 39017 AAAAAAGAAAGTCAGTTGCTCAAGGCCATTCCAACTCAACATT-----CACACTCGGGTC 39071
Qy 2613 ATTTCTCCTGAAGCATCTTTGGGGAAGTCATCCCCACCTGTTCCCTGAGAGTGGGAGGTGA 2672
Db 39072 TTTTGATACCAACGCCAGCGGCTGAAATGATCAAACTGTTT--TTAGATGGAGAAACTGA 39129
Qy 2673 GGGCTGACCTATTGCTCTGCACTTACTCCTATCTCAGCTGTCCCTCCCACTTTCAGGCTG 2732
Db 39130 GGCATGGA--AGGCGAGTGTCTGCACCAGTGTCTATGCTGGGACTCACCCCTGGGGAACT 39187
Qy 2733 CTGCCAGACACATGACAACTGCTAYGACCAGGCCAAGAGCTGGACAGCTGTAAATTCT 2792
Db 39188 GAGGAGGGGATTGTCCTTGTG---GGACTGGAGGAGCTGATGGATTTAGAAAGCTTGTGG 39243

Qy 2793 GCTGGACAMMCCGTACACCCACACCTATTTCATCTCGTCTGCTCTGGCTCGGCAATCACCTG 2852
Db 39244 GCAGGACACCGTGTCTCAGCCCTGGGCTGGGAGAGTAACACAGCCTCTGCATTCA---- 39299
Qy 2853 TAGCAGTAGGTTTATCCCTTCCCTTGACCTATGAATTCTAGTTGGTTCTCAGTAGGCCGGG 2912
Db 39300 -----AAAAAGCTTAG 39310
Qy 2913 GGGAAATAATAGTAACAACACAGCCATGATTTAGTGTAAATTTCTTGGTCTCGGCGAGTGT 2972
Db 39311 CCCAGTGAGACAAAACAGCATCTACTTTCTCTACTGAGCTCCAGAGCAGAGGCTAACTA 39370
Qy 2973 CTCCTTTAATCCTCAGAAACAACACTATGGGATAGGTACAATTATCCTCACTTAAACAGATA 3032
Db 39371 AGCCTCAGCTTCTACTTCTGCCATGAGAGTGAAAAATTTAACTTCACCATGTTCTCGTAA 39430
Qy 3033 AGAAAACTGAGGCTCAGAAGGCTGAGCTATTTGCCCAAGATCACACAGCTTGTAAAGTGGT 3092
Db 39431 GGATGCCAATTGCAGAAGCCACTTGCTTTGCCACTGTGGGGTGCCAGTGTAAAGATAA 39490
Qy 3093 GACAGTTTGGGTTTTTTTTTGTGTTGTTTGTGTTTAGACACAGGCTCTTGCTCTGACCCAGGC 3152
Db 39491 CAGAACTTTTTTATCTTTTTTTTTTTTTTTTGTGAGACGGAGTCTTGCTCTGCGCCAGGC 39550
Qy 3153 ATGAGCACAGTGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATC 3212
Db 39551 TGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAAGCTCTGCCTCCCAGGTTTCACACCACTT 39610
Qy 3213 TGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCACCGCTGGCTAA 3272
Db 39611 CTCCTGCTTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCACACCATGCC---CTAA 39667
Qy 3273 TTAAAAAAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACT 3332
Db 39668 TTTTCTGTACTTTTAGTAAGACAGGGTTTCACCATGTTAGCCAGGATGGTCTGGATCT 39727
Qy 3333 CCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAG 3392
Db 39728 CCTGACCTCATG--ATCCACTTGCCTCAGCTTCCCAAAGTCTGGGATTACAGGTGTGAG 39785
Qy 3393 CCACCATGTGCGGCTACTTATTTCTTTACATTCCTATCTTTCCAATAGAAATGTAAGATCCA 3452
Db 39786 CCACTGCGCCTGGCCTTTTTTTTTTTTTTTTCTTTTGAGA----- 39822
Qy 3453 CAGAACAGGGAATFACTGCCTATTTTCTTCTCTTCTTTTGTGAGACAGAGTCTCACTTCAT 3512
Db 39823 -----CTGAGTCTCGTTGTGTGCGCCAGGCTGGAGTGCAG 39857
Qy 3513 CACCTCAACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTTCTCCT 3572
Db 39858 TGGTCCAATC-----TTGGCTCACTGCAACCTCTGCCTCTCTGGGTTCAACAGATTCTCCT 39912
Qy 3573 GCCTAAGCCTCCTGAGTAGCTGGAATTACAAAGCGTGCACCACCATGCTTGGCTAATTTT 3632
Db 39913 GCCTCAGACTCCCAAGTATCTGGGATTACAGGCGCCTGCCAACACACCTGGCTAA-TTTT 39971
Qy 3633 TGTATTTTTTAGCAGAGATGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGAC 3692
Db 39972 TGTATTTTTTAGGAGAGACGGGGTTTCCACCATCTTGGCCAGACTGGTCTCAAACTCCCGAC 40031
Qy 3693 CTCAAGTGATCTGCTGCCTCAGTCTCCCAAGTGTGGAATTATAGGCGTGAGTCACTG 3752
Db 40032 CTCAGGTAATCCACCTGCCTTGGCCTCCCAAAGTGTGGGATTACAGGCGATGAGCCACCG 40091
Qy 3753 TGCCTGGCCGATTACTGTCTATTTTCTTTA-----TTGCTATATCCCCAGATCTAG 3803
Db 40092 AGCCTGGCCAGAAATAAGATAATCTTAAACAATCATGGAGTGTCTAGTAGTCCAGACAC 40151
Qy 3804 AGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATA 3863
Db 40152 GGCAGTGCAGGCTCTACCTACATCGCTCCATGAAACTTTTCATAAAAAACCCATCAGGAAG 40211
Qy 3864 TAAACTTTCTTTTCTTTTTTTTTTAAACAATCTTGACAACCTTTGCAGAAATAAATACAATCT 3923

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Db 40212 GTGTGATTATATCATCTCTGTTTTTATAGTAGAAGAACCCAGTCTTCAAGGGGTAAAAA 40271
QY 3924 TGCATTCTGCTTT-TTCACCTTATCACCTTGTTATGACTTTTTTCATATTGCCTCAAAACCTT 3982
Db 40272 ATCACTACCCCAAGGTCACACAAGCACAGGAGCCAGGACTTGAACCAAGATCAGTTTTAT 40331
QY 3983 TATTGTTACTGTTTTTTCATTGTTACTAATTTTAGTCACTGAATAATATGGCTTAATTTGC 4042
Db 40332 GCCAGGTTCAAACCCCTTAAGTCCAGTGATTTGATTTCACTAGAACGAGCATAAATGTTG 40391
QY 4043 TTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGAAGCTATGA 4102
Db 40392 TGGGAAAAGTACAAAAACACCTATCAGCTGTGACATCCAGTTTTAGTTCTGAACAGACTG 40451
QY 4103 ACCCTCTCCCCAGAGAAATACACACACACACACACTCA-----CACA 4146
Db 40452 CACATTAATTTGTTTAAATAGCCATGATAAAATGATGATAGCACTCATTTGTTGAGCATA 40511
QY 4147 CAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCAATTAGAGGATGTTTGTTC- 4205
Db 40512 CGCTTTTCTTGCAAGTATCACAATACTGATAACAGACCTCAGAGGAAAGTATTATTTTCC 40571
QY 4206 -----ATATTAATTAATAATACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACA 4256
Db 40572 TGACTTTTATAGATGAATAAACATCTCAGGGCCGAGGGCTGCTGCTGTAATCC 40631
QY 4257 CAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTTCGAGACCAGCCT 4316
Db 40632 CAGCACTTTGGAGGCCAAGGCAGGAGGATCGCTGAGGTGAGGATTCGAGACCAGCCT 40691
QY 4317 GGTCAATATGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGAT 4376
Db 40692 GGCCAACATGGCAAAACCCCATCTCTACTAAAAACACAAAAATTAGTTGGGTGTAGTGGC 40751
QY 4377 GCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGA 4436
Db 40752 AGTGCCCTGCAGTCCCACCTACTTTGGGAGGCTAAGGCAGGAGAAATCGCTTGAACCCAGGA 40811
QY 4437 GGCAGAGGTTGCAGTGAGCCGAGATCCCACCACCTGCATCCAGCCTGGCGGACACAGCGA 4496
Db 40812 GCGGAGATTGCAGTGAACCTGAGATCGTCCATTGCACTCCAGCCTGGGAGACAGAGCAA 40871
QY 4497 GACTCTATCTCAAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAAACTAATA 4556
Db 40872 GACTTCGTCTCAAAAACAAAACAATCTTAGAGAGATTGTTTGAAACTCACACAACACGTGAA 40931
QY 4557 AGATTCCCTGAAGGTAA--GCAGAGATACGTAAATATATATGTAATAAAGTTTAAATGCATT 4614
Db 40932 ATGTGGCTGATCCAAATTGAGATGCTCTGTGAAATATACACCAGATTTCAAAGACTTA 40991
QY 4615 TTAAGTGAATCTTATTGTTTATTTTGGTTAT 4646
Db 40992 GTATCAGAAAGAGAAATTAAATATTTTCTTTTT 41023
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RESULT 16
US-10-322-281-314/c
; Sequence 314, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314
; LENGTH: 227246
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(227246)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-314

Query Match      8.1%; Score 405.8; DB 7; Length 227246;
Best Local Similarity 59.7%; Pred. No. 1.3e-81;
Matches 898; Conservative 1; Mismatches 558; Indels 48; Gaps 11;

QY 3082 TTGTAAGTGGTGACAGTTTGGGTTTTTTTTTTTGTGTGTTTAGAGACAGGGTCTTGC-TC 3140
Db 140336 TGGTAATTGTAACTTTTTTTTCTTCTTTTTTTTATTTTCTGAGACGGAGTTTGTCTTC 140277
QY 3141 TGTCAACCCAGGCATGAGCACAGTGGTGCAACCACTAGGTCACTGCAGCCTCAACCTCCTGA 3200
Db 140276 TGTCAACCCAGGCTGGAGTGCAATGGCATGATCTTGGCTCACTGCAACCTCTGCAATCCCG 140217
QY 3201 GCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCAACACC 3260
Db 140216 GTTCAAGCAATTCTCCTGCCTCAGCCACCTGAGTATCTGGGATTACAGGCACGTCGCCACC 140157
QY 3261 ACGCCTGGCTAATTAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGC 3320
Db 140156 ACACCTGGCTAATTTTGTGTA--TTTTAAGTAGGACAGGGTTTCGCAATGTTGGCCAGGC 140099
QY 3321 TTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCCAAAGTGTGGGAT 3380
Db 140098 TGGTTTCAAACCTCTGACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGTGGGAT 140039
QY 3381 TACAGGGGTGAGCCACCATGTGCGGCTACTTAATTTCTTTTACATTTCCAAATAGA 3440
Db 140038 TACAGGCGTGAGCCACCACACTTGGCCCTACTTTTGTGTTGTTTCTTTTT----- 139988
QY 3441 ATGTAAGATCCACAGAACAGGGATTACTGCCCTAATTTTCTTCTTTTGTGAGACAGA 3500
Db 139987 -----GAGATAAGGTCTCACTTTGTTGCCAGGCTGGAGTGCAGTG 139947
QY 3501 GTCTCACTTCATCACCTCAACCTCCGTTTCAGTCTCACTGCAACCTCTGCCCTCCGGGTTCA 3560
Db 139946 GTGTAATCTTGGCTCAGTAGCATGATCTTGGCTCACTGCAACCTCTGCATCCCAGGTTCA 139887
QY 3561 AGYGATTCTCCTGCCCTAAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCCACCACCATGCT 3620
Db 139886 AGCAATTCTCCTGCCCTCAGCCACCTGAGTATCTGGGATTACAGGCACGTGCCACCACACC 139827
QY 3621 TGGCTAATTTTGTATTTTACGACAGATGGGTTTATCCATGTTGCCCAGGCTGGTCT 3680
Db 139826 TGGCTAA-TTTTTGTATTTAAGTAGGGACAGGGTTTCGCAATGTTGGCCAGGCTGGTTT 139768
QY 3681 CAAACTCCTGACCTCAAGTGATCTGCCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGG 3740
Db 139767 CAAACTCCTGACCTCAGGTGATCCGCCCGCCTCGGCCTCCCAAAGTGTGGGATTACAGG 139708
QY 3741 CGTGAGTCACTGTGCCTGGCCGA--TTACTGTCTATTTTCTTTTATTTGCTATATCCCCAGA 3798
Db 139707 CGTGAGCCACCACACTTGGCCCTACTTTTTTGTGTTGTTTCTTTTGTAGATAAGGTCTCAC 139648
QY 3799 TCTAGAGCAGTGTCTGACATATAGTAG-GTGCTCAATAAAATAAATTTGATGAATGCACAGCC 3857
Db 139647 TTTGTTGCCCAGGCTGGAGTGCAGTGGGTAGTCTTGGCTCAGTAGCATGATCTTGGCTC 139588
QY 3858 TAGATATAAACTTTTCTTTTCTTTTAAACAAATCTTGACAACCTTTGCAGAATAAATA 3917
Db 139587 ACTGCAACCTCTGCCTCCTGGGTTCAAGTAATTTCTCCTGCCTCAGCCTCCAGAGTAGCTG 139528
QY 3918 CAATCT-TGCATTTCTGCTTTTTCACCTTATCACCTTGTATGACTTTTTTTCATATGCGCTCA 3976
Db 139527 GAATTACAGGGCGCCGCCACCATACCTAGATAAATTTTATATTTTGTAGTAGAGATTTCAC 139468
QY 3977 AACCTTTTATTGTTACTGTTTTTTTTCATTGTTACTATTTTGTAGTCACTGAATAATATGGCTTA 4036
Db 139467 CATGTTGGCCAGGCTAGTCTCGACATCCGACCTCAGGTGATCGCCTGCCTCAGCCTCCCA 139408
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Qy 4037 ATTTGCTTATACATCCTCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAG 4096
Db 139407 AAATGCTGAGATTACAGCATGTGCCACCGCACCCAGCCTATGTTGATTTTGTGGAAC 139348
Qy 4097 CTATGAACCCCTCTCCCCAGAGAAA--TACACACACACACACACACTCACACACAGTTTT 4153
Db 139347 CACCATGCTTGTTTCCACAGTGACTTCACCATTTTACGTTCTCTACCAGTGGTGATGAA 139288
Qy 4154 TTTTAAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATAAT 4213
Db 139287 GGTCCCAATTTCTCCACATCCTCACCAACACTTATTATCTGTCTGTTTGGTTATAGTCCT 139228
Qy 4214 TAAAAATAAACTCAGTTG-----GGCACAGTGACTCAAGCCTGTAACCCACAGTACTTTG 4266
Db 139227 AAGAAAGTGGTATCTCAGGGGCCAGGTGCAGTGGCTCATGGCTGTAATTCAGGAGTTTG 139168
Qy 4267 GAAGTCCAAGGTGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATG 4326
Db 139167 GGAGSCCAAGGTGGACAGATCACTTTAGGTcAGGAGTTCGAGACCAGCCTGGCCAAcATG 139108
Qy 4327 GTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCGTGT 4386
Db 139107 GTGAACAGCATCTCTACT-AAAAATACAAAAATTAGCTGGGTGTGGGGCAGGCACCTGT 139049
Qy 4387 AGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAG-GCAGAGGT 4445
Db 139048 AATCCAGCTACTCGGGAGGCTGAGGCAGGAGAAATTGCTTAAATCTGGGGGTGCGGAGGT 138989
Qy 4446 TGCAGTGAGCCGAGATCCCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATC 4505
Db 138988 TGCAGTGAGCCAAGATCGCGCCACTGCACCTCCAGCCTGGGAGACAGAGCAAGACTCGTC 138929
Qy 4506 TCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAAACTAATAAGATTCTCTG 4565
Db 138928 TTGGAAAAAATAAATAAATAAAGAGAAAAAGAAAAAGTGGTATCTCATTTAGTG 138869
Qy 4566 AAGGT 4570
Db 138868 ATGAT 138864

RESULT 17
US-09-740-043-3/c
; Sequence 3, Application US/09740043
; Publication No. US20020086810A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000972
; CURRENT APPLICATION NUMBER: US/09/740,043
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23639
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(23639)
; OTHER INFORMATION: n = A,T,C or G
US-09-740-043-3

Query Match      8.1%; Score 403.6; DB 3; Length 23639;
Best Local Similarity 59.6%; Pred. No. 1.1e-81;
Matches 882; Conservative 1; Mismatches 545; Indels 52; Gaps 10;
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Qy 3099 TTGGGTTTTTTTTTGTGTTAGACACAGGGTCTTGCTCTGTCAACCCAGGCGATGAGC 3158
Db 10204 TTTCTTTTTTTTTTTTTTTTGAACACAGAGTCTTGGTCTGTGCGCCAGGCTGGAGT 10145
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Qy 3159 ACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGA 3218
Db 10144 GCAGTGGTGCAATCTCAGCTCACTGCAACCTCTGCCTCCAGGTTCAAGCAATTTCTCTG 10085
Qy 3219 CCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGGTGCACCACCACCGCCTGGCTAAATTA 3278
Db 10084 TCTCAGCCTCCCGAGTAACCTGGGATTACAGGCTCCTGCCACCATACCCGGCTAATT-T 10026
Qy 3279 AAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGC 3338
Db 10025 TGTGTTTTTTAGTGGAGATGGGGTTTCACCACGTAGGCCAGGCTGTTCTCAAACCTCTGAC 9966
Qy 3339 TTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCA 3398
Db 9965 CTCAGGTGATCCTCCTGCCTCGGCTCGGCTCCCAAAGTGTGGGATTCCAAGCATGAGCC 9906
Qy 3399 TGTGCGG-----CTACTATTCTTTTACATTCCTTTCCAA 3436
Db 9905 CGCCCGCCTAGAGATTCTATCTCTTAAACTTTTAACTCTCTTCGATTTTCATTTCTGAA 9846
Qy 3437 TAGAATG--TAAGATCCACAGAACAGGGATTACTGCCTATTCTTCTCTTTCTTTTGA 3494
Db 9845 ATGATTGCTTTACAACTCCATTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTGA 9786
Qy 3495 GACAGAGTCTCATCTCATCACCTCAACCTCCGT-----TCAGCTCACTGCA 3540
Db 9785 GACAGAGTCTCACCATGTCACCCAGGCTGGAGTGCAGTGGTGTGATCTCGGCTTACTACA 9726
Qy 3541 ACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCCTAAGCCTCCTG-AGTAGCTGGAATT 3599
Db 9725 GCCTCCACCTCCCGAGTTCGAAGCGATTCTTATGCGCTCAGCCTCCTTAAAGTAGCTGA 9666
Qy 3600 ACAAGCGTGCAACCACCATGCTTGGCTAAATTTTTTGTATTTTGTAGCAGAGATGGGGTTTA 3659
Db 9665 ACAAGCGTGCAACCACCATGCTCCTGGCTAA-TTTTTATATTTTAGTAGAGACAGAGTTTA 9607
Qy 3660 CCATGTTGCCCAGGCTGCTCAAACCTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTC 3719
Db 9606 CCATGTTGCCCAGGTTGGTCTCGAACTCCTGGCCTCAGGTTATCTGCC-----CGGTCTC 9552
Qy 3720 CCAAAGTGTGGAATATATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTCT 3779
Db 9551 CCAAAGTGTGGGATTACAGGCGTGAGCCACTGCACTCAGCCTACACCTCTACTCT--A 9494
Qy 3780 TTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAATA 3839
Db 9493 TTCTGAACACCCAAACAAATCTGAAATAACAGATTGTAATGTTTCTGTTGACTCTAAG 9434
Qy 3840 ATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTCTTTTAAAAACAATCTTGAC 3899
Db 9433 TTTTATGAGGCGAGTGTCTGTCTGATCTAGGCACTAATGTATGTCTGTTGCTCCTAGCAT 9374
Qy 3900 AACTTTGCAGATAAATAACAATCTTGCAATCTGCTTTTCTACTTTTCTACTATTTAGTCA 3959
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Qy 3960 TTTTTCATATTGCCCTCAAAACCTTTATTGTTACTGTTTCTTTTCTACTATTTAGTCA 4019
Db 9313 AATGAAAGGGAGTAAGAGTTTAGACCCAGAAATACCTTGATCACTTGTCCAGCTCTCATTC 9254
Qy 4020 CTGAATAATATGGCTTAATTTGCTTTATACATCCTCTGCTCCACTTTTAGAAGGCCAAATT 4079
Db 9253 ATCCCATCTCTTATCTCTCATTTCTCAAGAGAGGCGCAACCAATAAGAGTCAGATGACCTGGGT 9194
Qy 4080 TACAAATCTGATGAAGCTATGAACCTCTCCTCCAGAGAGAAATACACACACACACACAC 4139
Db 9193 TTGAATCTCAGTTCCTCTCTCATTAGCTGTGATGTTTGAGCAAGTCATTTGAATCTTTCTA 9134
Qy 4140 TCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAAACTGCAATTAGAGGATGT 4199
Db 9133 AACCTCAGTTTTTCTCTTTTATACAACCTGACTTAAATAACAGGACCCCATTTCAACAGGTCA 9074
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; NUMBER OF SEQ ID NOS: 73997									
; SOFTWARE: FastSEQ for Windows Version 4.0									
; SEQ ID NO 17664									
; LENGTH: 46878									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-741-600-17664									
Query Match 8.0%; Score 400; DB 8; Length 46878;									
Best Local Similarity 49.9%; Pred. No. 1.1e-80;									
Matches 1923; Conservative 11; Mismatches 1671; Indels 247; Gaps 28;									
QY	802	TATTATTCTTATTATTATTATTGAGACAGAGTCTTGCTTTGTGCGCAAGGCTGGAGTACAGTG	861						
Db	34282	TTTTKTTTTTTTTTTTTTGAGATGGAGTCTTGTTCTGTGTGCCAGGCTGGAGTGCAGTG	34223						
QY	862	GTGCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGTTACGGSCATTCTCCCGCCTCAG	921						
Db	34222	GCACGATCTCGGCTCACTGCAAGCTCTGCCTCCYGGGTTACGGCATTTCTCTGCCTCAG	34163						
QY	922	CCTCCCCAGTAGCTGGGACTAAAGGCGCTGCCACCACGCCCGCTAAATTTTTTGTGA--	979						
Db	34162	CCTCCCAAGTAGCTGGGACTACAGGTGCCTGCCACCACGCCCTGGCTAATTTTTTATATT	34103						
QY	980	TTTTTTAATAAAGACGGGGTTTCATCTGTGTTAGCCAGGATGGTCTCGATCTCATGACCTTG	1039						
Db	34102	TTTTTTAGTAGAGCTGGGGTTTCACCAATGTTAGCCAGGATGGTCTTGATCTCCTGACCTCA	34043						
QY	1040	TGATCCGCGCTCGCTCGGCCCTCCCAAAGTCTGGGATTACAGGATGAGCCACCGTGCCCG	1099						
Db	34042	TGATCTGCCRCCTCAGCTTCCCAAAGTCTGGGATTACAGGCTAAGCCACTGTCACCCG	33983						
QY	1100	GCCTTATCACATTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATCTGTT	1159						
Db	33982	GCC----AGGATTTTTTTTTTTTTTTTGTGAGACAGGGTCTCACTCTGTGCCAGGC	33927						
QY	1160	TTAGAGATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATCTGTT	1219						
Db	33926	TGGAGTGCCATGGCTCAGTCATAGCTTACTGCCTCAACCTCCCGGCTCAAGCGATCCTCC	33867						
QY	1220	CACCTGCTGATCTCTAGCTCCTAGGACAGAGCCTGGCACATAGTAAGTGTCTCAATAAATA	1279						
Db	33866	CACCCCAGCCTCCCGAGTAGCTGGGAC-TACATGTGCGCACCAACACACCTGGCTAATTT	33808						
QY	1280	TTCACTGGATAAACAGTGCAGATAGTTTAAAACTATCTGACCTAGGGAGGCTGAGGCGAGG	1339						
Db	33807	TTTTTTTTTTTTTTTTTGAGGTGGAGTTTCGCTCTCTTTTGCCAGGCTGGAGTGCATG	33748						
QY	1340	AGAATGGCGTG-----AACCCGGGAAGCAGAGTTTGGAGTGAGCTGAAATCGTGTCT	1390						
Db	33747	GTATGATCTCGGCTCAATGCAACCTCTGCCTCCAGGTTTCAAGTGATTTCTCTGCCTCAG	33688						
QY	1391	ACTGCACCTCAAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAACTAT	1450						
Db	33687	CCTCCCAAGTAGCTGGGATTACAGGTGCCACCATCACGCCCAGCTAAATTTTGTATTTT	33628						
QY	1451	CAGGCCTAGCTGGGTGGCACATGCCCTGTAATCCTAGCTGAGGGGTAGGGTCCCAGAG-	1509						
Db	33627	AGTAGAGATGGGGTTTGGCCATGCTGGCCAGGCTGGTCTTTGAACTCCTGACCTCAGGTGA	33568						
QY	1510	--AAGAAGAAGAAAAAGAAGATATATATATATATACACACACACAAAGATATA	1566						
Db	33567	TCCACCTATCTCGGCCTCCCTAAGTGTGGGATTACAGGTGTGAGCCACCGCACCTGGCC	33508						
QY	1567	AACCTTTATATATAAAGTTTTTCATTAATAAAAAAAAAAAAAAACCCTCTACCCACTTTTCACTT	1626						
Db	33507	ATATTTTTTTTTTTTTTTTTTTTGTAGACGAGGTTTACCATGTGGCCCCAGGCTGG	33448						
QY	1627	TACCAAGTTCTGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGGCAGGGGTACAGGAGGCA	1686						
Db	33447	TCTCAAACTCTAAGCTCAAGCAATCTGCCTGCCTTGGCTTCCCAAAAATGCTGGGACTAC	33388						
QY	1687	CGTGGGACCCGAGGAGCAGGAAGGAGTGTCCTCCCGGGTGCTGGCAGACCGATTTG	1746						

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QY	1747	AACCTCTGGCTATGTCTTTCAGTGGCCCGCGCMCAGCGGCATCAGCCCTCGGGCCG	1806						
Db	33327	TCTGCTGACCACCTGCCCTTGGTCACACCCCCACATCTCTGATCACAGAGACCGGTGCT	33268						
QY	1807	TGTGGCAGTTCGCGAAAAATGATCAAGTGCGTGATCCCGGGGAGTGACCCCTTYYTTGGAAT	1866						
Db	33267	TGGGATCATGTCCCTCCTGGCCTAAAACTTTCAAAAGGGTTTTCACAC----TCAGAAT	33212						
QY	1867	ACAACAACCTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGTGGATGAACCTGG	1926						
Db	33211	AAATCCAAACTCCTTCACCTTAGTCTTGCAGTTCCCCCATCCCCCTCATTCATTCCTTTG	33152						
QY	1927	ACAAGTAAGTATCCGCCTGCAGGAAAAATTGGAGTGCCTGCCGGGGGGGGTGGGGCAC	1986						
Db	33151	TTTTCTTTGTAAATTTTTTCTTAGAGATGGAGTCCCGCTCTGTTGCCAGGCTGGACTG	33092						
QY	1987	AGCCCAAGGATCTCACGAGGCATACAAAGGGGACTTGACATATCTGCTAAGGATAACATAT	2046						
Db	33091	CAGTGGCGTGATCTCGGCTCACTACAAGCTCCGCTTCCGGATTACGGCCATTCTCTGTC	33032						
QY	2047	TTTCACCTCTTGTCAAATAAACAATATGTTCCAAGAGGACCCTGTAGCGAACGACCCCC	2106						
Db	33031	CTCCGCCTCCAGAGTAGCTGGGACTACAGGGCGCTGCCACCATGCCTGGCTAAATTTGT	32972						
QY	2107	GTTAGAGATGGAACAATGACCGACGCTGCAAAACAGATGGGCGATGCTGCCCTCCAGTGGC	2166						
Db	32971	TTTTGTATTTTAGTAGAGACAGGGTTTCACCA-TGTTAGCCAGGATGGTCTTGATCTCC	32913						
QY	2167	AGATGTAGCAACAGTAAACATCACAGCAACTATCCACGTGTCAATTTCTAGCAGTGGTT	2226						
Db	32912	TGACCTCGTGATCCG-----CTCGCCTCAGCCTCCCAAAGTGTGGGATTACAGCGTGA	32858						
QY	2227	GTCACCTGCACCTTCTGAATACAGGATTTTACTGTATTCTTGCAACCATGTTAAAAATCGC	2286						
Db	32857	GCCACCACACCTT-----GCCAGGCCACTTACCT	32829						
QY	2287	TTTCAGGCCAGGCGGTGGCTCATGCCGTGTAATCCAGCACTTTGGGAGGCCGAGGCGG	2346						
Db	32828	CTACTAGCCCGGCACAGTGGCTCATGTCTGTAATCCAGCACTTTGGGAGGCCAAGGCAG	32769						
QY	2347	GCGGATCACTTGAGGTCAAGGATTCGAGACCAGCTGGCCAAACATGGTGAAACCTGTCT	2406						
Db	32768	GCAGATCAACTGTGTCAGGAGTTTGAGACCACCCCTGGCCAAACATGGCGAAACCCCATCT	32709						
QY	2407	CTACTAAAAAATACAAAAATTAGCCGGACATGTGGCGAGCGCCTGTAAACCCAGCTACT	2466						
Db	32708	CTATTAAAAATACAAAAACTTAGCCGGCATGGTGGCAGTTGCCTGTAATCCAGCTACT	32649						
QY	2467	TGGGAGACT-----GAGTTGGAGGTTTCAGTGAGCCAAG	2500						
Db	32648	CGGAGGCTAAGGCAGGAGAATCACTTGAAACCTTGAGGTTGAGGTTGCAGTAAGCCAAG	32589						
QY	2501	GTCGTGTCACTGCTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAAAAAAAAAATG	2560						
Db	32588	ATCATGCCATTGCACTCCAGCCTGGGTGATAGCGAGACTCTGTCTCARATAAATAAT	32529						
QY	2561	CTTTCAATAAATATATGATAAAAGGACTTATATTTTCAAGCCATAGGATCATTTCTCC	2620						
Db	32528	GAACAAAATAAATCTATCTCACATTCCAATCCCTGTCTTAGACTATTGGCYGCTGGATTCC	32469						
QY	2621	TGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCTCTGAGAGTGGGCAGGTGAGGCTGAC	2680						
Db	32468	AGAACAGAACTTTAGGTAGGCCCTTTCATAAACCCCTCCCAAATATCTTCCCTTTAATGA	32409						
QY	2681	CTATTGCTCTGCACCTTACTCCTATCTCAGCTGTCCCTCCCACCTTTCAGGTGCTGCCAGA	2740						
Db	32408	TAAATCAGGATCCCTGATATATTTCATCCCAAAGCAAAACCTATATATTTCTCTCCAGA	32349						
QY	2741	CACATGACAACTGCTAYGACCAGGCCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACA	2800						

Db 32348 CAACCTTCCCAAGTTGGTCATAAATTATGATTTACCTGTGGGATTATTGTCCCTATTAG 32289

Qy 2801 MMCGGTACACCCACACCTATTTCATACTCGTGTCTGGCTCGGCAATCACCTGTAGCAGTA 2860

Db 32288 ACCGAAATGGATGTGAGATGACAGAGGCCCTAATTGTTTTGTATAT-TGCTGCCTGACGC 32230

Qy 2861 GGTTTATCCCTTCCTTGACCTATGAATTCAGTTGGTTCTCAGTAGGCCGGGGGAAATA 2920

Db 32229 GCAGTAGGTATTTCATAGAAAGGCAGACACAGATTAGTGGCTACAATGGACTGGTGAGTCTA 32170

Qy 2921 ATAGTAACAACAGCCATGATTTAGTGTTAATTTTCTTGTTCTGGCAGTGTCCTCTTA 2980

Db 32169 GTATTGTCACCTCACTTGCCCTTAGACCAGGTCTACTTAACCTGGGGTTTAGTTGCCTCAT 32110

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Db 32109 CT-----ATAATAGGGAATAACAGTCTCTACTACTCAAGTTGTCATGAAGATT 32062

Qy 3041 GAGGCTCAGAAAGGCTGAGCTATTTGCCCCAAGATCACACAGCTTGTAAGTGGTGACAGTTT 3100

Db 32061 CAGTCAGTGAATATTTATTAAATGTTAAAGACATATATATATATATATATATATT 32002

Qy 3101 GGGTTTTTTTTTGTGTTGTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCAC 3160

Db 32001 TTTTTTTTTTTTTTTTTTTTGAGACA--GTCTCACTCTGTGCCCCAGGCTGGAGTGC 31944

Qy 3161 AGTGTGCAACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGGATCTGTGACC 3220

Db 31943 AGTGGCGTGATCTTGCTCACTGCAAGCTCCACCTCCCGGTTCAATGCCATTCTCCTGCC 31884

Qy 3221 TCAGCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGGCTAATTAAAAAA 3280

Db 31883 TCAGCTCCCGAGTAGCTGGGACTACAGGCGCCGCCACACGCCACCTAATTTTTTGT 31824

Qy 3281 ATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTT 3340

Db 31823 ATTTTAT-TAGAGACGGGGTTTCACCATTTTAGCCAGGATGGTCTCTATCTCCTGACCT 31765

Qy 3341 CAAGCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATACAGGGGTAGCCACCATG 3400

Db 31764 C--GTATCCGCCCGCCCTCGGCCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCACCGC 31707

Qy 3401 TCGGGTACTTATTCTTTACATTCCATCTTTCCAATAGAAATGAAGATCCACAGAACAG 3460

Db 31706 CCTGGCCTTTTTTTTT----- 31690

Qy 3461 GGATTACTGCCATATTTTCTCTCTTTCTTTTGTAGACAGAGTCTCACTTCATCACTCAA 3520

Db 31689 -GTTTGTGTGAGACAGAGTCCCGCTCTGTCAATGCAGCCTGGAGTGCAGTGGTGCCATC-- 31633

Qy 3521 CCTCCGTTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGC 3580

Db 31632 -----TTGGCTCACTGCAACCTCTGCCTCCCAAGTTCAAGTGATTCTTGTGCCTCAGC 31580

Qy 3581 CTCCTGAGTAGCTGGAATTACAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTT 3640

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Db 31520 TTGTAGAGACAGGGTTTCGCCATGTTGGCCAGACTAGTCTCAAACTCCTGTCTCAAGTG 31461

Qy 3701 ATCTGCCTGCCTCAGTCTCCCCAAAGTCTGGAAATTATAGSCGTGAGTCACTGTGCCTGGC 3760

Db 31460 AGTCGCTGCCTYGGCCTCCCAAAGTGTGGGATTACAGGCAATGAGCCACTGYGCCTGGA 31401

Qy 3761 CGATTACTGTCTAT-----TTTTCTTTATGCTATATATCCCCAGATCTAGAGCAGTGTCTGA 3815

Db 31400 CAAGAAATTTCTATTATTATTTTTTCTCTCAACAAATTATCAACATCTGTTACATCYTGA 31341

Qy 3816 CATATAGTAGGTGCTCAATAAATAATTGATGAAATGCACAGCCTAGAT----- 3862

Db 31340 CAGGCAACAGATAAGCATGAATAAGGACATGGGTCAACCAATCTCACTGGGGACAGATGA 31281

Qy 3863 -----ATAAACTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTG 3906

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Qy 3907 CAGAAATA-----ATACAATCTTGCAATCTGCTTTTTCACCTTATCACCTTTGTATGACT 3960

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Qy 3961 TTTTCATATTGCCTCA-----AACCTTTATTGTTACTGT 3994

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Qy 3995 TTTTTCATTGTTACTATTTTAGTCACTGAATAATATATGGCTTAATTTGCTTATACATCCTC 4054

Db 31100 TGAGAAGTGCTATATATCATATCACACTGATAAGACAGAGTAACCTAGGGCATGGGTACTT 31041

Qy 4055 CTGCTCCACT--TTAGAAAGGCCAAATTTACAAATCTGATGAAAAGCTATGAACCTCTCCC 4112

Db 31040 CAGCTGGGCTGAGGGAATGGGATTGTTAGGGACATGACATTTACACTGAGGTCTGAAG 30981

Qy 4113 CAGAGAAATACACACACA-----CACACACACTCACACACAGTTTTTTTTTAAATGT 4163

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Qy 4164 TTGCAACTAAGACAGAAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAAC 4223

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Qy 4284 GATCACTTGAGGTGAGAAAGTTTCGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTA 4343

Db 30803 GATCACCT---TTCAGGAGTTTGAGACCAGCCTGGCCAAATGTGGTGAAACCCCGTCTCTA 30747

Qy 4344 CTAAAAATACAAAAATTAGCTGGGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGG 4403

Db 30746 CTAAAAATACAAAAATTAGCTGGGCTTGGTGGTGGCGCCTGTAATCCCAGCTACTCTGG 30687

Qy 4404 AGGCTGAGGCAAGAGAATTGCTTGAAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCC 4463

Db 30686 AGGCTGGGCGAGGAGAAACGCTTGAAACCCGGGAGGTGGAGTTGCAGTGAGCTGAGGTGC 30627

Qy 4464 ----CACCACTGCATCCAGCCTGGGCGAC-ACAGCGAGACTCTATCTCAAAAAATAAA 4518

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Qy 4519 TAAATAAAAAATA 4530

Db 30566 AACAAAAAGAAA 30555

RESULT 23

US-10-087-192-1978

; Sequence 1978, Application US/10087192

; Publication No. US20020182586A1

; GENERAL INFORMATION:

; APPLICANT: Morris, David W.

; APPLICANT: Engelhard, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: CANCER

; FILE REFERENCE: 529452000122

; CURRENT APPLICATION NUMBER: US/10/087,192

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 09/747,377

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/798,586

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 2059

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1978

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; LENGTH: 87687
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(87687)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1978

Query Match      8.0%; Score 399; DB 5; Length 87687;
Best Local Similarity 60.1%; Pred. No. 2.8e-80;
Matches 900; Conservative 1; Mismatches 511; Indels 85; Gaps 11;

Qy 3111 TTGTTGTTGTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCACAGTGGTGCAA 3170
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Db 5754 TTTTNTTTTTTTTTTGAGACAGTCTCGCTCTGTCAACCCAGGCTGGAGTGCAGTGGCGGA 5813

Qy 3171 CCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGA-TCTGCTGACCTCAGCCTCC 3229
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Db 5814 TCTTGGCTCACTGCAAGCTCTGCCCTCTCTGGGTTCAAGCCATTCTCCTGTGCTCAGCCTCC 5873

Qy 3230 CAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGGCTTAATAAAAAATTTTTTTG 3289
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Db 5874 CGAGTAGCTGGGACTACAGGTGCCGCCACCATGCCTGGCTAAATTTTTTGGTATTTTTAG 5933

Qy 3290 TAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATC 3349
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Db 5934 TAGAGACTGGGTTTCACT--GTTAGCCAGGATAGTCTCGATCCCCTGAC--CTTGTGATC 5989

Qy 3350 CTCCTACCTTGGCATCCAAAGTCTGGGATTACAGGGTGAGCCACCATGTGCGGCTAC 3409
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Db 5990 TGCCCGCCTCAGCCTCCCAAAGTGGTGGATTACAGGCGTGAGCCACTGCGTCTGTCTT 6049

Qy 3410 TTATTTCCTTACATTCATCTTTCCAAATGTAAGATCCACAGAACAGGGATTA--C 3467
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Db 6050 ACCTTTATACAATGTATAGAAATGTATAGGAGGCTTTAGGTAAGAGACTGGCAATTAGTT 6109

Qy 3468 TGCCTATTTTCTTCTCTTTTGGAGACAGAGTCTCACTTCATCACCTCAACCTCCGT 3527
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Db 6110 TTTTAAATTTGTTACTTTTTTTTTTGAGACAGACTCTCACTCTGTGTCCTGGACTGGAGT 6169

Qy 3528 TCA-----GCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTG 3573
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Db 6170 GCAGTGGCATGATCTTGGCTCACTGCAACCTCTGCCTCCCGGTTCAAGTGATTCTCCTG 6229

Qy 3574 CCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCAATGCTTGGCTAATTTTT 3633
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Db 6230 CCTCAGCCTCCCTAGTAGCTGGGATTACAGGCATGTGCCACCATTGCCAGCTAATTTTT 6289

Qy 3634 GTATTTTTAGCAGAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACC 3693
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Db 6290 GTATTTTATAGAGACAGGGTTTCGTCTATGTTAGCCAGGCTGGTCTCGAACTCCCAACG 6349

Qy 3694 TCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGTCTGGAATTATAGGCGTGAGTCACTGT 3753
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Db 6350 CCAGGTGATCTGCCACCTCAGCCACCCCAAAGTGTGGGATTACAGGCGTGAGGCCACAC 6409

Qy 3754 GCCTGGCCGATTACTGTCTATTTTCTTT-----ATTGCTATATCCCCAGATCTAGA 3804
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Db 6410 ACATGGCCTAAAAAATGTTCTTCTTATTGAAAAATGAGTTTATAGGGGACATTTTGTCAA 6469

Qy 3805 GCAGTGTCTGACATATAGTAGGTGCTCAATAAAATAATTGATGAATGCACAGCCTAGATAT 3864
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Db 6470 TCTGGCTTCAAAAAAAGATGAATGAATCAATGGTAAAAAATTTGTTAAACGTGCTCGTTTC 6529

Qy 3865 AAACCTTTCTTTTCTTTTAAAAACAATCTTGACAA-----CTTTGCAGAT 3912
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Db 6530 AGCAGCACATACACTAAAATTAGACTGATACAGAGAAGATTAGCATGGCCCCCTGCGCAAA 6589

Qy 3913 AAATACAATCTTGCATTTCTGCTTTTTTCACTTATCACCTTGTATTGACTTTTTTCATATTGC 3972
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Db 6590 GATGACACGCAAAATTTCATTTTTAAAAAAGCAATAAATAATTTTGTAAATAATCATTTTTA 6649
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Qy 3973 CTCAAAACCTTTATTGTTACTGTTTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGG 4032
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Db 6650 ATCATGTAAGTATTTTCTCCATTTTTCAGACTGTTTCTCTTTTCATCATTTTAAACAATAA 6709

Qy 4033 CTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAAGGCCAAAATTTACAAATCTGATG 4092
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6710 ATAATAGGGCTGCTCTTATATACTTTTCAGTTTCAGGAATGATAAATCTGAAGAAAAAGT 6769

Qy 4093 AAAGCTATGAACCCCTCTCCCAGAGAAATACACACA----- 4128
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Db 6770 GAATGGTTCAATCACCGATACAAAAATTAAACAACATGATAGTGGCAAGCAACATCAGGT 6829

Qy 4129 -----CACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACT-----AA 4173
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Db 6830 GGGTTTTGTTTATTAGCGATGTTTTCGCCATTTTTTTTATGTTGTTGTGTTGAAA 6889

Qy 4174 GACAAGAAACCTGCTATGAGGATGTTTGTTCATATTAAATAAATAAATACTCAGTTG--- 4230
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6890 AGCCAGACACATTAATTCCAAGGCTCATTTGGCTGCTAAGAAAAAATTGTCACTGTGGCCA 6949

Qy 4231 GGCACAGTGACTCAAGCCTGTAACCAACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACT 4290
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6950 GGCACAGTGGCTCATGCTATAAACCCAGCACTTTGGAGGCCAAAGGCGGCAGATCACC 7009

Qy 4291 TGAGGTGAGAAAGTTCGAGACACAGCCTGGTCAATATGGTGAAACCCCTATCTCTAC-TAAAA 4349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7010 TGAGCCAGGAGTTTGAGATCAGCCTGGGCAACATGGCAAAACCCCGTCTCTACGAAAAA 7069

Qy 4350 ATACAAAAATTAGCTGGGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGSGAGGCTG 4409
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7070 ATACCAAAATTAGCTGGGTGGTGGCGCCCACTGTAGTCCCAACTACTCAGGGGGCTA 7129

Qy 4410 AGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTCAGTGAGCCGAGATCCCACCAC 4469
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7130 AGGTGGAGGACTGCCAGAGCCTAGGAGGTGAGGTTCAGTGAGCTGAGACTGACCCAC 7189

Qy 4470 TGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAATAA 4526
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7190 TGCACCTCCAGCCTGGGTGACACAGCAAGAGCGCTGTCTCAAAAAACAACAAACAAAAA 7246

RESULT 24
US-10-087-192-148
; Sequence 148, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 174448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(174448)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-148
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Query Match 8.0%; Score 398.6; DB 5; Length 174448;
Best Local Similarity 59.8%; Pred. No. 5.1e-80;
Matches 879; Conservative 0; Mismatches 524; Indels 66; Gaps 10;

Db 147414 CCTCAGGTGATATGCCACCTTGGCCTCCAAAAGTGTGGGATTACAGGCATGAGCCACT 147355

Qy 3398 ATGTGCGG-CTACTTATTTCTTTACATTCCATCTTTTCCAATAGAAATGTAAGATCCACAGA 3456

Db 147354 GTGCCGTGGCCTAAATTTATTTTTATGTTTGTGTTTTTGTGTTTTTTTTTTTTTTTGA 147295

Qy 3457 ACAGGGAATTACTGCCCTATTTTCTCTCTCTTTTCTTTTGTGAGACAGAGTCTCACTTCATCACC 3516

Db 147294 GACCGACTCTCTCTGTGTGCCTAGGCTGGAGTGCAGTGTCAAGATCTCTGCTCACTCTC 147235

Qy 3517 TCAACC----TCGGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCT 3572

Db 147234 TCCTCCGCAACCTCTCAAGATTTTCGGCAACCTCTGCCTCCTGAGTTCAGCGATTCTTGT 147175

Qy 3573 GCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCAACATGCTTGGCTAATTTT 3632

Db 147174 GCTTCAACCCTCTGGAGTAGGTGAGATTACAGGTGTGTGCCACCATGCCTGGCTAA-TTTT 147116

Qy 3633 TGTATTTTTCAGAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGAC 3692

Db 147115 TGTGTTTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGAC 147056

Qy 3693 CTCAAGTGATCTGCCTGCCTCAGTCTCCAAAAGTGTGGAATTATAGGCGTGAGTCACTG 3752

Db 147055 CTCAGGTGGTC-ACCTGCTTTCGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCTCCA 146997

Qy 3753 TGCCCTGGCCGA-----TTACTGTCTATTTTCTTTTATGCTATATCCCCAGATC 3800

Db 146996 TGCCCGACCCATAGCTCCTATTTTAAATTGTACCTGTAAATGTTGGCTGCCCTTTTAATC 146937

Qy 3801 TAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAAATAAATTGATGAATGCACAGCCTAG 3860

Db 146936 AAACCTACCCCCATGTTAATGCATCAGTCACTAAACTAGGATAAAGGTAGGATTACTGAA 146877

Qy 3861 ATATAAACTTTCTTTTCTTTTAAACAATCTTGACAACTTTGCAGAATAAATA--- 3917

Db 146876 ATGCTGCTTTCACCTGGCACCACCTTTGTGAGGAAAAGGAAACCTTAGAAAAATAACATTG 146817

Qy 3918 ----CAATCTTGCATCTGCTTTTTCACCTATCACCTTGTTATGACTTTTTCATATTGCC 3973

Db 146816 TGGGCATGATTTCTTTATCGTACGGTGAATTCAGCCTTGCAGTGATTTTTCAGAGATGA 146757

Qy 3974 TCAAACTTTATTTGTACTGTTTTCATTTGTACTATTTTAGTCACTGAATAATATGGC 4033

Db 146756 ACAGAAATTTAAAGTGTAGAACTCATTTGGGAGGCTAAGGCAGTAAAGTGTGTGAGCCC 146697

Qy 4034 TTAATTTGCTTATACATCTCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGA 4093

Db 146696 AGGAGTTTGAGACA-AGGCTGGGTAAACATAATGAGAACCTGTCTCTACAAACAAACAA 146638

Qy 4094 AAGCTATGAACCCCTCTCCCCAGAGAAATACACACACACACACACTCACACACAGTTTT 4153

Db 146637 AAACCTATGTTCTCCGCTTTCCCAACATTTAACTTTTACATACACAGTTGATGTTTTCA 146578

Qy 4154 TTTTAAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATA----- 4208

Db 146577 TCCCTTAAG-TAGCAAAAGAGGAGATGGAGTTGCTGAAGTGTGTAATTGTGATAACTGTT 146519

Qy 4209 -----TTAATTAATAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAG 4259

Db 146518 TGCTTTCCTTAGAATAATGTTTTTCTGGCCAGGAGCGTTTGGTGCAACGCTGTAAATCCCGAG 146459

Qy 4260 TACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGT 4319

Db 146458 CAGTTTGGGAGGCCAAGGTGGGTGGATCAGCTGAGGTTCAGGATCGAGACCATCCTGGC 146399

Qy 4320 CAATATGGTGAACCCCTATCTCTACTAAAAATAC--AAAAATTAGCTGGGTGTAGTGATG 4377

Db 146398 TAACATGGTGAACCCCTGTCTCTACTAAAAATAACAAAAAATTAGCCGGGCATGGTGGTG 146339

Qy 4378 CATGCCTGATGCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAG 4437

Db 146338 GGCACCTATAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGATGGCATGAAACCAGGAG 146279

Qy 4438 GCAGAGGTTGCAGTGAGCCGAGATCCCACCACCTGCACCTCCAGCCTGGGCGACACAGCGAG 4497

Db 146278 GCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCACCTCCAGTCTGGGCAACCCGAGCGAG 146219

Qy 4498 ACTCTATCTC 4507

Db 146218 ACTCCTTCTC 146209

RESULT 26

US-09-964-824A-273/c

; Sequence 273, Application US/09964824A

; Patent No. US20020102531A1

; GENERAL INFORMATION:

; APPLICANT: Horrigan, Stephen

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatur

; TITLE OF INVENTION: Sets

; FILE REFERENCE: 689290-73

; CURRENT APPLICATION NUMBER: US/09/964,824A

; CURRENT FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US/60/236,033

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236,032

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US/60/236,028

; PRIOR FILING DATE: 2000-09-28

; NUMBER OF SEQ ID NOS: 583

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 273

; LENGTH: 167343

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-964-824A-273

Query Match 8.0%; Score 398.4; DB 3; Length 167343;

Best Local Similarity 60.1%; Pred. No. 5.5e-80;

Matches 872; Conservative 1; Mismatches 532; Indels 45; Gaps 11;

Qy 3098 TTTGGGTTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAG 3157

Db 147653 TTTTTTTTTTAATTAAATTATTTTTTGAGACGGAGTCTTGCTCTGTCACTAGGCTGGAG 147594

Qy 3158 CACAGTGGTGCAACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTG 3217

Db 147593 TGCAGTGGCACAATCTTGGCTCACTGCAGCCTCCGCCTCCCGGTTGAAGCGATTCTCCT 147534

Qy 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGGTGCACCAACCAACCGCTGGCTAATTAA 3277

Db 147533 GCCTCTGCCTCGCCAGTAGTTGGATTACAGGTGTGTGCTACCACGCCAGCTAATTTT 147474

Qy 3278 AAAAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGG 3337

Db 147473 TGTA-TTTTGTAGAGACGGAGTTTTCACCATGTGTGGCTAGGCTAGTCTTGAACCTCTGA 147415

Qy 3338 CTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGGTGAGCCACC 3397

Db 147414 CCTCAGGTGATATGCCACCTTGGCCTCCCAAGTGCTGGGATTACAGGCATGAGCCACT 147355

Qy 3398 ATGTGCGG-CTACTTATTTCTTTTACATTCCATCTTTCCAATAGAAATGTAAGATCCACAGA 3456

Db 147354 GTGCCTGGCCTAATTTTATTTTATGTTTGTGTTTTTTTTTTTTTTTTTTTTTTTGA 147295

Qy 3457 ACAGGGATTACTGCCTATTTTCTTCTTCTTTTGTAGACAGAGTCTCACTTCATCACC 3516

Db 147294 GACCGACTCTCTCTGTGTGCCTAGGCTGGAGTGCAGTGTACGATCTCTGCTCACTCTC 147235

Qy 3517 TCAACC----TCCGTTCAAGCTCACTGCAACCTCTGCCTCCCGGTTTCAAGYGATTCTCCT 3572

Db 147234 TCCTCCGCAACCTCTCAAGATTTCGGCAACCTCTGCCTCCTGAGTTCAAGCGATTCTTGT 147175

Qy 3573 GCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGGTGCACCAACCATGCTTGGCTAATTTT 3632

Db 147174 GCTTCAACCTCTGGAGTAGGTGAGATTACAGGTGTGTGCCACCATGCCTGGCTAA-TTTT 147116

Qy 3633 TGTATTTTATAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACCTCCTGAC 3692

Db 147115 TGTGTTTTAGTAGAGATGGGTTTCACCATGTTGGCCAGGCTGGTCTTTGAACCTCCTGAC 147056

Qy 3693 CTCAGTGATCTGCCTGCCTCAGTCTCCCAAGTCTCGGAATTATAGGCGTGAGTCACTG 3752

Db 147055 CTCAGGTGGTC-ACCTGCTTTTCGCTTTCCCAAGTCTGGGATTACAGGCATGAGCCTCCA 146997

Qy 3753 TGCCTGGCCGA-----TACTGTCTATTTTCTTTATTTGCTATATCCCCAGATC 3800

Db 146996 TGCCAGCCCATAGCTCCTATTTTAATTGTACCTGTAAATGTTGGCTGCCCCCTTTAATC 146937

Qy 3801 TAGACAGTGTCTGACATATAGGTGCTCAATAAATAAATTAATGATGAATGCACAGCCTAG 3860

Db 146936 AAACCTCACCCCATGTTAATGCATCAGTCACTAAACTAGGATAAAGGTAGGATTACTGAA 146877

Qy 3861 ATATAAACTTTCTTTTCTTTTAAAAACAATCTTGACAACACTTTGCAGAATAAATA--- 3917

Db 146876 ATGCTGCTTTCACACTGGCACCACTTTGTGAGGAAAAAGGAAACCCCTAGAAAAATAACATTG 146817

Qy 3918 ----CAATCTTGCAATCTGCTTTTTCACCTTATCACCCTTGTATGACTTTTTTCATATGCC 3973

Db 146816 TGGGCATGATTTCTTTATCGTACGTGAATTCAGCCTTGCACTGATTTTTTTCAGAGATGA 146757

Qy 3974 TCAAACTTTATTTGTTACTGTTTTTTTTCATTTGTTACTATTTTAGTCACTGAATAATATGCC 4033

Db 146756 ACAGAAATTAAAGTTTAGAACTCAATTTGGGAGGCTAAGSCAGGTAAGTGCCTTGAGCCC 146697

Qy 4034 TTAATTTGCTTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGA 4093

Db 146696 AGGAGTTTGAGACA-AGGCTGGGTAAACATAATGAGAAACCTGTCTCTACAAAACAAAACA 146638

Qy 4094 AAGCTATGAACCCCTCTCCCCAGAGAAATACACACACACACACTCACACACAGTTTT 4153

Db 146637 AAACCTATGTTCTCCGCTTTCCCAACATTTTAACTTTTACATACACAGTTGATGTTTCA 146578

Qy 4154 TTTTAAATGTTTGCAACTAAGACAAGAAACCTGCATTTAGAGATGTTTGTTCATA----- 4208

Db 146577 TCCCTTAAAG-TAGCAAAAGAGAGATGGAGGTTGCTGAAGTGTGTAATTTGTGATAACTGTT 146519

Qy 4209 -----TTAATTAATAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAG 4259

Db 146518 TGCCTTCCCTTAGAATATGTTTTCTGGCCAGGAGCGTTTGGTGCACGCTGTAAATCCAG 146459

Qy 4260 TACTTTGGAAGTCCAAGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGT 4319

Db 146458 CAGTTTGGGAGGCCAAGGTGGGTGGATCACGTGAGGTCAGGAGATCGAGACCATCCTGGC 146399

Qy 4320 CAATATGGTGAAACCCCTATCTCTACTAAAAATAC--AAAAATTAGCTGGGTGTAGTGATG 4377

Db 146398 TAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAAATTAGCCGGGCATGGTGGTG 146339

Qy 4378 CATGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGAG 4437

Db 146338 GGCACCTATAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGCATGAAACCGAGG 146279

Qy 4438 GCAGAGTTGCAGTGAGCCGAGATCCCACCACCTGCACCTCCAGCCTGGGCGACACAGCGAG 4497

Db 146278 GCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCACCTCCAGTCTGGCAACCCGAGCGAG 146219

Qy 4498 ACTCTATCTC 4507

Db 146218 ACTCCTTCTC 146209

RESULT 27
US-10-843-641A-2740/c
; Sequence 2740, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2740
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-2740

Query Match 8.0%; Score 398.4; DB 9; Length 167343;
Best Local Similarity 60.1%; Pred. No. 5.5e-80;
Matches 872; Conservative 1; Mismatches 532; Indels 45; Gaps 11;

Qy 3098 TTTGGGTTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCAGGCATGAG 3157

Db 147653 TTTTTTTTTTAAATTAATTTATTTTTTGAGACGGAGTCTTGCTCTGTCACTAGGCTGGAG 147594

Qy 3158 CACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTG 3217

Db 147593 TGCAGTGGCACAATCTTGGCTCACTGCAGCCTCCGCCTCCCGGTTGAAGCGATTCTCCT 147534

Qy 3218 ACCTCAGCCTCCCAAGTAGCTGGACTACGAGCGCTGCACCAACCACGCCTGGCTAATAAAA 3277

Db 147533 GCCTCTGCCTCGCCAGTAGTTGGATTACAGGTGTGTGTACCAACGCCAGCTAATTTT 147474

Qy 3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACCTCTGG 3337

Db 147473 TGTA-TTTTGTAGTAGACGGAGTTTTCACCATGTGTGGCTAGGCTAGTCTTTGAACCTCTGA 147415

Qy 3338 CTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGTGGATTACAGGGGTGAGCCACC 3397

Db 147414 CCTCAGGTGATATGCCACCTTGGCCTCCCAAGTGTGGATTACAGGCATGAGCCACT 147355

Qy 3398 ATGTGCGG-CTACTTTATTTCTTTACATTCCTTTTCCAAATAGAAATGAATGCCACAGA 3456

Db 147354 GTGCCTGGCCTAAATTTATTTTATGTTTGTGTTTTTGTGTTTTTTTTTTTTTTTGA 147295

Qy 3457 ACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTGTAGACAGAGTCTCACTTCATCACC 3516

Db 147294 GACCGACTCTCTCTGTGTGCCTAGGCTGGAGTGCAGTGTACGATCTCTGCTCACTCTC 147235

Qy 3517 TCAACC---TCCGTTCAAGTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCT 3572

Db 147234 TCCTCCGCAACCTCTCAAGATTTCGGCAACCTCTGCCTCCTGAGTTCAAGCGATTCTTGT 147175

Qy 3573 GCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTT 3632

Db 147174 GCTTCAACCTCTGGAGTAGGTGAGATTACAGGTGTGTGCCACCATGCCTGGCTAA-TTTT 147116

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QY      3633  TGTATTTTTCAGAGAGATGGGGTTTTTACCATGTTTGCCAGGCTGGTCTCAAAACTCCTGAC 3692
Db      147115 TGTGTTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGAC 147056

QY      3693  CTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTG 3752
Db      147055  CTCAGGTGGTC-ACCTGCTTTGCGCTCCCAAAGTGCTGGGAATTACAGGCATGAGCCTCCA 146997

QY      3753  TGCCTGGCCGA-----TTACTGTCTATTTTCTTTTATTGCTATATCCCCAGATC 3800
Db      146996  TGCCCGACCCCATAGCTCCTATTTTAAATTGTACCTGTAAATGTTGGCTGCCCTTTTAATC 146937

QY      3801  TAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAG 3860
Db      146936  AAACCTCACCCCATGTTAATGCATCAGTCACTAAACTAGGATAAAGGTAGGATTACTGAA 146877

QY      3861  ATATAAACTTTCTTTTCTTTTAAAAACAATCTTGACAACCTTTGCAGAATAAATA--- 3917
Db      146876  ATGCTGCTTTCCACTGGCACCACTTTTGTAGGAAAAAGGAAACCCCTAGAAAAATAACATTG 146817

QY      3918  ----CAATCTTGCAATTCTGCTTTTTCACCTTATCACCTTGTTATGACTTTTTCATATTGCC 3973
Db      146816  TGGGCATGATTTCTTTTATCGTACGGTGAATTCAGCCTTGACAGTATTTTTCAGAGATGA 146757

QY      3974  TCAAACCTTTATGTGTACTGTTTTCATTTGTACTATTTTAGTCACTGAATAATATGGC 4033
Db      146756  ACAGAAATTTAAAGTGTAGAACTCATTTGGGAGGCTAAGGCAGTAAAGTCTTGAGCCC 146697

QY      4034  TTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGA 4093
Db      146696  AGGAGTTTGAGACA-AGGCTGGGTAAACATAATGAGAACCCCTGTCTACAAACAAACAA 146638

QY      4094  AAGCTATGAACCCCTCTCCCCAGAGAGAAATACACACACACACACTCAACACAGTTTT 4153
Db      146637  AAACCTTATGTTCTCCGCTTTTCCCAACATTTAACTTTTACATACACAGTTGATGTTTCA 146578

QY      4154  TTTTAAATGTTGCAACTAAGACAAGAAACCTGCATTAGAGGAATGTTTGTTCATA----- 4208
Db      146577  TCCCTTAAG-TAGCAAAAGAGGAGATGGAGGTTGCTGAAAGTGTGTAATTGTGATAACTGTT 146519

QY      4209  -----TTAATTAATAAATAAATCACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAG 4259
Db      146518  TGCTTTCCTTAGAAATATGTTTTCTGGCCAGGAGCGTTTTGGTGACGCGCTGTAATCCCGAG 146459

QY      4260  TACTTTGGAAGTCCAAAGGTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGT 4319
Db      146458  CAGTTTGGGAGGCCAAAGGTGGGTGGATCAGGTGAGGTCAGGAGATCGAGACCATCCTGSC 146399

QY      4320  CAATATGGTGAACCCCTATCTCTACTAAAAATAC--AAAAATTAGCTGGGTGTAGTGATG 4377
Db      146398  TAAACATGGTGAACCCCTGTCTCTACTAAAAAATACAAAAAATTAGCCGGGCATGGTGGTG 146339

QY      4378  CATGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATGCTTGAACCTGGGAG 4437
Db      146338  GGCACCTATAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAAATGGCATGAAACCGAGGAG 146279

QY      4438  GCAGAGGTTGCAGTGAGCCGAGATCCCACTGCACTCCAGCTCCAGCTGGGCGACACAGCGAG 4497
Db      146278  GCGGAGCTTGCAGTGAGCCGAGATCGTGCACCTGCACCTCCAGTCTGGGCAACCGAGCGAG 146219

QY      4498  ACTCTATCTC 4507
Db      146218  ACTCCTTCTC 146209
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RESULT 28
US-10-843-641A-5576/c
; Sequence 5576, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using

```
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5576
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5576
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Query Match      8.0%; Score 398.4; DB 9; Length 167343;
Best Local Similarity 60.1%; Pred. No. 5.5e-80;
Matches 872; Conservative 1; Mismatches 532; Indels 45; Gaps 11;

Qy      3098  TTTGGGTTTTTTTTTGTGTTGTTTAGAGACAGGGTCTTGCTGTACCCAGGCATGAG 3157
Db      147653  TTTTTTTTTTAATTATTTTTTTGAGACGGAGTCTTGCTGTACCTAGGCTGGAG 147594

Qy      3158  CACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTG 3217
Db      147593  TGCAGTGGCACAATCTTGGCTCACTGCAGCCTCCGCTCCCGGTTGAAGCATCTCCT 147534

Qy      3218  ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGACACCAACCGCCTGGCTAAATAA 3277
Db      147533  GCCTCTGCCTCGCCAGTAGTGGGATTACAGGTGTGTGTACCAACCGCCAGCTAAATTT 147474

Qy      3278  AAAATTTTTTTGTAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGG 3337
Db      147473  TGTA-TTTTGTAGTAGACGGAGTTTCACCATGTGGCTAGGCTAGTCTTGAACCTCTGA 147415

Qy      3338  CTTCAAGCAATCCTCCTACCTTGGCATCCCCAAAGTGCTGGGATTACAGSGGTGAGCCACC 3397
Db      147414  CCTCAGGTGATATGCCCACTTGGCCTCCCAAAAGTGCTGGGATTACAGGCATGAGCCACT 147355

Qy      3398  ATGTGCGG-CTACTTATTTCTTTACATTCCATCTTTCCAATAGAAATGTAAGATCCACAGA 3456
Db      147354  GTGCCTGGCCCTAAATTTATTTTATGTTTTTGTGTTTTTTTTTTTTTTTGA 147295

Qy      3457  ACAGGGATTACTGCCTAATTTTCTTCTTTTGTGAGACAGAGTCTCACTTCAFCACC 3516
Db      147294  GACCGACTCTCTCTCTGTGCTTAGGCTAGGCTGGAGTGAGTGTCAAGATCTCTGCTCACTCTC 147235

Qy      3517  TCAACC---TCCGTTTCAGCTCACTGCAACCTCTGCTCCCGGTTTCAAGYGATTTCTCCT 3572
Db      147234  TCCTCCGCAACCTCTCAAGATTTCGGCAACCTCTGCTCCTCTGAGTTCAAGCGATTCTTGT 147175

Qy      3573  GCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGGTGCACCAACCATGCTTGGCTAATTTT 3632
Db      147174  GCTTCAACCTCTGGAGTAGGTGAGATTACAGGTGTGTGCCACCATGCCTGGGCTAA-TTTT 147116
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QY	2979	TAATCCTCAGAACAAACACATATGGGATAGGTACAATATCCTCACTTAACAGATAAGAAAA	3038
Db	131534	GAAGACGGGGCTCTTCGAAAAACAGGTAGCACCAAAAGTCCTAGTTACACCCTTAAATAGGA	131593
QY	3039	CTGAGGC-----TCAGAAGGCTGAGCTATTTTGGCCCAAGATCACACAGC	3081
Db	131594	GCTAAGCAGCTGGGAATGCAGAAAAACGCAACAATAAGTGATGTGCCCGGTGGGCTCTC	131653
QY	3082	TTGTAAG-----TGGTGACAGTTTGGGTTTTTTTTTTGTTGTTTAGAGACAGGGTCTT	3136
Db	131654	CTGTGTGCACCTTCCCTGCCACATTTCTATTTTTTTTTTTTTTTTTTTTGAGATGGAGTCTC	131713
QY	3137	GCTCTGTCAACCCAGGCATGAGCACAGTGGTGCACCATAGGTCACTGCAGCCTCAACCTC	3196
Db	131714	GCTCTGTCAACCCAGGCTGGAATGCAGTGGTCTGATTTTCAGCTCACGGCAACCTCTGCTTT	131773
QY	3197	CTGAGCTCAAGGGATCTGTGACCTCAGCCCTCCCAAGTAGCTGGGACTACGAGCGTGAC	3256
Db	131774	CCAGGTTACGGGATTTCTCTGCCTCAGTCTCCGAGTAGCTCGGATTACAGGCACCTGC	131833
QY	3257	CACCACGCCCTGGCTAATTAAAAAAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCC	3316
Db	131834	CACCATGCCCCAGCCAAATCTTTTGTATTTTTTAGTAGAAACAGGATTTTGCCATGTTGCC	131893
QY	3317	AGGCTTGCTTTAAACTCTGGCTTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGCTG	3376
Db	131894	AGGCTGGTTTCGAACCTCTGACCTCAAGTGATCCACCAGCCCTTGGCCTCCCAAGTGCTA	131953
QY	3377	GGATTACAGGGGTGAGCCACCATGTGCGGTACTATTCTTTACATTCATCTTTCCAA	3436
Db	131954	GGATTACATCGTGAGACACCATGCCCCCTGGCCTCCTCCCCACATTATTATTAT----	132009
QY	3437	TAGNATGTAAGATCCACAGAACAGGATTACTGCGCTATTTTCTTCTCTTTTGTGAGA	3496
Db	132010	-----TTATTATTATTATTGTGAGACGGAGTCTTGCTCT	132042
QY	3497	CAGAGTCTCACTTCATCACCTCAACCTCCGTTCCAGCTCACTGCAACCTCTGCCCTCCCGG	3556
Db	132043	ATCGCCAGGCTGGAGTGAGTGGCACAACTCTCAGCTCACTGCAAGCTCCGCCCTCCCGG	132102
QY	3557	TTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGACCACCA	3616
Db	132103	TTACGCCATTCTCCTGCCTCAGCCTCCCAAGTAGTGGGACTACAGGCGCCCCACCA	132162
QY	3617	TGCTTGGCTAATTTTTTGTA-----TTTTTAGCAGAGATGGGGTTTT	3658
Db	132163	TGCCAGCTAATTTTTTCTTTTTTTTCTTTTTTTTTTTTAGTAGAGACGGGGTTTT	132222
QY	3659	ACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTGCCTCAGTCT	3718
Db	132223	ATGGTGTAGCCAAGATGGTCTCGATCTCCTGACCTCA--TGATCGGCCCGCCTTGCGCT	132280
QY	3719	CCCAAAGTCTGGAATTAPAGGCGTGAGTCACTGTGCGCTGGCCGATTACTGTCTATTTTC	3778
Db	132281	CCCAAAGTCTGGATTACAGGCATGAGCCACTGTGCCGCGCTCCCCACATTTTTTAAAG	132340
QY	3779	TTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAAT	3838
Db	132341	TCCATGG-----CCCAGATCTTCTCCTCCCTGACTCTCCTGTGATC-----	132379
QY	3839	AATTGATGAATGCACAGCCTTAGATATAAACTTTCTTTTTTTTAAACAAATCTTCA	3898
Db	132380	-----AGATCGTGGAGGGGGTTTGCTTCTCCTCCCAAAAGGCCCTGT	132419
QY	3899	CAACTTGCAGAAATAATACAATCTTGCAATCTTGCTTTTTTCACITTTATCACCTTGTATGA	3958
Db	132420	TTAGGCCCCAG-----CACCTCACTCTTGACTTTGTTTCCCAAAATCTTGTATTGG	132471
QY	3959	CTTTTTTCATATTGCCCTCAACCTTTATTGTTACTGTTTTTTTCATTGTTACTATTTTAGTC	4018
Db	132472	AGCTGTGCGTCCGGCAGTCTTCGGGAATCAGCAGCTGTGGGAAGCGGGGGGTGTTGTGTC	132531

RESULT 30
US-09-880-107-3949
; Sequence 3949, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3949
; LENGTH: 76798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z84718
US-09-880-107-3949

	Query Match	7.9%;	Score 396;	DB 3;	Length 76798;
	Best Local Similarity	53.6%;	Pred. No. 1.3e-79;		
	Matches 1300;	Conservative	2;	Mismatches 942;	Indels 180; Gaps 16;
QY	2278	AAAAATCGCTTTCAGGCCAGCGCGCGTGGCTCATGCTGTAAATCCAGCACACTTTGGGAGG	2337		
Db	12199	AAAAAAAAAAAAAGGCCAGTGGCGGTGCTTATACGTGTAATCACAGCACACTTTGGGAGG	12258		
OY	2338	CCGAGGCGGGCGGATCACTTGAGGTTCAGGAGTTCGAGACCGAGCCTGGCCAAACATGTTGAA	2397		

Db 12259 CCGAGCAGGCAGATCAC--AAGGTCAGGAGTTCGAGACCATCCTGGCTAAATATGTTGAA 12316
Qy 2398 ACCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTAAACC 2457
Db 12317 ACCCATCTCTACTAAAACTACAAAAAATTAGCCAGGCATGGTGGCAGCGCACCTGTAGTT 12376
Qy 2458 CCAGCTACTTGGGAGACT-----GAGTTGGAGGTTTCAG 2491
Db 12377 CCAGCTACTTGGGAGGCTGAGGCAGGAGAAATCACTTGAAACCCGGGAGGTGGAGGTTGCAG 12436
Qy 2492 TGAGCCAAGGTGCGTCACTGCTGTCCAGCCTGGGTAACAGAGCAAACTCTGTCTCAAAA 2551
Db 12437 TGAGCCAAGATCGCACCACTGCACTCCAGCCTGAGCGACAGAGCGAGACTCCGTATCAAA 12496
Qy 2552 AAAAAAATGCTTTCAAATAAATATATGATAAAAAGGACTTATATTTTTCAAAGCCATAGGAT 2611
Db 12497 AAAAAAAGCGACTATGTATGAAATACCCAGCACAGTGCCTTCCCTTACCCATCAT 12556
Qy 2612 CATTTCTCCTGAAGCATCTTTGGC-----GAAGTCATCCCC 2646
Db 12557 GACCCCCACACCCACAGTGTGGCCATCCTGCTCTACCTGACCGCAATATAAGGTCCT 12616
Qy 2647 ACCTGTTCTCTGAGAGTGGGAGGTGAGGGCTGACCTATTGCTCTGCACCTTACTCCTATCT 2706
Db 12617 GACTACTGGTACCTTCAGGACCTGCAGGCCCGTGTCCCGTGTGGATGAGTACCTGGCATGG 12676
Qy 2707 CAGCTGTCCCTCCCACTTTCAGGTGCTGCCAGACACATGACAACTGCTAYGACCAGGCC 2766
Db 12677 CAGCACGACTCTGCGGAGAAAGCTGCCTCCGGGC-C TTGTGGCATAAAGTGAGGCTGGG 12735
Qy 2767 AAGAACTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCGACACCTATTTCATAC 2826
Db 12736 AATGTGGGGCGGCAGCGAGAGCATTCCCCAAAGGTGTTCAGGCACCACTCTCTCTTT 12795
Qy 2827 TCGTGTCTTGGCTCGGCAATCACCTGTGAGCAGTAGGTTTATCCCTTCCCTTGACCTATGAA 2886
Db 12796 TCAGTTTGGATTAATTTCTACTGACCTGTCTTTGCGCTTCACAGATTCTTTCCCTCTGTGT 12855
Qy 2887 TTCTAGTTGGTTCTCAGTAGGCCGGGGGAAATAATAGTAACAAACAGCCATGATTTAGTG 2946
Db 12856 GCCAAATGCTATTAAAGCCCATCCAATACATTCTTTGTTGAGATATGATATTTTTCAGCT 12915
Qy 2947 TTAATTTCTTGGTTCGGGAGTGTCTCTTTAATCCTCAGAAACAACACTATGGGATAG 3006
Db 12916 CTGGAATTCATTTGGTTGTTTTTAGAAATTTCCACTTCTCTGATGAAATTCACCATCT 12975
Qy 3007 GTACAATATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGGCTGA----- 3057
Db 12976 GTTCATCCATTTTATCTGTCTTTCTGTAAATTTCTTTAACAATTTATCACTGTTAACCT 13035
Qy 3058 -----GCTATTTGCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTT 3111
Db 13036 AAAAACTTTGTCAACTAATTTCAACAGTAGGTGTTCTGTGGGTCTGGTTTTTTTGT 13095
Qy 3112 TGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGAGCACAGTGGTGCAAC 3171
Db 13096 TGTTTTGTTTTGAGATGGGTCTCACTCTGTCACCCAGGC-TGAGTGCAATGGTGGCAT 13154
Qy 3172 CATAGGTCAGTCAGCCCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCA 3231
Db 13155 CTCAGCTCACTGCAACCTCCACCTCCAGGCTCAAGCGATTCTCCTGCCTCAGCCTCCTG 13214
Qy 3232 AGTAGCTGGGACTACGAGCGGTGCACCAACCGCCTGGCTAAATTAATAAAAAATTTTTTGT 3291
Db 13215 CGTAGCTGGGATTACAGGCACCCACAGCACACCTGGCTAACTTTTGTTA-TTTGTAGTG 13273
Qy 3292 GAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCT 3351
Db 13274 GAGACCAGGTTTACCATGTTGGCCAGGCTGGTTTCGAACTCTCCACCTGAAGTGAITCG 13333
Qy 3352 CCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCGG----- 3405

Db 13334 TCCTCCTTGGCTTCCCAAAGTGTTGGGATTACAGGCATGAGCCACCATACCCAGCCTACG 13393
Qy 3406 -----CTACTTATTTCTTTACATTCATCTTTTCCAATAGAATGTAAGATCCACAGA 3456
Db 13394 GGTCTATTTCTATTGATGTGTTTTTCTCCCTCTTGATTATGGGTCACATTTGCCTGCTT 13453
Qy 3457 ACAGGGATTACTGCCTAT-----TTTCTCTCCTTTCTTTTTTGAGACAGAGTCTCACT 3508
Db 13454 CTTTGCATGTCTCATGATGATTATCAATTAATTTTTTATTTTTTTTGAGACGGACTCTCACT 13513
Qy 3509 TCATCACCTCAACCTCCGTTCA-----GCTCACTGCAACCTCTGCTCCTCCCG 3554
Db 13514 CCATTGCCCAGGCTGGCGTGCAATGGCACGATCTTGGCTCACTGCAACCTCCGCTCCTG 13573
Qy 3555 GGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCAC 3614
Db 13574 GGTTCAAAGCGATTCTCCACCTCAGCCTCCCAAGTAGCTAGAATTACAGGCACCTGCCAT 13633
Qy 3615 CATGCTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGGTTTTTACCATGTTGCCCCAGGC 3674
Db 13634 CATGCCTGGCTAAATTTT- -GTATTTTGTAGACAGAGGTTTTTACCATGTTGGCCAGGC 13691
Qy 3675 TGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTGGAAT 3734
Db 13692 TGGTCTTGAACCTCCTGACCTCAGGTGATCCTCCCATCTCGGCCTCCCAAAGTGCTGGAT 13751
Qy 3735 TATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCCC 3794
Db 13752 TGTAGGCATGAGCCACCATGCCCGCCTCATGATGATCTCTTGTGTGCCAGACATTATGA 13811
Qy 3795 CAGATCTAGAGCAGTGTCTGACATATAGTAGTGGTCAATAAATAAATTGATGAATGCAC- 3853
Db 13812 TAAAAGAAGACAGAGATTGAATTGCATAATAAACACCCCCAAGAAAGGCTTGCACTTC 13871
Qy 3854 -----AGCCTAGATATAAACTTTCTTTTCTTTTAAAAACAATCTTGACAA 3901
Db 13872 CCTGTGTCAGGTAGCCAGGATGTGAGGCTGTTCTCTCTTAAGCTAATCAGGAGGTGGCT 13931
Qy 3902 CTTTGCAGAAATAAATACAAATCTTGCAATCTGCTTTTTCACCTTATCACCTTGTATGACTT 3961
Db 13932 GGGTTGCAGGTTTAGTTGGTTTCAGTTTATCTTTGGTTTCAAAATATCTTGAATGTGAGAT 13991
Qy 3962 TTTCATATTGCTCAAACTTTATTGTTACTGTTTTCATTTTTCATTTACTATTTTTFAGTCACT 4021
Db 13992 CAGGTCACTAGCTCAGTCTAGCATGGCTTTGGAACTAATCACCAACTACGATGTTGCCT 14051
Qy 4022 GAATAATATGGCTTAATTTGCT-----TATACATCCTCCTGCTCCACTTTTAGA 4069
Db 14052 GTAAGATCTCTCTGTCTTTTCATCCCTGCCCCAGTTCCCAAACCTGCTGCTCAGTCAGAAA 14111
Qy 4070 AGCCCAAATTTTACAAATCTGATGAAAGCTATGAACCTCTCTCCCAG-----AGA 4118
Db 14112 AGCCCATGCCTGTGACAGTCTTTCTCCCAGCCTGCTTGGGCCCCAAGGAATGAATTTGA 14171
Qy 4119 AATACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCACCTAAGACAA 4178
Db 14172 ATGAAAGTAGTCTCATCTAGGAACGGCTTATGCCTCTCTGGAATTTAGTTCAATTAGTCAA 14231
Qy 4179 GAAACCTGCATTAGAGGATGTTTGT-----C 4205
Db 14232 GTGCTGTCCGATAGAAGTATAAAGTGAGCCACATPACGTAATTTTAAATTTTCTFAGTAGGC 14291
Qy 4206 ATATTAAATTAATAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCAACAGTACTTT 4265
Db 14292 ACATTTAAAAAGTAAAAAGAGTCCAGGCACAGTGTGCTCATGCCAATAATCCTAGCACTTT 14351
Qy 4266 GGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAATTTCGAGACCAGCCTGGTCAATAT 4325
Db 14352 GGGAGGCCAAGG-CAGTGGATCACCTGAGGTGAGAGTTCGAGACCAGCCTGGTCAACAT 14410
Qy 4326 GGTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTG 4385
Db 14411 GGGGAAACCTTGTCTCTACTAAAAACCACAAAAATTAGCCAGGCTTGGTGGCCTGTGCCTA 14470

Db 11860 CTGGGTGACAGAGTAAGACCCCATCTCAAAAAATAAAAAATTTAAAAAAAAG 11911

RESULT 35

US-10-843-641A-1242

; Sequence 1242, Application US/10843641A

; Publication No. US20050064454A1

; GENERAL INFORMATION:

; APPLICANT: Avalon Pharmaceuticals, Inc.

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using

; TITLE OF INVENTION: Signature Gene Sets

; FILE REFERENCE: 689290-189

; CURRENT APPLICATION NUMBER: US/10/843,641A

; PRIORITY FILING DATE: 2004-05-12

; PRIOR APPLICATION NUMBER: US/09/873,367

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US/09/954,531

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: US/09/954,456

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/962,436

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/962,832

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/964,824

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US/09/967,768

; PRIOR FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: US/09/968,007

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US/09/969,347

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US/09/969,708

; PRIOR FILING DATE: 2001-10-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 8447

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1242

; LENGTH: 15000

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-843-641A-1242

Query Match 7.8%; Score 390.8; DB 9; Length 15000;

Best Local Similarity 54.7%; Pred. No. 8e-79;

Matches 1275; Conservative 3; Mismatches 920; Indels 134; Gaps 20;

QY 2288 TTCAGGCCAGGCGGGTGGCTCATGCTGTGAATCCCAGCACATTTGGGAGGCCGAGCGGG 2347

Db 9627 TTCTGGCCGGGTGGTGGCTCATACCTGTATCCAGCACATTTGGGTGGCCGAGCGAG 9686

QY 2348 CGGATCACTTGAGGTCAGGAGTTCGAGACAGCCTGGCCAAACATGCTGAAACCCCTGCTC 2407

Db 9687 TGGATTGCTGAGCTCAGGAGTTTGAGACCAGCCTGGGCAACATAGTGAAACCCCTGTCTC 9746

QY 2408 TACTAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTAAACCCACGCTACTT 2467

Db 9747 TACTAAAATACA-AAAAAATTAGCCAGGTGTGGCGCGGTGTCCTGT-AGTCCAGCTACTT 9804

QY 2468 GGGAGACTGAGTTGGAGGTTTCAGTAGGCCAAGGTCGTGCTACTGCTGTCCAGCCTGGGT 2527

Db 9805 GGGAGGC-----AGAGGTTGCAGTTAGCTGAGATCATGCGACTGCACTCCAGCCTGGCA 9858

QY 2528 A-ACAGAGCAACTCTGTCTCAAAAAAATAAATGCTTTCAATAAATATATGATAAAAGGA 2586

Db 9859 ACAGAGTGAGACTCTATCTCAAAAAAACAATATATATATATATACATATATATACG 9918

QY 2587 CTTATATTTTCAAGCCCATAGGATCAATTTCTCCTGAAGCATCTTTGGCGAAGTCATCCCC 2646

Db 9919 TATATATATATACA---CATATATATACGTATATATATATATATATATATATATATAT 9975

QY 2647 ACCTGTTCTGAGAGTGGGCAGGTGAGGCTGACCTATTGCTCTGCACTTACTCCTATCT 2706

Db 9976 ACGTATATATATATGTTGTTATATATATATACGTATATATATATGTTATATATATATGTTTTT 10035

QY 2707 CAGCTG-----TCCCTCCCACCTTTCCAGGTGCTGCCAGACACATGACAACTGCTAYGA 2759

Db 10036 TTTTGTGAGATAGATATATATATATATATATACGTATATATATATGTTATATATATATAT 10095

QY 2760 CCAGGCCAAGAAG-CTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCACACCT 2818

Db 10096 ACGTATATATATGTTATATATATGTTATATATATATATATATATATATATATATATATAT 10155

QY 2819 ATTCACTACTCGTGTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCTT-- 2876

Db 10156 ATACGTATATATATATGTTATATATATATATATATAAAAAATATTTTACTGCATCTTTC 10215

QY 2877 GACCTATGAATTTCTAGTTGGTCTCTCAGTAGGCCGGGGGAAATAATAGTAACACACGCCA 2936

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QY 2937 TGATTTAGTGTTAATTTTCTTGGTCTCTGGCAGTGTCTCTCTTTAATCCTCAGAAACAC 2996

Db 10276 TAAACATGCTACACAGGTTGTAGACCAGGAGCAATAAGCTACACTATATAGCCTAGGTGT 10335

QY 2997 TATGGGATAGGTACAAATATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAAGGCTG 3056

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Db 10396 GTGAAATTGCCTAACACACACACTTCTCAGAAATGCATCCCTGTCTATTAGGTGATGATGAC 10455

QY 3106 TTTTGTGTTGTTTAGAGACAGGGTCTTTGCTCTGTACCCAGGCATGAGCACAGTGG 3165

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QY 3226 CTCCCAAAGTAGCTGGGACTACGAGCGTGCACCACACAGCCTGGCTAA-TTAAAAAATTT 3284

Db 10576 CACCTGAGTAGCAGGGACACAGGCGTGCGCCACCAACACTGGCTAAATTTTGTATTTTT 10635

QY 3285 TTTTGTAGAGACTGGGTCTTACTACGTTTGGCCAGGCTTG-TCTTAAACTCCTGGCTTCAA 3343

Db 10636 TTTTGTGGAGACAGGGTTTCAACACGTTTGGCCAGGTGGCTCTTTGAACCTCCTGGACTAA 10695

QY 3344 GCAATCCTCCTACCTTGGCATCCCAAAGTCTGGSATTAACAGGGGTGAGCCACCATGTGC 3403

Db 10696 AGATCCTCCTGCCTCGGCCTCCCAAAGTCTGGSATTAACAGGCGTGAGCTACCCACCT 10755

QY 3404 GGCTACTTATTTCTTACATTCATCTTTCCCAATAGAATGTAAGATCCACAGAACAGGGA 3463

Db 10756 GGCCACTGACTATTCTCTTTTTTTTTT----- 10783

QY 3464 TTACTGCCATATTTTCTCTCTTTTCTTTTGTGAGACAGAGTCTCACTTCACTCACTCAACCT 3523

Db 10784 TTTTTTTTTTTCTGAGACAGTTTCACTCTTTGTGCCCAGGCTGGAGTGCAATGGCGT 10843

QY 3524 CCGTTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTTCTCCTGCCCTAAGCCTC 3583

Db 10844 GATCTCAGTTCACTGCAGCTCCCCCTCCTGGTTCAAGTGATTTCTCCTGCCTCAGCCTC 10903

QY 3584 CTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTTTTGTATTTTAG 3643

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QY 3644 CAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGCTCAAACTCCTGACCTCAAGTGATC 3703

Db 10962 TAGAGACGGAGTTTCTTCATGTTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGTGATC 11021

QY 3704 TGCCTGCCTCAGTCTCCCAAAGTCTGGAATTTATAGGCGTGAGTCACCTGTGCCTGGCCGA 3763

Db 11022 CACCTACCTCAGCCTCCCAAAGTCTGGGATTACAGGTGTGAGCCACCACCGCCGCCAA 11081

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QY 3764 TTA-----CTGCTAATTTCTTTATTGCTAT 3789
Db 11082 CTATTCATTTTGTGGCGAGATTTTGTGTTTTTGTATTTCTTCCTTC 11141
QY 3790 ATCCCCAGACTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAAT 3849
Db 11142 TTAGGAGCTGTAGACTATTTCAGAGAGTTCAGAAAGGCACAAAATGGAAGTAAATGGCT 11201
QY 3850 GCACAGCCTAGATATAAACTTTCT-----TTTTCTTTTTTAAAAACAATC 3894
Db 11202 TCCACTTTCTCTTAAAGGAACHTACTAAATACAGTGTCTGGGTATTTTCTAAAGTTT 11261
QY 3895 TTGACAACTTTGCAGAATAAATAACAATCTTGCAATCTGCTTTTTCATTTGTTACTATTTT 3954
Db 11262 TTAATAAATGAAATATTATTGCAATTTGTTTCTAGGAGTTATGTGGTTTACATTGTAAGAACTT 11321
QY 3955 ATGACTTTTTCATATTCCTCAAACTTTTATTGTTACTGTTTTCATTTGTTACTATTTT 4014
Db 11322 AGTATAATTATCTTTCGCATGTTTTTCTAGGAGTTATGTGGTTTACATTGTAAGAACTT 11381
QY 4015 AGTCACCTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTTAGAGGCC 4074
Db 11382 TAGAAAAATACATTTAGCCAGTTCTGTAACACTGAAATTGTATCTAGGTTTTAGCTGACA 11441
QY 4075 AAATTTACAAATCTGATGAAAGCTATGAACCC---TCTCCCAGAGAAATACACACAC 4131
Db 11442 TAAGCAGTGTGCAGTCCCTTTTATATGTACCTATTGTTAGGTACAACTGGTCCCTGGC 11501
QY 4132 ACACACACTCACACACAGTTTTTTTTTAAATGTTTGCAACTAAGACAAGAAACCTGCA--- 4188
Db 11502 TTATGAAGTTTGACCTGATTTTTTTTCGACTTTACAATGGTGTATAACCATATTTTGAGCA 11561
QY 4189 -TTAGAGGATGTTGTTTCATATTAAFTAAAAA-----TAACTCAGTTGGGCACAGTGA 4240
Db 11562 CTCACAGTGTGTTTTTTTCTTTCTTTAAGAGACAGGGTCTCTTGGCTGGGAGCAGTG 11621
QY 4241 CTCAAGCCTGTAACCACACAGTACTTTTGGAAAGTCCAAGGTGGTGGATCACTTGAGGTGAGA 4300
Db 11622 CTCACGCCTGTAATCCCAACACTTTGAGAGGCCAGGGTGGC--GGATCACTTGAGCTCAGG 11680
QY 4301 AGTTGAGACACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATACAAAATT 4360
Db 11681 GGTTTGAGAACAGCCTGGGCAACATAGTGAGACCTTGTCTCTAAAAAACACA-AAAAATT 11739
QY 4361 AGCTGGGTAGTGATGCATGCCCTGTAGTCCAGCTACTCGGAGGCTGAGGCAAGAGAA 4420
Db 11740 AGCCTGGGTAGTGGCACGCACCTGTGGTCCCAGGTACTCAGGAGGCTGAGGTGGGAGAG 11799
QY 4421 TTGCTTGAACCTGGGAGGCAGAGGTGCGAGTGAGCCGAGATCCCACCACTGCACTCCAGC 4480
Db 11800 TAACTTGAGCCTTAGGAGGTGGAGGCTACAGTGGGCCACAGTGCATGCCACTACACTCTAGC 11859
QY 4481 CTGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAAG 4532
Db 11860 CTGGGTGACAGAGTAAGACCCCATCTCAAAAAATAAAAAATTAAAAAAAAG 11911
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RESULT 36
US-09-764-853-897/c
; Sequence 897, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ06
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 897
; LENGTH: 13224
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-897

Query Match      7.8%; Score 390; DB 3; Length 13224;
Best Local Similarity 58.6%; Pred. No. 1.1e-78;
Matches 855; Conservative 1; Mismatches 516; Indels 86; Gaps 7;

QY 3105 TTTT---TTGTTGTTTAGAGACAGGGTCTTGTCTGTCAACCAGGCATGAGCACAGTG 3164
Db 7663 TTGTTT---TTGTTT---TTAAGATGGACTCTCACTCTGTCAACCAGGCAGGATGCGAGTG 7604
QY 3165 GTGCAACCATAGGTCACTGACAGCCTCAACCTCCCTGAGCTCAAGGGATCTGCTGACCTCAG 3224
Db 7603 GCGTGATCTCTGCTCACTGACAGCCTCCGCTTCTCGATTCAAGCAATTCTCCTGCCTCAC 7544
QY 3225 CCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACCGCCTGGCTAATTAAAAAAATTT 3284
Db 7543 CCTCCTGAGTCGCTGGGACTACAGGTGCCCGCCACCATGCTGCTGGCTAATTTTGTGA- 7486
QY 3285 TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCTCTGGCTTCAAG 3344
Db 7485 TTTTGTAGAGACAGGGTTTGTCTGTGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTTAAG 7426
QY 3345 CAATCCTCCTACCTTGGCATCCCAAAGTGTCTGGATTAAGGGGTGAGCCACCATGTGCG 3404
Db 7425 TGATCTGCCACCTCAGCCTCCCAAAGTGTCTGGATTACAAGCATAAACTACCAAGCCTG 7366
QY 3405 GCTAC-----TTATTTCTTTTACATTTCCATCTTTTCCAATAGAAATGTA 3445
Db 7365 GCCTCCAAGACTCTGGAGAGAGGGTGACATTTGCTGACACCTTGATTTTGAACCTTCTAGCT 7306
QY 3446 AGATCCACAGAACAGGGATTACTGCCTATTTTCTCTCTTTTCTTTTGTGAGACAGAGTCTC 3505
Db 7305 TCTAGAAATATCAGAGAAATCGATTTCTGTGGTTTGTGTTTGTGTTTGTGAGACAGAGTCTA 7246
QY 3506 ACTTCATCACCTCAACCTCCGTTCA-----GCTCACTGCAACCTTCGCCTC 3551
Db 7245 GCTCTGTGCTCAGCGCGGAGTGCAGTGGCACAAATCTTGGCTCACTGCAACCTTCGCCTC 7186
QY 3552 CCGGGTTCAAGYGATTTCTCTGCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAC 3611
Db 7185 TTGGGTTCAAGCAATTTCTCTGCTCAGCCTCCTGAGTAGTGGGATTACAGGCGCCAC 7126
QY 3612 CACCATGCTTGGCTAATTTTGTATTTTGTAGCAGAGATGGGTTTACCATGTTGCCCCA 3671
Db 7125 CACCATGCCCAGCTAA-TTTTGTATTTTGTAGTAGACAGAGGTTTCACTGTGTGGCCA 7067
QY 3672 GGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGTGG 3731
Db 7066 GGATGGTCTCAAACTCTGACTTCAAGTGATCTGCCCGCCTCGGCCTCCCAAAGTGTGGG 7007
QY 3732 AATTATAGGCGTGACTGCTGCTGGCCGATTACTGTCTATTTTCTTTATTGCTATAT 3791
Db 7006 GATTACAAGCATGAGCCACTGTGCCCAGCTGATTTCTATGGTTT----- 6963
QY 3792 CCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGC 3851
Db 6962 -----TAAGCCACGTGGATTGTGGTCTCTTTTTCGTGACAGTACCAG 6922
QY 3852 ACAGCCTAGATATAAACTTTCTTTTCTTTTAAAAACAATCTTGACAACCTTTGCAGAA 3911
Db 6921 GAAGCCACACAGGGAATCATCAGGATT-----AGAAATAAGATCTGCTGGGCTGGG 6872
QY 3912 TAAATACAATCTTGCATTTCTGCTTTTTCACCTATACCTTGTATGACTTTTTCATATTG 3971
Db 6871 CGCAGTGGCTCATGCCCGCAGTCCCAGCACTTTGGGAGGCCGAGGCGGATCGCCTG 6812
QY 3972 CCTCAAAACCTTTATTGTTACTGTTTCTTTTTCATTGTTACTATTTTAGTCACTGAATAATG 4031
Db 6811 AGCCCGGAGTTAGAGACCAGCTTGACCAACATGGAGAAACCCCGTCTGTACTAAAAATA 6752
QY 4032 GCTTAATTTGCTTTATACATCTCTCTCTGCTCCACTTTAGAAAGGCCAAATTTACAAATCTGAT 4091
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Db      6751  CAAAAAATACCAAGGGCATGGTGACCGCATGTAATCTCAGCTATTTCGGAGGCTGG 6692
QY      4092  GAAAGCTATGAACCCCTCTCCCCAGAGAAATACACACACACACACACTCACACACAGTT 4151
Db      6691  GGCAGGAGATAACTTGAACCCAGAGCGGAGGTTGCGGTGAGCCAAAGATTGCGCCATT 6632
QY      4152  TTTTTTAAATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTA 4211
Db      6631  GCATGCCAGCTGGGCAACAAAAGCGAAACTCGGCCTCAAAA-----AATAAAGAAAGAA 6577
QY      4212  ATTAAAAATAAACTCAGTTGGGCACAGTGACTCAAGCCCTGTAACCAACAGTACTTTGGAGT 4271
Db      6576  ATAAGATCAGCTCAGGCGCGGCATGTGGCTTACGCCCTGTAATCCCAGCACTTTGGGAGG 6517
QY      4272  CCAAGGTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAA 4331
Db      6516  CCGAGGTGGCGGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAA 6457
QY      4332  ACCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCC 4391
Db      6456  ACCCGCCTCTACTAAAAATACAAAAATTAGTTGGGTGTGCTGGTACACACCTATAATCC 6397
QY      4392  CAGCTACTCGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGTTGCAGT 4451
Db      6396  CAGCTACTCGGAGGCTGAGGCAGAAATGCTTGAATCTGGGAGGCAGAGTTGCAGT 6337
QY      4452  GAGCCGAGATCCCACCACCTGCACCTCCAGCCTGGCGACACAGCGAGACTCTATCTCAAAA 4511
Db      6336  GAGCCGAGATCACCCCACTGCACCTCCGSCCTGGCGACAGAGCAAGACTCAGTCTCAAAA 6277
QY      4512  AAATAAATAAATAAATA 4529
Db      6276  AAAAAAAAAAAAAAAAAAGA 6259
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RESULT 37

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US-10-322-281-64/c
; Sequence 64, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 23456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-281-64
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Query Match 7.8%; Score 389.6; DB 7; Length 23456;
Best Local Similarity 59.1%; Pred. No. 2e-78;
Matches 854; Conservative 1; Mismatches 535; Indels 54; Gaps 9;

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QY      3108  TTTTTTGTGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCACAGTGGTG 3167
Db      4452  TATTTTTCCTTTTTTGAGACAGAGTCTTGCTCTGTGCGCCACGGCTGGAGTGCAATGGCG 4393
QY      3168  CAACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGAFTCTGCTGACCTCAGCCT 3227
Db      4392  CCATCTTGGCTCACTGCAACCTCTGCCTCCCGGTTTCAAGCGAFTCTCCTGCCTCAGCCT 4333
QY      3228  CCCAAGTAGCTGGGACTACGAGCGTGCACCAACCAACCGCTGGCTGAATTAACAAAAATTTT 3287
Db      4332  CCTGAGTAGCTGGGATTACAGGCAACCAACCAACCCACCCAGGTAATTTTGA---TTTTT 4276
QY      3288  TGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCTGGCTTCAAGCAA 3347
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Db      4275  AGTAGAGATGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCCGACCTCAGGTGA 4216
QY      3348  TCCTCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGGCT 3407
Db      4215  TCCGTCTGCCTTGGCCTCCCAAAGTGTGGGATTACAGGTGTAAAGCCACACACCGGCC 4156
QY      3408  ACTTATTCTTTACATTCCATCTTTCCAATAGAAATGTAAAGATCCACAGAACAGGGATTAC 3467
Db      4155  TTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 4096
QY      3468  TGCCTATTTTCTCTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGT 3527
Db      4095  CGCCCTCTGTCACCAG-----GCTGGAGTGCAATGGTGGCATC 4058
QY      3528  TCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGA 3587
Db      4057  TCAGCTCACTGCAACCTCCACCTCCCGAGTTCAAGCGATTCCCTGCCTCAGCCTACTGA 3998
QY      3588  GTAGCTGGAATTACAAGCGTGCAACCATGCTTGGCTAAATTTTTTGTAT-TTTTAGCAG 3646
Db      3997  GTAGCTGGGACTACAGGCGGTGCCACCACGCCAGCTAAATTTTGTATTTTAGTAG 3938
QY      3647  AGATGGGJTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACC---TCAAAGTGAT 3702
Db      3937  AGACGGGTTTTCACCATGTTGGCCAGGATGGTCTCCGTCTCCATCTCCTGACCTGTGTAT 3878
QY      3703  CTGCCTGCCCTCAGTCTCCCAAAGTGCTGGAATTATAGGCGTGAGTCACTGTGCTGGCCG 3762
Db      3877  CCGCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGTGCCAGCCT 3818
QY      3763  ATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAG 3822
Db      3817  ATT--TTATTTTAAATAAAACAGAGTGGGGTCTCTCTGCCTCCTGGCCACCTTCTCA 3760
QY      3823  TAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTTCTTTTCTTTT 3882
Db      3759  GCCTTAAGGGCCAGCTTCAGGCTGCCTTCTCCAGGAAGCCTGCCATGACTTCTCCTCT 3700
QY      3883  TTTAAAAACAATCTTGACAACTTTGCAGAAATAAATAACAATCTTGCAATCTTGCT-TTTTCAC 3941
Db      3699  TCTACTCTAACAGCAGAAAGGTTTCTGTCTCAGAAAAGGGCAGTGACCCAGCAGGATCAC 3640
QY      3942  TTATCACCTTGTTATGACTTTTTCATATATTGCCTCAAAACCTTTATTGTTACTGTTTTTCA 4001
Db      3639  CCAGTAAGGGCACAGCCAGGAGCTGAAGGGCCTTTTGCTTGAGCAGCTCCTGGATCACA 3580
QY      4002  TTGTTACTATTTTAGTCACTGAATAA--TATGGCTTAATTTGCTTATACATCCTCCTGC 4058
Db      3579  CTGCTCCTGCATGCAGCACACCGTCACTGACCAGCCGGACATGCTTCCAGAGTTAACTGG 3520
QY      4059  TCCACTTTTAGAAGGCCAAATTTACAAATCTGTGTAAGAGCTATGAACCTCTCCTCCAGAGA 4118
Db      3519  CACTGTTTTGAGAAATGAGAAAAGCACCCCTGAAGAAAAGCAAGCAATTCCTTAAGACAGA 3460
QY      4119  AATACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAA 4178
Db      3459  TCTTAAATGAGAGAGAGAGCAAGAGAAACAACAAGTTTAATGGCATCAGGAGGAAAGCAA 3400
QY      4179  GAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAATAAAATAAATACTCAGTTGGGCACAGT 4238
Db      3399  CAGGTTTCTCTCAGAAATGAGGTATTAGGGGT-----GCTGGGTGTAGT 3356
QY      4239  GACTCAAGCCTGTAACCAACAGTACTTTTGAAGTCCAAGGTGGGTGGATCAGTCACTTGAGGTGA 4298
Db      3355  GGCTCATGCTGTAAATCCAGCACTTTGGAGGCTGAGGCAGGCAGATCAC--GAGGTCA 3298
QY      4299  GAAGTTCGAGACCAGCCTGGTCAAATATGGTGAACCCCTATCTCTACTAAAAATAACAAAAA 4358
Db      3297  AGAGTTTAAGACCAGCCTGGCCCAACATAATGAACCCCACTCTACTAAAAAGTACAAAAA 3238
QY      4359  TTAGCTGGGTGTAGTATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGSCAAGAG 4418
Db      3237  TTAACCGAGTATGGTGTGCACACCTATAGTCCCAGCTACTCGGGAGGCTGCGGCAGGAG 3178
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; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 904
; LENGTH: 75252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-904

Query Match          7.8%; Score 388; DB 5; Length 75252;
Best Local Similarity 60.5%; Pred. No. 8.9e-78;
Matches 868; Conservative 1; Mismatches 511; Indels 54; Gaps 12;

Qy 3107 TTTTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCAGGCATGAGCACAGTGGT 3166
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3025 TTATTATTACTATTTTGGAGACAGAGTCTCGCTCTGTCA-CCAGGCTGGAGTGCAGTGGC 3083

Qy 3167 GCAACCATAGGTCACCTGCAGCCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCC 3226
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3084 GCAATCTGGCTCACTGCAAGCTCACTTCCGGGTTTACGGCATTTCTCTGCCTCAGCC 3143

Qy 3227 TCCCAAGTAGCTGGGACTACGAGCGTGCACCCACCCAGCCCTGGCTAAATTAATAAATTTT 3286
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3144 TCCCGAGTAGCTGGGACTGCAGGCATCGCCACCCAGCCCGACGTAATTTTGTA--TTT 3201

Qy 3287 TTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCAAGCA 3346
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3202 TAGTAGAAACGGGTTTCACCATGTGTCCAGGATGGTCTCTAACTCTTGACCTC--GTG 3259

Qy 3347 ATCCTCTACCTTGGCATCCCAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCGGC 3406
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3260 ATCTGCCACCTCAGCCTCCCAAAATGCTGGGATTACAGGCATGAGCCACTGTGCGCTGGC 3319

Qy 3407 TACTTATTTCTTTACATTTCCATCTTTCCAATAGAATGTAAGATCCACAGAACAGGGATTA 3466
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3320 CGGAAATATTATTATTATTATTATTTTATTTTATTTTATTTTGTGAGAGGAG----- 3373

Qy 3467 CTGCCTATTTTCTTCTCTTTCTTTTGGAGACAGAGTCTCACTTCATCACCTCAACCTCCG 3526
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3374 -----TCTCACTCTGTCAACCAGGCTGGAGTGCAGTGGCATGATC----- 3413

Qy 3527 TTCAGTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCTGCCTAAGCCTCCTG 3586
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3414 -TCGGCTCACTGCAAGCTCTGCCTCCTGGGTTTCATGCCATTCTCTGCCTCAGCCTCCTG 3472

Qy 3587 AGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTGTG-----TATT 3638
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3473 AGTAGCTGGGACTACAGACGCCCGCCACCCACCTGGCTAATTTTCTTTTATATATT 3532

Qy 3639 TTTAGCAGAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAG 3698
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3533 TTTAGTAGAGATGGGGTTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTC--G 3590

Qy 3699 TGATCTGCCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGCGTGAGTCACTGTGCGCTG 3758
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3591 TGATCCACCCGCTCAGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCGTGCCCG 3650

Qy 3759 GCCGATTAAGTCTATTTTCTTTAATGCTATATCCCCAGATCTAGAGCAGTGTCTGACAT 3818
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3651 GCCAGAAATTATTAAATTATAATCATGATGAGTGC----TTCTAGAATGCTAAAAAAAAG 3706

Qy 3819 ATAGTAGTGCTCAATAATAATATTGATGAATGCACAGCCTAGATATAAACTTCTTTTTC 3878
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3707 ATTTTATTATTATTTTATTTTATTTTATTTTGGACGGAGTCTGTGTCT--GTTGCCAGGC 3763

Qy 3879 TTTTTTTAAACAATCTTGACAACCTTTCAGAAATAAATAACAATCTTGCATTTCTGCTTTT 3938
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3764 TGGAGTGCAAATGGTGGATCTCAGCTCACTGCAACCTCCACCTCCTGGGTTTGAGTGATT 3823

Qy 3939 CACTTATCACCTTGTATGACTTTTTCATATTGCTTCAAACTTATTTATTGTTACTGTTT 3998
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3824 CTCCTCCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGTGTGCCACCACACCTGGCTAA 3883
```

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Qy 3999 TCATTGTTACTATTTTAGTCACTGAATAATATATGGCTTAATTTGCTTATACATCCTCCTGC 4058
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3884 TTTTGTATTTTGTAGACCGGGGAGTTTACCATATTTGGCCAGGCTGTTGATC 3943

Qy 4059 TCC--ACTTTAGAGGCCAAATTTACAAATCTGATGAAAAGCTATGAACCTCTCCCCAGA 4116
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3944 TCCTGACCTCAGGTGATTCATCTGCCCTTGGCCCTCCCAAAGTGTGATTGACGGTGTGAGC 4003

Qy 4117 GAAATACACACACACACACACTCACACAGTGTTTTTTTTAAATGTTTGCAACTAAGAC 4176
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4004 CACCAGCCTGTCCCAAAAAAAGATTTTAAATAACAGGGCTGACATAGTTCAGCAGGTGAG 4063

Qy 4177 AAGAAAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATAAAGTGGGCACA 4236
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4064 GGAACAGTTTCTGAGAAAATGATT-TTTAGGTTAAAAACCCCAAAATAGGCCAGGCGTA 4122

Qy 4237 GTGACTCAAGCCTGTAACCCACAGTACTTTTGGAGTCCAAAGTGGGTGATCACTTGAGGT 4296
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4123 GTGGCTCATTCGGGTAATCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCAC--GAGGT 4180

Qy 4297 GAGAAAGTTCGAGACCCCTGGTCAATATGTTGNAACCCCTATCTCTACTAAAAATACAAA 4356
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4181 CAGGCATTGGAGACCAACCTGGCCAAACATGGTGAAACCCCGTCTCTACTAAAAATACAAA 4240

Qy 4357 AATTAGTGGGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAG 4416
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4241 AATTAGCCAGGTAGTGGCGCGCCAGTAATCCAGCTACTCGGGAGGCTGAGGCAGG 4300

Qy 4417 AGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAAGTCCAGTCCAGTCCCACTGCACTC 4476
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4301 AGAATTGCTTGAACCTGGAGGCAGAGGTTGCAGTGGGCGGAGATTGTGCCATTGCACTA 4360

Qy 4477 CAGCCTGGCGACACAGCGAGACTCTATCTCAAAAAAATAAAATAAAATAA 4530
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4361 CAGCCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAATAAAACCAAA 4414
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RESULT 43
US-10-304-107-4
; Sequence 4, Application US/10304107
; Publication No. US20040101855A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PPAR BINDING PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0433
; CURRENT APPLICATION NUMBER: US/10/304,107
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 4
; LENGTH: 48001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1662, 1665, 1668, 1671, 12844, 13431-13530, 13749, 15475, 15509, 15576,
; LOCATION: 20466, 22014, 23090, 23092, 23094, 26394, 30518, 30524, 30673, 36595, 43474
; LOCATION: 46942, 47193, 47198
; OTHER INFORMATION: n = A,T,C or G
US-10-304-107-4
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Query Match          7.8%; Score 387.8; DB 7; Length 48001;
Best Local Similarity 58.2%; Pred. No. 7.7e-78;
Matches 891; Conservative 1; Mismatches 559; Indels 79; Gaps 9;

Qy 3089 TGGTGACAGTTTGGGTTTTTTTTTGTGTTGTTTAGAGACAGGGTCTTGTCTGTCAACC 3148
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 19249 TGGCCAGTTTTTTTTTGGTTTTTTTGTGTTTTTTTGGAGACAGAGTCTCGCTCTGCCA-CC 19307

Qy 3149 AGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGG 3208
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 19308 AGGCTGGAATGCAATGGCATGATCTCGGTTCACTGCAACCTCCACCTCCCGGTTCAAGC 19367
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Qy	3209	GATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGG	3268
Db	19368	AAATTCTCTGGCCTTAGTCTCCCAAGTAGCTGGGACTACAGGCGATGCTGCCACGCCTGG	19427
Qy	3269	CTAATTAAAAAATT-----TTTTTGTAGAGACTGGGTCTTTACTACGTTGGCCAGGCTTGT	3324
Db	19428	CTAATTTTTTTTTTTTGTATTTTATAGAGACGGGTTTTCACCGTGTGCCCAGGCTGCT	19487
Qy	3325	CTTAAACTCCTGGCTTCAAGCAATCCTCCCTACCTTGGCATCCAAAAAGTGTGGGATTACA	3384
Db	19488	CTCAAACTCCTGAGCTCAGGCAATCTGCCCTCCTCGGCTTCCCAAATTGCTAGGATTATA	19547
Qy	3385	GGGTTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTCCATCTTTTCCAATAGATGT	3444
Db	19548	GGCATGAGCCACTGCGCCTGGCCAGTTTTTAAAAATATATATATATTTTTTGCCTTCAAT	19607
Qy	3445	AAGA-----TCCACAGAACAGGGATTA	3466
Db	19608	TAGACTTGCTCTTTAGGCCCTTCTATGTCACTGTTTGTGTCTGTATATATATGTGTATT	19667
Qy	3467	CTGCCTATTTCTTCTCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACTCAACCTCGG	3526
Db	19668	TTTCAACTTTTTTTTTTTTTTTTTTTTGTAGATGGAATCTTGTCTGTCAACCCAGGCTGGAG	19727
Qy	3527	TTCA-----GCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCT	3572
Db	19728	TGCAGTGGTATGATCTTGGCTCACTGCAACCTCTTCTCTCGGTTCAAGCAATTCTCCT	19787
Qy	3573	GCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTT	3632
Db	19788	GCCTCACCCCTCCGAGCAGCTGGGATTACAGGTGCCTGCCACCAGCTCGGCTAA-TTTT	19846
Qy	3633	TGTATTTTACGAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGAC	3692
Db	19847	TGTAGTTTATGAGATGGGGTTTTTGCCATGTTGGCCAGGCGGCTCTCAAACTCCTGAC	19906
Qy	3693	CTCAAGTGTATGCCTGCCTCAGTCTCCCAAAGTGTGGAAATTATAGGCGTGAGTCACTG	3752
Db	19907	CTCAGGTGATCTGCCCCCTCAGCCTCCCAAAGGTGCTGGGATTACAGGCTGAGCCACCC	19966
Qy	3753	TGCCCTGGCCGATTACTGTCTATTTTTCTTTTATTGCTATATCCCCAGATCTAGAGCAGTGC	3812
Db	19967	GCTTGGTCAATATTTTCAACTATTAACTCATGTTCTTCTCATCTACTCTCCAGCAAAC	20026
Qy	3813	TGACATATAGPAGGTGCTCAATAAAATAATTGATGAATGCACAGCCTAGATATAAACTTTC	3872
Db	20027	AAGACTAAAAATGTAATTGGCTCTCCAATCCTTAGAACAAGATCTTCTAAAAATGGCAATT	20086
Qy	3873	TTTTTTCTTTTTTAAAAACAATCTTGCACAACTTTGCAGAAATAAATACAAATCTTGCAATCTG	3932
Db	20087	ATGTACTGGTAAGACTGCTAAAAACCTTAAATCTACATGATCCCTTGAGTTTTTCTCTGGG	20146
Qy	3933	CTTTTTTCATCTATCACCTTGTATTGACTTTTTTCATATTGCCCTCAAA-----	3978
Db	20147	GAGATTAGGGTCCCTATTTTATACATCTCTATTAAAGCCTGTATGATAAATATGTCCTTCTC	20206
Qy	3979	--CCTTTATTGTTACTGTTTTTTTCATTGTTACTATTTTGTAGTCACTGAATAATATGGCTTA	4036
Db	20207	TTCCAAAATGATGATTGTATTTTGAACCTTCTGAGTATCAGTATCGCTAAAGTTGTGGTTAC	20266
Qy	4037	ATTTGCTTATACATCCTCCTGCTCCACTTTTAGAAGGCCAAATTTACAAAATCTGATGAAAG	4096
Db	20267	CATAGGTTTTTATCTCAAGACTCATCAGACCTGGAGTCCCATCTGAGAAAATAATAGTCTAA	20326
Qy	4097	CTATGAACCTCTCTCCCCAGAGAAAATACACACACACACACTCAACAGTATTTT	4156
Db	20327	GTGTAATTTTGTTCACCATACTACATACTGGTGTGTACTTTGGAATAATCCCTTTACTT	20386
Qy	4157	TTAATGTTTGCAACTAAGACAAGAAACCTGTCATTAGAGGATGTTTGTTCATATTAATTA	4216
Db	20387	TGGAGGTGAAATACATTTTGCTATATGCCCAATTACAAGACAGAACCATTATGATAGTATT	20446

Qy	4217	AAATAAECTCAG---TTGGGCACAGTGACTCAAGCCTGTAACCAACACAGTACTTTTGGAAGTCC	4273
Db	20447	ATAAGACTTTGGGCTGGCNGCGGTGGTGCACGCCTGTAATCCAGCACACTTTGGGAGGCC	20506
Qy	4274	AAGTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAAAC	4333
Db	20507	GAGCGGGCGGATCACTGAGGTCAAGGTTCGAGACCAGCCTGCCCAATATGGTGAAAC	20566
Qy	4334	CCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCC	4392
Db	20567	CCCGTCTCTACTAAAAATACAAAAAATTATCTGGCGTGGTGGCGGCCTGTATATCCC	20626
Qy	4393	AGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGTTGCAGTG	4452
Db	20627	AGCTACTCGGGAGGCTGAGGCAGGAGAAATCACTGGAACCTGGGAAGCGGAGTTGCGGTG	20686
Qy	4453	AGCCGAGATCCCACCCTGCACTCCAGCCTGGGCAC-ACAGCGAGACTCTATCTCAAAA	4511
Db	20687	AGCTGAGATTGTACCCTGCACTTCAGCCTGGGCACAAGAGCGAANACTCCGCTCTCAAAA	20746
Qy	4512	AAATAAATAAATAAAAAAAGGATCGGAGA	4541
Db	20747	AAAAAAAAGACAAGACTTCGGAGAGGTGA	20776
RESULT 44			
US-10-262-552-33			
; Sequence 33, Application US/10262552			
; Publication No. US20030125289A1			
; GENERAL INFORMATION:			
; APPLICANT: Gelb, Bruce D.			
; APPLICANT: Tartaglia, Marco			
; TITLE OF INVENTION: NOONAN SYNDROME GENE			
; FILE REFERENCE: 2420/1J859-US1			
; CURRENT APPLICATION NUMBER: US/10/262,552			
; CURRENT FILING DATE: 2002-10-01			
; PRIOR APPLICATION NUMBER: US 60/326,532			
; PRIOR FILING DATE: 2001-10-01			
; NUMBER OF SEQ ID NOS: 35			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 33			
; LENGTH: 300000			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; LOCATION: (1)..(300000)			
; OTHER INFORMATION: where n may be a or g or c or t/u, unknown or other			
US-10-262-552-33			
Query Match 7.8%; Score 387.8; DB 6; Length 300000;			
Best Local Similarity 58.0%; Pred. No. 2.2e-77;			
Matches 849; Conservative 1; Mismatches 558; Indels 57; Gaps 7;			
Qy	3067	CCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTAGAG	3126
Db	146243	CCAACACTGGAAATCATATTTTTCATATCTCTTTTGTGTTGTTTGTGTTGAG	146302
Qy	3127	ACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCAC	3186
Db	146303	ACGAGTCTTGCTCTGTCAACCCAGGCTGAATTGCAGTGGCGGATCTTGGCTCACTGCAA	146362
Qy	3187	CCTCAACCTCCTGAGCTCAAGGGATCTGTGACCTCAGCCTCCCAAGTAGCTGGGACTAC	3246
Db	146363	CCTCCACCTTCTGGGTTCAAGCAATTCTCCTGTCTCAGCCTCTCGAGTAGCTGGAAC	146422
Qy	3247	GAGCGTGCACCACCGCTGGCTAAATTAAAAAAATTTTTTGTAGAGACTGSGTCTTAC	3306
Db	146423	AGACACATGCCACCACCGTCAGGCTAATTTTGTGA--TTTTTAGTAGACAGAGGTTTCAC	146480
Qy	3307	TAGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCAAGCAATCCTCTACCTTGGCATCC	3366
Db	146481	CATATTGCTCAGGCTGTTCTTGAATTCCTGACCTCAGGTGATCCACCCGCTCAGCCCTCC	146540

QY	3367	CAAAAGT	GCTGGG	ATTACAG	GGGTGAG	CCACC	ATGTG	CGGCTAC	TATTAT	TCTTTAC	ATTCC	3426			
Db	146541	CAAAAGT	GCTGAG	ATTACAG	GGGTGAG	CCACC	ATGTG	CGGCTAC	TATTAT	TCTTTAC	ATTCC	146594			
QY	3427	ATCTTTT	CCAATAG	AATGTA	AGATCC	ACAGAA	CAGGGA	TACTGC	CTATTT	TCTTCCT	TTTC	3486			
Db	146595	TTTTTTT	GAGATAG	AGTG	-----	-----	-----	-----	-----	-----	TC	146613			
QY	3487	TTTTTTT	GGAGAC	GAGAGT	CTCACT	TCAATC	ACCTCA	ACCTCG	GTTCAG	CTCACT	GCAAC	CTCT	3546		
Db	146614	TCTCTGT	TGCCCA	AGCTGG	AGTGCA	GTGGCG	CAATC	-----	TCAG	CTCACT	GCAAC	CTCT	146668		
QY	3547	GCCTCC	CGGGTT	CAAGYGA	TCTC	CTGCCT	TAAGC	CTCCTG	AGTAG	CTGGA	ATTACA	AGCG	3606		
Db	146669	GTCTCC	CAGGTT	CAAGTGA	TTCT	CGTGC	CTCAG	CCTCC	CAAGT	AGTGG	ATTAC	AGCG	146728		
QY	3607	TGCACCA	CCATG	CTGGCT	AAATTTTT	TTTGT	ATTTTT	TAGC	AGAGAT	GGGGT	TTTTAC	CATGTT	3666		
Db	146729	CCTGCC	CAAGAC	CAAGCT	AA-TTTTT	TGTAT	TTTTTT	TAGC	AGAGAT	GGGGT	TTTTAC	CATGTT	146787		
QY	3667	GCCCAG	GCTGGT	CTCAAA	CTCCTG	ACCTCA	AGTGAT	CTGCCT	GCCTC	AGTCT	CCCCAA	AGT	3726		
Db	146788	AGCAAG	GCTGGT	CTTGA	ATCTTG	ACCTTA	AGTGAT	CTGTCC	GCCTC	AGCCT	CCCCAA	AGT	146847		
QY	3727	GCTGGA	ATTATAG	GGGTGAG	TCAC	TGTG	CCCTG	CGCCG	ATTACT	GTCTAT	TTTTCT	TATTGC	3786		
Db	146848	GCTGGG	ATTACAG	GTGTG	AGCCACT	GTG	CCCCG	ACCTGT	GCCCC	AGGAAT	CATAT	TTTCA	ATGAGA	146907	
QY	3787	TAT-AT	CCCCAG	ATCTAG	AGCAGT	GTCTG	ACATAT	ATAGT	AGTGCT	CAATAA	ATAATT	GTAT	3845		
Db	146908	CATAAA	AGGAATA	AAACAT	CCAAAC	CATATAC	ATATTT	GATTG	AGTAA	AGTAA	AGTACT	ACT	146967		
QY	3846	GAATGC	ACAGC	CTAGAT	ATAAA	ACTTT	CTTTT	TCTTTT	TTTAAAA	CAATCT	TGACA	ACTTT	3905		
Db	146968	ATGAAA	AGAAAT	AGTGTG	CAAAA	AATGACT	GAGAAA	CAGGAG	ACCTAT	TGTGTT	TGGGG	147027			
QY	3906	GCAGAA	TAAATACA	ATCTTG	CAATCT	GCTTTT	TTTTC	ACTTAT	CACCTT	GTTATG	ACTTTT	TC	3965		
Db	147028	AATCAG	ATGCTCT	ACGAG	GAAGCT	GATAA	CTGG	AGATAG	GTAG	GAGTTT	TGCCA	AGTG	147087		
QY	3966	ATATTG	CCCTCAA	ACCCTTT	TATTG	TACTG	TTTTTT	TTCATT	GTACT	ATATTT	TAGTCA	CTGAAT	4025		
Db	147088	AAGCAG	TGGCG	GAAGG	CATTCT	GCGAG	GGGGA	CAGCA	AGTG	CAAA	GGCCTA	GAGGTAG	147147		
QY	4026	AATATG	GCTTAA	TTTGCT	TATAC	ATCCT	CTCTGC	-TCC	ACTTTT	AGAG	CCCAA	ATTAC	AA	4084	
Db	147148	GAAAAT	GGTACA	ATTTG	TAAAG	AAACTG	CAAGC	AGTC	AGG	TGCTG	AGATGA	AGA	147207		
QY	4085	ATCTGA	TGAAAG	CTATGA	ACCCTC	TCTCCC	CAGAG	AAATAC	ACACAC	ACACAC	ACTC	ACA	4144		
Db	147208	TGGGCAT	TGTATG	CCTAAG	ATCTC	AGAAG	CACAG	ACAAC	AAAAAC	AGACA	AAACAG	GA	147267		
QY	4145	CACAGT	TTTTTT	TTTAA	TGTTT	GCAACT	TAAG	CAAGAA	ACCTG	CAATT	TAGAG	GATGTT	4204		
Db	147268	AAACCA	AAAAAG	CTTCTG	TACAG	CAAAA	AGAAATA	ATCA	AGATA	TAATGA	ACCA	CAAC	ACA	147327	
QY	4205	CATATT	TAATTAA	AAATAA	CTCAG	TGGGC	CACAGT	GACTCA	AGCCTG	TAAC	CAAC	AGTACT	4264		
Db	147328	CAATGA	AAAGAAA	ATATCT	GTGG	CCAGG	CACAGT	AGCTCA	CACTTGT	AAATCC	CAGCAT	TT	147387		
QY	4265	TGGAAG	TCCAAG	GTGGT	GGATCA	CTTGA	GGTG	AGAGT	TCGAG	ACCAG	CCTGGT	CAATA	4324		
Db	147388	TGGAGG	CCCAAG	GTGGC	AGATCAC	CTTG	AGGT	CAGAG	CTTG	AGACC	AGCCTG	GGCCA	ACA	147447	
QY	4325	TGGTGA	AAACCT	TATCT	TACTAA	AAAAAT	ACAAAA	ATTAG	CTGG	TGTAG	TGATG	CATG	CCT	4384	
Db	147448	TGGTAA	AAACCC	CAATCT	CTACTA	AAAAAT	GTAAAA	ATTAG	CTGG	TGTGG	TGG	CA	TGTAC	CT	147507
QY	4385	GTAGT	CCCAG	CTACT	CTGG	GAGG	CTGAG	GCAAG	AAATTG	CTTTGA	ACCTGG	GAGG	CAGAG	4444	
Db	147508	GTAAT	CCCAG	CTACT	TTGG	GAGG	CTGAG	GCAAG	AAATTG	CTTTGA	ACCCG	GAGAT	GATG	147567	

Qy	4445	TTGCAGT	GAGCCG	AGATCCC	ACCAC	TGCAC	TCCAG	CCCTGG	CGGAC	ACACAG	CAGACT	CTAT	4504
Db	147568	TTTCAGT	GAGCCA	AGATTG	CACCA	CTGC	ACTCC	AGCCTGG	GAGAC	AGAGT	GAGACT	GTCT	147627
Qy	4505	CTCAAAA	AAAAATA	AAAA	TAAAA	TATA	4529						
Db	147628	CAAAAA	AAAAAT	CAATAC	ATAAAA	AAAA	147652						
RESULT 45													
US-10-703-210-33													
; Sequence 33, Application US/10703210													
; Publication No. US20040121384A1													
; GENERAL INFORMATION:													
; APPLICANT: Gelb, Bruce D.													
; APPLICANT: Tartaglia, Marco													
; APPLICANT: Niemeyer, Charlotte													
; TITLE OF INVENTION: PTPN11 (SHP-2) Mutations And Cancer													
; FILE REFERENCE: 02420/100M124-US1													
; CURRENT APPLICATION NUMBER: US/10/703,210													
; CURRENT FILING DATE: 2003-11-05													
; PRIOR APPLICATION NUMBER: US 60/424,170													
; PRIOR FILING DATE: 2002-11-05													
; NUMBER OF SEQ ID NOS: 39													
; SOFTWARE: PatentIn version 3.1													
; SEQ ID NO 33													
; LENGTH: 300000													
; TYPE: DNA													
; ORGANISM: Homo sapiens													
; FEATURE:													
; NAME/KEY: misc_feature													
; LOCATION: (1)..(300000)													
; OTHER INFORMATION: where n may be a or g or c or t/u, unknown or other													
US-10-703-210-33													

Query Match													
Best Local Similarity 7.8%; Score 387.8; DB 7; Length 300000;													
Matches 849; Conservative 1; Mismatches 558; Indels 57; Gaps 7;													
Qy	3067	CCAAGATCACACAGCTTGTAAAGTGGTGACAGT	TTTGGGTTTTTTTGTGTTGTTAGAG	3126									
Db	146243	CCAACACTGGAATCATATTTTTCATATCTCTTTTGTGTTGTTTGTGTTTGAG	146302										
Qy	3127	ACAGGGTCTTGCTGTCA	CCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAG	3186									
Db	146303	ACGGAGTCTTGCTGTCA	CCAGGCTGAATTGCAGTGGCGGATCTTGGCTCACTGCAA	146362									
Qy	3187	CCTCAACCTCCTGAGCTCA	AGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTAC	3246									
Db	146363	CCTCCACCTTCTGGGTTCA	AGCAATTTCTCCTGTCTCAGCCTCTCGAGTAGCTGGAACCTAC	146422									
Qy	3247	GAGCGTGCACACACCGCCTGGCTAA	TTAAAAAATTTTTTTGTAGAGACTGGGTCTTAC	3306									
Db	146423	AGACACATGCCACACCGTCAGGCTAA	TTTTTGTAGTAGAGACAGGGTTTTTCAC	146480									
Qy	3307	TACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCA	AGCAATCCTCCTACCTTGGCATCC	3366									
Db	146481	CATATTGCTCAGGCTGTTCTTGAATTCCTGACCTCAGGTGATCCACCCGCTCAGCCTCC	146540										
Qy	3367	CAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTC	3426										
Db	146541	CAAAGTGTGAGATTACAGGCATGAGCCACCACACCCAG-----AGGTTTTTTTGATCGT	146594										
Qy	3427	ATCTTTCCAATAGAAATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCCTTTC	3486										
Db	146595	TTTTTTTGAGATAGAGTG-----TC	146613										
Qy	3487	TTTTTTTGAGACAGAGTCTCACTTTCATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTCT	3546										
Db	146614	TCTCTGTTGCCCAAGCTGGAGTGCAGTGGCGCAATC-----TCAGCTCACTGCAACCTCT	146668										
Qy	3547	GCCTCCCGGGTTCAAGYGATTCTCCTCGCTAAGCCTCCTGAGTAGCTGGAATTACAAGCG	3606										

Db 146669 GTCTCCAGGTTCAAGTGATTCTCGTGCCTCAGCCTCCCAAGTAGCTGGATTACAGCGG 146728

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Db 146729 CCTGCCACCAAGACCAGCTAA-TTTTGTATTTTGTAGTACAGACAGGGTTTCACCATGTT 146787

QY 3667 GCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTCAGTCTCCCAAAGT 3726

Db 146788 AGCAAGGCTGGTCTTGAATTTCTTGACCTTAAGTGATCTGTCCGCTCAGCCTCCCAAAGT 146847

QY 3727 GCTGGAATTATAGCGGTGAGTCACGTGCTGCCTGGCCGATTACTGTCTATTTTCTTTATTC 3786

Db 146848 GCTGGGATTACAGGTGTGAGCCACTGTGCCCGACCCCGGGAATCATATTTCAACATGAGA 146907

QY 3787 TAT-ATCCCCAGATCTAGAGCAGTGTCTGCATATAGTAGTGTCTCAATAAATAATTGAT 3845

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Db 147028 AATCAGATGCTCTACGAGGAAGCTGATAACTGGAGAAATAGTAGGAGTTTGCCAAGTG 147087

QY 3966 ATATTGCCTCAAACTTTTATTGTTACTGTTTTTTTCATTGTTACTATTTTGTACTGAAT 4025

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QY 4026 AATATGGCTTAATTTGCTTATACATCCTCCTGC-TCCACITTTAGAAGGCCAAATTTACAA 4084

Db 147148 GAAAATGGTACAATTTGTTAAAGAACTGCAAGCAGTCAAGGTGCGCTTGCTGAGATGAAGA 147207

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QY 4385 GTAGTCCAGTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGG 4444

Db 147508 GTAATCCCAGTACTTGGGAGGCTGAGGCACGAGAGTTGCTTGAACCCCGGAGATGGATG 147567

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Db 147628 CAAAAAATAATCAATACATAAAAAA 147652

RESULT 46

US-10-271-416-1

; Sequence 1, Application US/10271416

; Publication No. US20040043021A1

; GENERAL INFORMATION:

; APPLICANT: Keith, Tim

; APPLICANT: Little, Randall D.

; APPLICANT: Van Eerdewegh, Paul

; APPLICANT: Dupuis, Josee

; APPLICANT: Del Mastro, Richard G.

; APPLICANT: Allen, Kristina

; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES

; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY

; FILE REFERENCE: 2976-4045

; CURRENT APPLICATION NUMBER: US/10/271,416

; CURRENT FILING DATE: 2002-10-11

; PRIOR APPLICATION NUMBER: 60/328,424

; PRIOR FILING DATE: 2001-10-11

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 304905

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-271-416-1

Query Match 7.7%; Score 386.4; DB 7; Length 304905;

Best Local Similarity 53.3%; Pred. No. 4.7e-77;

Matches 1246; Conservative 2; Mismatches 923; Indels 167; Gaps 14;

QY 2277 TAAAAATCGCTTTTCAGGCCAGGCGCGGTGGTGCATGCCTGTAATCCCAGCACACTTTGGGAG 2336

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QY 2337 GCCGAGCGGGCGGATCACTTGAGGTCAGGATTCGAGACCAGCCTGGCCACATGGTGA 2396

Db 13114 GCCGAGGTGGGCGGATCATCTGAGGTCAGGAGTTCAGAGCCAGCCTGGCCACATGGTGA 13173

QY 2397 AACCCCTGTC-----TCTACTAAAAAATACAAAAATTAGCCGGAC 2435

Db 13174 AACCCCTTCTCTATAAAATACAAAAAATAAAAAAATTAGCCAGGC 13233

QY 2436 ATGGTGGCAGCGCCTGTAAACCCAGCTACTTGGGAGACTGAGTTGGAGGTTTCAGTGAG 2495

Db 13234 ATGGTGGTGACGCGCTGTAATCCTAGCTACTTTGGGAGGCTGAGGTAGAAGAATCACTTGA 13293

QY 2496 CCAAGGTCGTCACTGCTGTCCAGCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAA 2555

Db 13294 ACCCGGGAG-GCGGAGGTGGCAGTGAGCAGAGACCACGCGCTGTACTCCAGCCTGGGTG 13352

QY 2556 AAATGCTTTCAATAAATATATGATAAAAGGACTATATATTTTCAAGCCATAGGATCATT 2615

Db 13353 ACAGAGTAAGACTCTGTCTCAAAAAAATAAAAAAGAAATTTGAGAATTCCTTGGCCTTGAG 13412

QY 2616 TCTCCTGAAGCATCTTGGCGAAGTCATCCCCACCTCTTCTTGAGAGTGGGCGAGGTGAGGG 2675

Db 13413 TTTCTAGTGGCAATCACAGTTGGTTTTTGGCCGACTCTCTTCTTAGCAACCA----- 13464

QY 2676 CTGACCTATTGCTCTGCACTTACTCCTATCTCAGGTGTCCCTCCCACCTTTCAGGTGCTG 2735

Db 13465 -----GCAACCCCAATTTTCTTGGGAGCAGCCCTTTCCCCACTTCTGGTCTCA 13514

QY 2736 CCAGACACATGACAACTGTAYGACCAGGCCAAGAAGCTGGACAGCTGTAAATTCTGCT 2795

Db 13515 GTAGTTAGCTGACTCCACCTCCCCCAGCTGTCTCTGGCCAAATCAGAGCACTACCTCTCT 13574

QY 2796 GGACAMMCCGTACACCCACACCTATTTCATACTCGTGTCTTGGCTCGGCAATCACCTGTAG 2855

Db 13575 GG-----GGGTTGCTATGATTGGTTCAGGACTGAGCCAGTGAGAAATGAGAAGAGGAGG 13627

QY 2856 CAGTAGGTTTATCCCTTCTTGGACCTATGAATTTCTAGTTGGTTCTCAGTAGGCCGGGGG 2915

Db 13628 CTCTGTGTCCTTACCCGAGGATATAGAGCTGGGAGGATGGAATTTGGAGCCACTGAGGG 13687

QY 2916 AAATAATAGTAAACACAGCCATGATTTAGTGTAAATTTTCTTGGTTCTGGGCAGTGTCTC 2975

Db 13688 GCATCCTTGCCACTAGAAAAAGGGAGCCCACTCGGGGGTGAGGCTGGGAGAAAGCCAGCC 13747

QY 2976 CTTTAATCCTCAGAACAAACACTATGGGATAGGTAGCAATTATCCTCACTTAACAGATAAGA 3035

Db	13748	CAGAAAGAAACGAGAGTTGAGAGATGGCAAGAGAAAAAT--TGCTAATGTTCATGAGTCAAG	13805
QY	3036	AAACTGAGGCTCAGAAGGCTGAGCTATTTTGGCCCAAGATCACACAGCTTGTAAAGTGGTGAC	3095
Db	13806	TTCTTGATCCAAACCATACCTGAAGCTGTAATATTGCACTTGTCAATGAGCCTGGGTAGT	13865
QY	3096	AGTTTGGGTTTTTTTTTGTGTTGTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATG	3155
Db	13866	AAATTTCCCTTTTTTTTTTTTTTTTTTTTGTAGATGGAGTCTCGCTCTGTGCGCCAGGCTAG	13925
QY	3156	AGCACAGTGTGCAACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGC	3215
Db	13926	AGTGCAGTGGCGCAATCTCAGCTCACTGCAAGCTCCGTCTCTGGGTTTCATGCCATTCTC	13985
QY	3216	TGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGGCTAAATTA	3275
Db	13986	CTGCCTCAGCCTCCTGAGTAGCTGGGACTACAGGTGCCCGCACCAAGCCTGGCTAAATTT	14045
QY	3276	AAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCT	3335
Db	14046	TTTGTA-GTTTTAGTAGAGACAGGGTTTACCGTGTTAGCCAGGATGGTCTCGATCTCCT	14104
QY	3336	GGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCA	3395
Db	14105	GACCTC--GTGATCCACCCACCTTGGCCTCCCAAAGTCTGGGATTACAGGCGTGAGCCA	14162
QY	3396	CCATGTGCGGCTACTTATTTCTTTTACATTCCATCTTTTCCAATAGAAATGTAAGATCCACAG	3455
Db	14163	CCGCGCCCGGC--CTTATTTTTTTTTTTTAAATTTTTTTTTTTTGGAGACAAAG-----	14212
QY	3456	AACAGGGATTACTGCCTATTTTCTTCCTTTCTTTTTTTTGAGACAGAGTCTCACTTTCATCAC	3515
Db	14213	-----TCTCATTTCTGTCAACGAGGCTGGAGTGCACTGG	14245
QY	3516	CTCAACCTCCGTTTCACTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTTCTCCTGCC	3575
Db	14246	CACAATC----TCTGCTCACTGCAACCTCTGCCTCTCGGGTTCAAGCGATTCTCTCTACC	14300
QY	3576	TAAGCCTCCTGAGTAGCTGGAAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTTTTGT	3635
Db	14301	TCAGCCTCCTGAGTAGCTGGGATTACAAGCATGTGCCAACATGTCCAGCTAA-TTTTTGT	14359
QY	3636	ATTTTTAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACCTCCTGACCTC	3695
Db	14360	ATCTTTAGTGAGACGGGGTTTTCATCACGTTGGCCAGGCTGGTCTTGAACCTCTGGGCTC	14419
QY	3696	AAGTGATCTGCCTGCCTCAGTCTCCAAAAGTCTGGAATATATAGGCGTGAGTCACTGTGC	3755
Db	14420	AAGTGATCCGCCACCTCGGCCCTCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGGAC	14479
QY	3756	CTGGCCGATTACTGTCTATTTTCTTTATTG-----TCTTTTCTTTTCA-----	3785
Db	14480	CCGGCCACTTTTCTTTTTTTTGTGTTATCGTGGGAGTGGTGTGTTTAAATGACTGGCAAAA	14539
QY	3786	-----CTATATCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATA	3839
Db	14540	GAATGTTGATAAGCGCCTTTTCTGCGTAATGTGAAGATCTTGGAAATTTCTGGAATAGCT	14599
QY	3840	ATTGATG--AATGCACAGCCTAGATATAAACTTTTCTTTTCTTTTAAAAACAATCTT	3896
Db	14600	ATGGGGGAAAGCGCTAGGACCTGAGAGTCACTCCCAATTTATTTTATTATATATATT	14659
QY	3897	GACAACTTTCAGAAATAAATAACAATCTTGCATTTCTGCTTTTTC-----TCTCA-----	3940
Db	14660	GTCATAGACAGGGAGTCTTGTGCTGCGTTGCCAGGATGGTCTCAAACCTCCTGGCCTCAAG	14719
QY	3941	-----CTTATCACCTTGTGTTATGACTTTTTTTCATATTGCTCTCAAACTTT	3983
Db	14720	AGAACCTCTGCCTCCGCCCTCCCAAAGTACTGGCATTACAGGCATGAGCCGCGAGTGCCTG	14779
QY	3984	ATTGTTACTGTTTTTTCATTTGTTACTATTTTAGTCACTGAATAATATGGCTTAAATTGCT	4043

Db	14780	GCAGGTTCCACTTCCAAATTGTTAAGAGTCTGAAGCCAGAGACAGTTTGGTCTCTTTCATGCT	14839
Qy	4044	TATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAGCTATGAA	4103
Db	14840	CAAACTGGGTAGCGATGCTGCACCTGCAGGCGAGGGTGCCTAGCACCATGAGTGCAGTGAG	14899
Qy	4104	CCCTCTCCCCAGAGAAATACACACACACACACACTCACACACAGTTTTTTTTTAATGT	4163
Db	14900	GTGGCCCTGTGGCAAAACCCAGGAGCCTGGAGGGTCCAAAAGGCCACAATAGACTGGGG	14959
Qy	4164	TTCCAACCTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAATAATAAC	4223
Db	14960	GAGATTTGAAGAGAAAGCCTGAAAAACTCAAGGTTTCAAGTATCAGCAAAACCATGGGAG	15019
Qy	4224	TCAGTTGGGCACAGTGACTCAAGCCTGTAAACACAGTACTTTGGAAAGTCCAAGGTGGGTG	4283
Db	15020	ACGCCAGGTGAAATGGTGACATCTGTAAATCCCGCACCTTTGGGAGGCCGAGGCAGGTG	15079
Qy	4284	GATCACATTGAGGTGAGAAAGTTTCGAGACCAGCCTGGTCAATATGGTGAAACCTATCTCTA	4343
Db	15080	GCTCACCTGAGGTGAGGAGTTCGAGACCAGCCCGTCAACATGGTGTAACCCCGTCTCTA	15139
Qy	4344	CTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCCGACTACTCGGG	4403
Db	15140	CTAAAAATACAAAAATTATCCAGGCATGGTGGCAGGTGCCCTGTAATCCCGACTATTTGGG	15199
Qy	4404	AGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGCCAGAGGTTGCAGTGAGCCGAGATCC	4463
Db	15200	AGGCTGAAGTAGGAGAAATCACTGAACCTGAGAGGCGGAGGTTGCAGGGGAGCCAAAGATTG	15259
Qy	4464	CACCACTGCACTCCAGCTGGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAA	4521
Db	15260	CACCATTCACACCAGCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAATAAATAA	15317

RESULT 47

```

US-10-087-192-58
; Sequence 58, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 61103
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(61103)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-58

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	Query Match	7.7%;	Score 385.2;	DB 5;	Length 61103;
	Best Local Similarity	59.4%;	Pred. No. 3.5e-77;		
	Matches 869;	Conservative	1;	Mismatches 499;	Indels 95; Gaps 9;
Qy	3099	TTGGGTTTTTTTGTGTTTAGACAGAGGCTTGCTCTGTCAACCAGGCATGAGC	3158		
Db	34982	TTTATTATTATAATGTATTATTAGACAGAGTCTCGCTCTGTCAACCAGGCTGGAGT	35041		
Qy	3159	ACAGTGGTGCAACCATAGGTCACTGCAGCCCTCAACCTCCTGAGCTCAAGGGATCTGCTGA	3218		

Db 35042 GCAATGGCACAGTCTCTGCTCACTGCAACCTCCGCCCTCCTGAGTTCAAGCGATTCTCCTG 35101
Qy 3219 CCTCAGCCTCCCAAGTAGCTGGGACTPACGAGCGTGCACCACACGCTTGCTAAATTAATA 3278
Db 35102 TCTCAGCCTCCCAAGTAGCTGGGATTACAGGCCCATGCCGTCACGCCCAGCTGATT--TT 35159
Qy 3279 AAATTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGC 3338
Db 35160 TTGTATTTTAGTAGAAACGGGGTTTCACTGTGTTGCCAGGCTGGTCTCGAACTCCTGAG 35219
Qy 3339 TTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACCA 3398
Db 35220 CTCAGGCAGTCCACCCGCCCTTGGCCCTCTCAAAGTGCTGTGATTACAGGCGTGAGCCACTG 35279
Qy 3399 TGTGCGGCTACTATTCTTTACATTCCATCTTTCCAATAGAAATGAAGATCCACAGAAC 3458
Db 35280 CGTCCGGCCGCCCTTTT TTTT----- 35299
Qy 3459 AGGGAATTACTGCCTATTTTCTTCCCTTCTTTTGTAGACAGAGTCTCACTTCAATCACCTC 3518
Db 35300 -----TTTAGATGGAGTTTCGCTCTGTAGCCCAAGGCTGGAGTGCAGTGGCG 35346
Qy 3519 AACCTCCGTTCACTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAA 3578
Db 35347 AACTCGGT-----TCACTGCAAGCTCTGCCTCCCGGTTACGCCCATCTCTCCTGGCTCA 35401
Qy 3579 GCCTCCTGAGTAGCTGGAATTACAGCGGTGCACCACCATGCTTGGCTAATTTTTTGTAAT 3638
Db 35402 ACCTCCGAGTAGCTGGACCAACAGCGCCCCGCCACCACCGCCGCCAATTTTTTGTAAT 35461
Qy 3639 TTTAGCAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAG 3698
Db 35462 TTTAGTAGACGGGGTTTACCCGTGTAGCCAGGATGGTCTCGATCTCCTGACCT--TG 35519
Qy 3699 TGATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGGTGAGTCACTGTGCCTG 3758
Db 35520 TGATCTGCCGCCCTCAGCCTCCCAAAGTGTGGGATTACAGGGTGAGCCACCGCACCG 35579
Qy 3759 GCCGATTACTGTCTATTTTCTTTATGTCTATAT-----CCCCAGATCTAGAGC 3806
Db 35580 GCTCCCCCTTTTATTTTATTGATTTTTTTTTTTTTTTTGAGAGGCGAGTCTCGCTCTGTGCG 35639
Qy 3807 AGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATA 3866
Db 35640 CGAGGCTCGAGTGCAGTGGCACGATCTCGGCTCGTGCAACCTCCACCTCCTGGGTTCAA 35699
Qy 3867 A--CTTTCITTTTCTTTTTTAAACAACTTTTGACAACTTTTGACAGATAAATACAATCTT 3924
Db 35700 ATGATTCTCTGCCTCAGCTTCTGTAGTAGTGGGATTACAGGCACACACTACCAACGCCA 35759
Qy 3925 GCATTCTGTTTTTCACTTATCACCTTGTATGACTTTTTTCAATATGCTTCAAACTTTA 3984
Db 35760 GGCTCTTTTTTTTTTCTTTTTTGGTCAAGAGGGGGTTTTTACCATGTGAGCCAGGGTGGT 35819
Qy 3985 TTGTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGCTTAAATTTGCTT 4044
Db 35820 CTCAAACTCCTGACAAAGTGCTGAGATTACAAGCATGAGCCACTGTACCTGGCCTTTTTT 35879
Qy 4045 -----ATACATCCTCCTGCTCCACTTTTAGAAGGCCA--AATTTACAAATCTGA 4090
Db 35880 GCCTTTTTTAAAAAATGTTTTTCTTTGTACTATTATTAGTATGTAATCTTTGAAACACCTGA 35939
Qy 4091 TGAAGCTATGAACCCCTCTCCCCAGAGAAATACACACACACACACTCACACACAGT 4150
Db 35940 CTTCAGCCAGGCACAATGACTCATGCTGTAAATCTCAGCACTTTTGGGAAGTCAAAGGGG 35999
Qy 4151 TTTTTTTTAAATGTTTGAACATAAGACAAAGAACCTG-----CATTAGAGGATGTTTGTTC 4205
Db 36000 AGAATCTCTTGAGCCAGGAGTTGAAGAACAGCCTGGGCAACATAATGAGACACTACCTC 36059
Qy 4206 ATATTAAATTAATAAATAACTCAGTTGGGCACAGTGACTCAAGCCCTGTAAACCACAGTACTTT 4265
Db 36060 TACAAAAAATAAAAAAATAATGGCCAGGATGTTGGTCTCAGCCCTGTPAATCCCAGCACTTT 36119

Qy 4266 GGAAGTCCAAGGTGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATAT 4325
Db 36120 GGGAGGCTGAGGTGGCGGATCGCTTGAGGTCAAGAGTTTGAGACCAGCCTGGCCAACAT 36179
Qy 4326 GGTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTG 4385
Db 36180 GGC AAAACCCCTGCTCTACTAAAAATACAAAAATGAACTGGGCGTGGTGGCACATGCCTG 36239
Qy 4386 TAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGT 4445
Db 36240 TAATCCCAGCTACTTGGGAGGATGAGGCATGAAAAATCACTTGAACCTGGGAGGCAGATGT 36299
Qy 4446 TGCAGTGAGCCGAGATCCCACCACACTGCACCTCCAGCTGGCGACACAGCGAGACTCTATC 4505
Db 36300 TGCAGTGAGCTGGGATTACACCACACTGCACCTCCAGCTGGGTGACAGAGTGAGACTCTGTC 36359
Qy 4506 TCAAAAAAATAAATAAATAAATA 4529
Db 36360 TTAAAAA AAAAAAAAAAAAAAAAAA 36383

RESULT 48

US-10-482-065-22
; Sequence 22, Application US/10482065
; Publication No. US20040260058A1
; GENERAL INFORMATION:
; APPLICANT: AXARON Bioscience AG
; TITLE OF INVENTION: Novel endothelially expressed DNAs and proteins, and
; TITLE OF INVENTION: their use
; FILE REFERENCE: OZ0091/00010-AT
; CURRENT APPLICATION NUMBER: US/10/482,065
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 13104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-065-22

Query Match 7.7%; Score 385; DB 8; Length 13104;
Best Local Similarity 59.0%; Pred. No. 1.6e-77;
Matches 847; Conservative 1; Mismatches 511; Indels 76; Gaps 8;

Qy 3106 TTTT TTTTGTGTGTTTAGAGACAGGCTTGTCTGTCTGTACCCAGGCATGAGCAGTGG 3165
Db 11400 TATTCTTTTCC TTTT TTTT TGGAGTCTTGTCTGTCACCAGGCTGGAGTCCAGTGG 11459
Qy 3166 TGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGTGACCTCAGC 3225
Db 11460 CATGATCTCAGCTCACTGCAACCTCCGCTTCTGGTTCAGCGGATTCTCCTGCTTCAGC 11519
Qy 3226 CTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCAACCGCTGGCTAATT-----AAA 3277
Db 11520 CTCCTGAGTAGCTGGGATTACAGGCGCCCAACCAATTTTGTGTGTGT 11579
Qy 3278 AAAATTTT TTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGG 3337
Db 11580 GTGTATTTT TTAGTAGAGATGGGTTTTCACCATGTGGCCAGGCTAGTCTTGAACCTCTGA 11639
Qy 3338 CTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACC 3397
Db 11640 CCTCAAGTGATCCACACACCTTGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCGCT 11699
Qy 3398 ATGTGCGGCTACTTATTTCTTTTACATTCATCTTTCCAATAGAAATGTAAGATCCACAGAA 3457
Db 11700 GTGCCCATCCAATGCTCTTGGCTTTTCTGATTTT----- 11734
Qy 3458 CAGGGATTACTGCCTATTTTCTTCTTCTTTTGTAGACAGAGTCTCACTTCAATCACCT 3517
Db 11735 -----TTT TTTT TTAGACGGAGTTTGTCTCTTTTCGCCCAGGCTGGAGTACAG 11780

Db 69585 GATACAAATATCAGCTTGGTACTGGTCCCAAGTTATAGCAAGTTATGGGATTAAGTTTTTA 69526
Qy 3876 TTCTTTTTTAAAAACAATCTTTGACAACTTTGCAGAATAAAATACAATCTTGCAATTCGTCT 3935
Db 69525 AATGGCAAGTAGGGCATTTGTATCAGAAATGCAACTTGTGTGGAAACCTTAATGCTTATC 69466
Qy 3936 TTTCACCTTATCACCTTGTATGACTTTTTTCATATTGCCCTCAAACTTTATTTGTTACTGTT 3995
Db 69465 CTGGGAAGAAAAGAGAGAGAAAAATAGAAATCTCTACTATTCTCTTCTTAACCTTCTCRAA 69406
Qy 3996 TTTCATTTGTACTATTTTAGTCACCTGAATAATATGGCTTAATTTGCTTATACATCCTCC 4055
Db 69405 ATATGGCTCTAGCCCCATTATTCTATTAGAACCTTACCCAAAGAGAGACCCAGGACCACT 69346
Qy 4056 TGCTCCACTTTAGAAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCTCCAG 4115
Db 69345 TAACTTAATGCAATAGGTCTTCTCTCCATCCTTTTCCATTGCTCTGAGCCATGGGAATCT 69286
Qy 4116 AGAAATACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGA 4175
Db 69285 GCTCATCTGTATGCCATTCCAAAGTTGAGAAATGATGGGCAATTCCTTTTCT----- 69236
Qy 4176 CAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATAACTCAGTTGGGCAC 4235
Db 69235 -----CTCTCTCATCTCTCATGATAATCATTAAGATTTCCCACTACAGGCCGGGCAC 69184
Qy 4236 AGTACTCAAGCCTGTAAACCACAGTACTTTGGAAGTCCAAGTGGGTGGATCATTGAGG 4295
Db 69183 AGTGGCTCAGCCTGTAATCCCAGCACTTTGGAAGGCTGAGGTGGGCCGATCACA--AGG 69126
Qy 4296 TGAGAAAGTTGAGACCCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATAC-A 4354
Db 69125 TCAGGAGATTGAGACCATCCCGGCTAACATGGTGAAACCCCGTCTCTACTAAAAATACAA 69066
Qy 4355 AAAATTAGTGGGTGTAGTGATGCATGCCTGTAGTCCCAGTACTCGGAGGCTGAGGCA 4414
Db 69065 AAAATTAGTCAGGCATGGTGGTACACGCTGTAGTCCCAGTACTGTCAGGAGGCTGAGGCA 69006
Qy 4415 AGAGAAATTGCTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACTGCAC 4474
Db 69005 GGAGAATCGCTTGAACCTTGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCAATTGCAT 68946
Qy 4475 TCCAGCCTGSCGACACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAGGA 4534
Db 68945 TCCAGCCTGGCAACAGAATGAGACTCCGCTCTCAAAAAAATAAATAAATAAATAA 68886
Qy 4535 TCGGAGAGAAACAACAACTAATAAGATTCTCTGAAGGTAAGCAGAGATACGTAA 4586
Db 68885 ATAATAATAATAAAAAAGATTCCCACCTCCATTTCTTAAAAAANAANAANAANA 68834

RESULT 50
US-10-741-601-5712/c
; Sequence 5712, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5712
; LENGTH: 73237
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-5712

Query Match 7.7%; Score 384.2; DB 7; Length 73237;
Best Local Similarity 58.8%; Pred. No. 6.6e-77;
Matches 898; Conservative 3; Mismatches 526; Indels 100; Gaps 10;

Qy 3071 GATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTTAGAGACAG 3130
Db 17492 GATGAGGAACTTTCTAGTTGATGGCAATGGCCTATGCTCTTTTTTTTTTTTGTAGATGG 17433
Qy 3131 GGTCTTGTCTGTCAACCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTC 3190
Db 17432 AGTCTCACTCTGTCAACCAGGCTGGAGTACAGTGCACAGTCTCGGCTCACTGCAACCTC 17373
Qy 3191 AACCTCCTGAGCTCAAGGGATCTGTGACCTCAGCTCCCAAGTAGCTGGGACTACGAGC 3250
Db 17372 TGCCTCGCGGTTCAAGCGATTCTTCTGCCCTCGGCTTCTGAAATAGCTGTACTACAGGC 17313
Qy 3251 GTGCACCACACGCTGGCTAAATTAATAAAAT-TTTTTGTAGAGACTGGGTCTTACTAC 3309
Db 17312 ATGTGCCACACGCCCGAGCAATTTTTTTGTATTATTYAGTAGAGATGGGATTTACCAT 17253
Qy 3310 GTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAGCAATCCTCCTACCTTGGCATCCCAA 3369
Db 17252 GTTGGCCAGGATGGTCTTGAACCTCCTGCCTT--TGTGATCCACTTGCCTCGGCCTCCAA 17195
Qy 3370 AGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTACATTCCATC 3429
Db 17194 AGTGCTGGGATTACAGGTGTGAGCCACCGCACCCGGTCGTCTTTTTTTTTT----- 17145
Qy 3430 TTTTCAAATAGAATGTAAGATCCACAGAACAGGGAATTACTGCCTATTTTCTTCTTCTTTT 3489
Db 17144 TTTGAAACAGTCTCTCTTTGTGTACCCAGGCTGGAGTGCAG----- 17105
Qy 3490 TTTGAGACAGAGTCTCACTTTCATCACCTCAACCTCCGTTTTCAGTCTCACTGCAACCTCTGCC 3549
Db 17104 -----TGGCATGATCTTGGGTCACTGCAACCTCTGCC 17073
Qy 3550 TCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTAACAAGCGTGC 3609
Db 17072 TCCCGGGTTCAAGCAATTCTCCTGCCCTCAGCCTCCGAGTAGCTGGGATTACAGGCATGT 17013
Qy 3610 ACCACCATGCTTGGCTAAATTTTTGTATTTTTTAGCAGAGATGGGGTTTTTACCATTGTTGCC 3669
Db 17012 GCCACCACGCCAGCTAA-TTTTTGTATTTTTTAGTAGAGATGGGGCTTACCATTGTTGCC 16954
Qy 3670 CAGGCTGGTCTCAAACCTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAGTGCT 3729
Db 16953 CAGGCAGGTCTCGAACTCCTGGCCTCATGTGATCCACCCACCTCGGCCTCCCAAGTGCT 16894
Qy 3730 GGAATTATAGCGGTGAGTCACTGTGCCCTGGCCGATTACTGTCTATTTTCTTTTACTTAT 3789
Db 16893 GGGATTACAGGCATGAGCCACCGTGCCCTGGCC-TTATGTCTTGATTATGGTGGGTACT 16835
Qy 3790 ATCCCCAGAT-----CTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAA 3840
Db 16834 ATGAGTATATACATTTGTCAAAACTCACTGTACACTATAAACGGTATATTTCATTAAGAT 16775
Qy 3841 TTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTAAACAATC----- 3894
Db 16774 CTGTATATTGTACTGTATATAAATTATACCTTCAATTTTAAAAAATGAATAAGCAGTCCC 16715
Qy 3895 -----TTGACAACCTTTCAGAAATAAATAACAATCTTGCAATCTGCTTTTTCATTATCA 3947
Db 16714 CTAATAATCCAACAATGAGATGAGTTAGTGAATCATGATGTATCCATAAAACATTATGC 16655
Qy 3948 CCTTG--TTATGACTTTTTTCATATTGGCTCAAACCTTTATTGTTACTGTTTTTTTCATTGT 4005
Db 16654 ATTGGATTGCAGAAGGACAGAAAAATGACATAGAAGGTTATTTAGCACGTGCAGTTAAGGA 16595
Qy 4006 TACTATTTTAGTCACTGAATAAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTT 4065
Db 16594 AAAAAAGTTATGAAACTGTGATATACTTGTAGTAGTATTTTGTAAAAATAAAATGTATATACT 16535
Qy 4065 TAGAAGG-----CCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCTCCC 4112
Db 16534 TGAAAGAAAAATGACCAAAAGGAAATCTTCTATTCAATTTGTTCAATATAAAATTTCTCTGAG 16475

Db 12010 AAATAAACATTCACTACAACACAGAGAAGTGGACAATAAAAAATGACTTTTTATTGAAA 11951

QY 4171 TAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATAATAAACTCAGTTG 4230

Db 11950 TGAGGGATTAGGTGACGTATTAAATAAATTCTTACATGCATAGATTA---TCAGCCA 11895

QY 4231 GGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTGGAAAGTCCAAGGTGGGTGGATCACT 4290

Db 11894 GGCATGGTGTCTACGCTGTAAATCCCAACACTTTGGGAGACCAAAAGCGGTGGATCAC 11835

QY 4291 TGAGGTGAGAAGTTTCAGACCAGCCTGGTCAATATGGTGAACCCATCTCTACTAAAAA 4350

Db 11834 TGAAGTCAGGAGTTCGAGACTAGCCCGGCCAAACATGGTGAACCTGGTCTCTACTAAAAA 11775

QY 4351 TACAAAAATTAGCTGGGTGTAGTATGCATGCCCTGTAGTCCCAAGTACTCGGGAGGCTGA 4410

Db 11774 TACAAAAATTAGCTGGGCATGGTGGCATGTGCTGTAAATCCCAGCTACTAGTAGGCTGA 11715

QY 4411 GGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACT 4470

Db 11714 GGCAGAAGAATCACTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGATTGTGCCACT 11655

QY 4471 GCACTCCAGCCTGGGGGAC-ACAGCGAGACTCTATCTCAAAAAATAAATAAAAAATA 4529

Db 11654 GCACTCCAGCCTGGGCAACAAGAGCAAAACTCCATCTCAAAAAAAAAGCATAGATTATC 11595

QY 4530 A 4530

Db 11594 A 11594

RESULT 52

US-10-322-281-314

; Sequence 314, Application US/10322281

; Publication No. US20040126762A1

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc S. Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001000

; CURRENT APPLICATION NUMBER: US/10/322,281

; CURRENT FILING DATE: 2002-12-17

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 314

; LENGTH: 227246

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(227246)

; OTHER INFORMATION: n = A,T,C or G

US-10-322-281-314

Query Match 7.7%; Score 383.4; DB 7; Length 227246;

Best Local Similarity 59.6%; Pred. No. 1.9e-76;

Matches 885; Conservative 1; Mismatches 542; Indels 57; Gaps 12;

QY 3099 TTGGGTTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGC 3158

Db 138536 TTTTCTTTCTTTTTTTTTTTTTTTTGTAGATGGAGTCTCACTCTGTCAACCCAGGCTGGAGT 138595

QY 3159 ACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGTCAAGGGATCTGTGTA 3218

Db 138596 GCAGTGGTGCATCTCTGCTCACTGCAAGCTCCACCTCCCGGGTTCACGCCATTCTCCTG 138655

QY 3219 CCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCTGGCTAATTAAAA 3278

Db 138656 CCTTAGCCTCCCGAGTAGCTGGGACTACAGGCGCCCGCCACCACACTGGCTAATTTTTT 138715

QY 3279 AAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAAACTCCTGGC 3338

Db 138716 GTA-TTTTTGTAGAGAC-GGGTTTTCATCGTGTTAGCCAGGATGGTCTTGATCTCCTGAC 138773

QY 3339 TTCAAGCAATCCTCTTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCA 3398

Db 138774 CTCTTG--ATCCGCCACCTCGGCCTCCCAAAGTCTCGGATTACAGGCGTGAGCCACCG 138831

QY 3399 TGTGCGGCTA-CTTATTTCTTTTACATTCATTCCTTTCCAAATGAATGTAAGATCCACAGAA 3457

Db 138832 CACCCGGCCAGAAATAATAATTCTGTAAAGAATCATCACTAAATGAGATACCACCTTCT 138891

QY 3458 CAGGGATTACTGCCATATTTCTTCTTTTCTTTTGTGAGACAGAGTCTCACTTTCATCACCT 3517

Db 138892 TTTTCTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 138951

QY 3518 CAACCTCCGTTCA-----GCTCACTGCAACCTCTGC-CTCCCGGTTCAAG 3562

Db 138952 AGCTGGAGTGCAGTGGCGCGATCTTGGCTCACTGCAACCTCCGCACCCCGAGATTTAAG 139011

QY 3563 YGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCACCATGCTTG 3622

Db 139012 CAATTCTCCTGCCTCAGCCTCCGAGTAGCTGGGATTACAGGTGCCTGCCCCCACACCCA 139071

QY 3623 GCTAATTTTGTATTTTAGCAGAGATGGGGTTTACCATTGTTGCCAGGCTGGTCTCA 3682

Db 139072 GCTAATTTTT--GTAATTTAGTAGAGATGCTGTTTACCATTGTTGGCAGGCTGGTCTCG 139129

QY 3683 AACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCCTCCAAAGTCTGGAAATTATAGGCG 3742

Db 139130 AACTCCTGACCTAAAGTGATCTGTCCACCTTGGCCTCCCAAACTCCTGGAATTACAGGCA 139189

QY 3743 TGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTCTTTTATTTGCTATATCCCCAGATCTA 3802

Db 139190 TGAGCCACTGCACCTGSCCCTGAGATACCACCTTC-TTAGGACTATAACCAAAACAGACA 139248

QY 3803 GAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAAATTGATGAATGCACAGCCTAGAT 3862

Db 139249 GATAATAAGTGTGGTGAGGATGTGGAGAAATTGGAGCCTTCATACACCACCTGGTAGGAA 139308

QY 3863 ATAAACTTTCTTTTCTTTTAAACAATCTTGACAACCTTTGCAGAAATAAATACAATC 3922

Db 139309 CGTAAAAATGGTGAAGTCACTGTGGAAAAACAAGCATGGTGGTTCTCAAAAAATCAACAT 139368

QY 3923 TTGCATTCTGCTTTTTCATTATCACCTTGTGATGACTTTTTCATATTGGCCTCAAACTT 3982

Db 139369 AGGCTGGGTGCGGTGGCACATGCTGTAATCTCAGCATTTTGGAGGCTGAGGCAGCGAT 139428

QY 3983 TATTGTTACTGTTTTTTTCANTGTTACTATTTTAGTCACTG-----AATAATATGG 4032

Db 139429 CACCTGAGGTGCGATGTGAGACTAGCCTGGCCAACATGGTGAAATCTCTACTAAAAATA 139488

QY 4033 CTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAAGGCCAAATTTACAAATCTGATG 4092

Db 139489 TAAAAATTATCTAGGTATGGTGGCGGCGCCTGTAATTCAGTACTCTGAGGCTGAGG 139548

QY 4093 AAAGCTATGAACCTCTCCCCAG---AGAAATACACACACACACACTCACACACA 4148

Db 139549 CAGGAGAATTACTTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCAAGATCATGCTACTGA 139608

QY 4149 GTTTTTTTTAAATGTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATA 4208

Db 139609 GCCAAGACTACACCACTGCACCTCCAGCCTGGGCAACAAAGTGAGACCTTATCTCAAAAAG 139668

QY 4209 TTAATTAA-AAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTGG 4267

Db 139669 AAAACAAACAAAAAAGTAGGCCAAAGTGTGGTGGCTCAGCCTGTAATCCAGCACCTTGG 139728

QY 4268 AAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGG 4327

Db 139729 GAGGCCGAGGCGGCGGATCACCTGAGGTGAGGAGTTTGAAAACCAGCCTGGCCAACATG 139788

QY 4328 TGAACCCCTATCTCTACTAAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTA 4387

Db 139789 CGAAACCTGTCCCTACTTAAAAATACAAAAATTAGCCAGGTGTGGTGGCACGTGCCTGTA 139848

Qy	4388	GTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGTTG	4447
Db	139849	ATCCAGATACTCAGGTGGTGAGGCAGGAGAATTGCTTGAACCTGGCATGCAGAGTTG	139908
Qy	4448	CAGTGAGCCGAGATC-----CCACCACCTGCACCTCCAGCCTGGSCGA	4488
Db	139909	CAGTGAGCCAAGATCATGCTACTGAGCCAAGATTACCACTGCACCTCCAGCCTGGGCCAA	139968
Qy	4489	CACAGCGAGACTCTATCTCAAAAAAATAAATAAAAATAAAGG	4533
Db	139969	CAAAGTGAGACCTTATCTCAAAAAAGAAAACAACAAAAAAGTAGG	140013

RESULT 53

US-09-764-877-3770/c

; Sequence 3770, Application US/09764877

; Patent No. US20020147140A1

: GENERAL INFORMATION:

APPLICANT: Rosen et al.

AFRICANA: ROSEN ET AL.
: TITLE OF INVENTION: Nucleic Acids. Proteins, and Antibodies

FILE REFERENCE: PC005

FILE REFERENCE: FC003
CURRENT APPLICATION NUMBER: IIS/09/764.877

: CURRENT FILING DATE: 2001-01-17
: CURRENT APPLICATION NUMBER: US/0

; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PAlM or file wrapper

; PRIOR APPLICATION DATA FEM
 : NUMBER OF SEC ID NOS: 4031

; NUMBER OF SEQ ID NOS: 4031
: SOFTWARE: Paton1a Ver 3.0; SOFTWARE: PAT
: CEO ID NO 3370; SEQ ID NO 3770
: ENCTU: 5902

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Homo

Query Match	7.6%	Score 382.2;	DB 3;	Length 6892;
Best Local Similarity	60.1%	Pred. No. 5e-77;		
Matches 893; Conservative	1;	Mismatches 504;	Indels 89;	Gaps 12;

QY	3087	AGTGGTGACAGTTTGGGTTTTTTTTTTGTTGTTTGTAGAGACAGGCTCTTGCTCTGTCTCAC	3146
Db	6148	ACTTTTAAAAATTTTATTTTATTTTATTTTATTTTATTTGAGATGGAGTCTCCCTCTGTCTTAC	6089
QY	3147	CCAGGCATGAGCAGTGGTGCAACCATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAA	3206
Db	6088	CCAGGCTGAAGTCAGTGGCACAATCCTGACTCACTGCAGCCTCCGCCTCCTCGGTTCAA	6029
QY	3207	GGGATCTGCTGACCTCAGCCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACACAGCCT	3266
Db	6028	GCAATTCTCCTGTCTCAGCCCTCCCGAGTAGCTGGGACTACAGGCGTGTGCCAACACACCC	5969
QY	3267	GGCTAATTAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCT	3326
Db	5968	GGCTAATT-TTTGTATTTTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCT	5910
QY	3327	TAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGG	3386
Db	5909	CAAACTCCTGACCTCAGGTGATCCACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG	5850
QY	3387	GGTGAGCCACCATGTGCGGCTACTTATTTCTTTACATCCATCTTTCCAATAGAATGTAA	3446
Db	5849	CGTGAACCGCCATGCTTGGCCCAAGGTAAATATTCTATAACCAGTATAAGGAAACATAG	5790
QY	3447	GATCCACAGAACAGGATTACTGCCTATTTTCTTCTTCTTTTGTAGACAGAGTCTCA	3506
Db	5789	GCAAGTGATTCCAGCTAGCTTTTTTTTTTGAGATGGAGTTTGTCTT---GTTGCCAG	5734
QY	3507	CTTCATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGAT	3566
Db	5733	GCTGGAGTGCAATGGCACGGTCTCGTTTACTGCAACCTCCACTTTCCGGGTTCAAGTAAT	5674
QY	3567	TCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTA	3626
Db	5673	TCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAAGTGCCCCACCAACCGCTGGCTA	5614
QY	3627	A-TTTTTTGTATTTTAGCAGAGATGGGGTTTTACATGTTGCCAGGCTGGTCTCAAAC	3685

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; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3770
; LENGTH: 6892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3770

Query Match          7.6%; Score 382.2; DB 6; Length 6892;
Best Local Similarity 60.1%; Pred. No. 5e-77;
Matches 893; Conservative 1; Mismatches 504; Indels 89; Gaps 12;

QY 3087 AGTGGTGACAGTTTGGGTTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGCTGTGCAC 3146
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Db 6148 ACTTTTAAATTTTATTATTTTATTATTTGAGATGGAGTCTCCCTCTGCTTTAC 6089

QY 3147 CCAGGCATGACACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAA 3206
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Db 6088 CCAGGCTGAAGTCAGTGGCAGTGCCACAATCCTGACTCACTGCAGCCTCCGCCCTCCTCGGTTCAA 6029

QY 3207 GGGATCTGTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCCT 3266
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Db 6028 GCAATTCTCTGTCTCAGCCTCCCGAGTAGCTGGGACTACAGSCGTGTGCCAACACACCC 5969

QY 3267 GGCTAATTAATAAATAATTTTTTTGTAGAGACTGGGTCTTTACTAGCTTGGCCAGGCTTGCT 3326
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Db 5968 GGCTAATT-TTGTATTTTGTAGAGACAGGGTTTTCACCATGTTGGCCAGGCTGGTCT 5910

QY 3327 TAAACTCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGTGGGATTACAGG 3386
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Db 5909 CAAACTCCTGACCTCAGGTGATCCACTGCCTCGGCCTCCCAAGTGTGGGATTACAGG 5850

QY 3387 GGTGAGCCACCATGTGCGGCTACTTATTCTTTTACATTCATCTTTTCCAATAGAATGTAA 3446
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Db 5849 CGTGAACCGCATGCTTGGCCCAAGGTAATAATTCTATAACCATATAAGGAAAAACATAG 5790

QY 3447 GATCCACAGAACAGGGATTACTGCCTATTTTCTTCCCTTTCTTTTGTAGACAGAGTCTCA 3506
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Db 5789 GCAAGTGATCCAGCTAGCTTTTTTTGTGAGATGGAGTTTGTGTTCTT---GTTGCCCCAG 5734

QY 3507 CTTTCATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCTCCCGGTTTCAAGYGAT 3566
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Db 5733 GCTGGAGTGAATGGCACGGTCTCGTTTACTGCAACCTCCACTTCCGGGTTCAAGTAAT 5674

QY 3567 TCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTA 3626
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Db 5673 TCTCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAAGTGCCCAACCATCCAGCCTGGCTA 5614

QY 3627 A-TTTTTTGTATTTTAGCAGAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAC 3685
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Db 5613 ATTTTGTATTTTAGTAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAAC 5554
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QY 3686 TCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAAGTGCTGGAATTATAGGCGTGA 3745
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QY 3746 GTCACCTGTGCCTGGCCGATTACTGTCTATTCTTTTATTGCTATATCCCCAGATCTAGAG 3805
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Db 5493 GCCACTGCGACCAGCCCA--GCTAGCTTTTATACTGAGTCTAAATGTGTTCAATAAATCAC 5436

QY 3806 CAGTGTCTGACATATAGTAGGTGCTCAATAAAATAAATGATGAATGCACAGCCTAGATATA 3865
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Db 5435 TATTC-----CAACAAGATTATCACATACTAAGCC----- 5404

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Db 5403 -----TTATGCTGAGATCATATCCTACATGTCAATCAATAACATACTG 5359

QY 3926 CATTCGTCTTTTTCACCTTATCACCTTGTTATGACTTTTTCATATTGCCTCAAAACCTTTAT 3985
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Db 5358 CAAAC-----TCTCCTTTAGGAATTAGAGCCCCAGAGAATTAAATTACCTTCACCCCTCAC 5304

QY 3986 TGTTACTGTTTTTTCATTACTATTATTTTAGTCACTGAATAATATGGCTTAATTGCTTA 4045
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Db 5303 AGTTTCAGAAATAGCTGGAGTTGATTTCCAAAGAAAGGGCTGGGAATGAGAACATGAACAAA 5244

QY 4046 TACATCCTCCTGCTCCACTTTTGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACC 4105
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Db 5243 TATATAGGATGCTATGCTACTACCAAAAAAATCAATTGAAATTTTATATTGTAGATTAGGTAAC 5184

QY 4106 CTCTCCCAGAGAAATACACACACACACACTCAACACACAGTTTTTTTTTTTAAATGTTT 4165
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Db 5183 TTAT-----ATAGCACTATCAGGCTGAAGGCCACCAGTCACTGCACCTTGATACAAAAC 5133

QY 4166 GCAACTAAGACAAAGAACTGCATTAGAGGATGTTGTTTCATATTAAATTAATAAATAACTC 4225
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Db 5132 ACTACTTAGGAAA-----ACTAAAGGTATTCTGATGTAATAAAGAAACAAACAAA 5085

QY 4226 AGTTGGCACAGTGAAGCTGTAACCCACAGTACTTTTGAAGTCCAAGGTGGGTGGA 4285
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Db 5084 GGCCAGGCGTGGTGCCTCATGCCTATAATCCCAGCACTTTGGGAGACCGGCGGTGGA 5025

QY 4286 TCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCTACT 4345
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Db 5024 TCACTTGAGGTGAGAGTTTGAGACCAGCCTGGCCAAACATAGTGAAACCCCTGTCTCTACT 4965

QY 4346 AAAAAATAC-AAAAATTAGTGGGTGTAGTGTGATGATGCCTGTAGTCCCAGCTACTCGGA 4404
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Db 4964 AAAAAATACAAAAAATTAGCCAGGCATGGTGGTGGCTGTAAATCCCAGCTACTTGGGA 4905

QY 4405 GGCTGAGGCAAGAGAAATTGCTTGA-----ACCTGGGAGGCAGAGTTGCAGTGAGC 4455
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Db 4904 GGCTGAGACACGAGAAATCACGTGAGGTGGAGTTTGAGGTGGAGGTTGCAGGTGCAGTGAGC 4845

QY 4456 CGAGATCCCACCACTGCACCTCCAGCCTGGCGGACACAGCGAGACTCTATCTC--AAAAAA 4513
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Db 4844 TGAGATCGCGCCACTGCACCTCCAGCCTGGGTGACAAATGCAAGATGCTATCTCCAAAAACAA 4785

QY 4514 ATAAATAAATAAATAAAGGATCGGAGAGAAACAAAACTAATAAGAT 4560
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Db 4784 ACAAAACAAACAAACAAACAAACACCAGCTTACTATAACTAAGAAGTT 4738
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RESULT 55
US-10-699-941-10
; Sequence 10, Application US/10699941
; Publication No. US20040146900A1
; GENERAL INFORMATION:
; APPLICANT: Burmeister, Margit
; TITLE OF INVENTION: Ataxia Associated Gene and Protein
; FILE REFERENCE: UM-08441
; CURRENT APPLICATION NUMBER: US/10/699,941
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 62
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[illegible]

Db 11776 CTTAAGTGATCCTCCCAACTCGGCCTCCCAAGTCTGGGATTACAGGCATGAGTCAC-- 11833

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Qy 3564 GATTCTCTGCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGG 3623

Db 12014 AATTATCCTGCCCTCAGCCTCTTGAGTAGCTGGGATTACAGGTGCACGCCACCATGCCAG 12073

Qy 3624 CTAATTTTTGTATTTTGTAGCAGAGATGGGGTTTTTACCATGTTGCCCCAGGCTGGTCTCAA 3683

Db 12074 ATAA-TTTTTGTATTTTGTAGACAGCGGGTTTCACCATGTTGGTCAGGCTGGTCTCGA 12132

Qy 3684 ACTCTGACCTCAAGTGATCTGCCCTGCCTCAGTCTCCCAAGTCTGGAATTAAGCGGT 3743

Db 12133 ACTCCTGACGTCATG---ATCCGCCACTCAGCCTCCCAAGTCTGGGATCACAGCGT 12189

Qy 3744 GAGTCACTGTGCTGGCCGATTACTGTCTATTTTCTTTA---TTGCTATATCCCCAGATC 3800

Db 12190 GAGCCACTGTGCCCTGCCCTTCAGCCACCTTTTAAATTAAGCTTCTGTAGTGGAAATC 12249

Qy 3801 TAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAG 3860

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Qy 3861 ATATAAACTTCTTTTT-----CTTTTTTTAAACAATCTTGACAACTTTGCAG 3909

Db 12310 AGACAGAAGGAGATCTAAAGCAGGATGCTCTGCTAGGTGTTTGTGTAACACATGTATT 12369

Qy 3910 AATAAATACAATCTTGCAATCTGCTTTTTTCACTTATCACCTTGTTATGACTTTTTTCATAT 3969

Db 12370 ATCACCCACTTTTGTAGAAAGTGGCTTCTACCCCTCTGAACAGCAGGAGGTCTGGCTGAC 12429

Qy 3970 TGC-----CTCAAAACCTTTATTTGTTACTGTTTTTTCATTTGTACTATTTTAGTC 4018

Db 12430 TGCAAGGTCCAAGGTGTTTCCCCAGTTTACAGATGAGTGTCAAATTTCTACTACTACTAGTG 12489

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Db 12490 TCCACAACTGCCAAGAGTGAGCCTCCAGAAACCTCACTGGAATCTTTCTCTCGATGAAAC 12549

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Qy 4199 TTTGTTCATATTAATTAATAAATAAATACTCA--GTTGGGCACAGTGACTCAAGCCTGTAACCA 4256

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RESULT 58

US-09-764-877-2623

; Sequence 2623, Application US/09764877

; Patent No. US20020147140A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC005

; CURRENT APPLICATION NUMBER: US/09/764,877

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 4031

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2623

; LENGTH: 32193

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-764-877-2623

Query Match 7.6%; Score 380.8; DB 3; Length 32193;

Best Local Similarity 58.2%; Pred. No. 2.5e-76;

Matches 855; Conservative 1; Mismatches 568; Indels 44; Gaps 9;

Qy 3098 TTTGGGTTTTTTTTTGTGTTGTTTGTAGACAGGGTCTTGCTCTGTACCCAGGCATGAG 3157

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Qy 3158 CACAGTGGTGCAACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGAATCTGTG 3217

Db 13025 TCCAATGGCGCAATCTCAGCTCACTGCAACCTCTGCCTCCTGGTTCAAGTGATTCTTT 13084

Qy 3218 ACCTCAGCCTCCCAAGTAGTGGGACTACGAGCGTGCACACCAC-ACGCCTGGCTAATTAA 3276

Db 13085 GCCCAGCCTCTCAAGTAGTGGGATTACAGGCCACTACAACGGCTAATTTTGTATTT 13144

Qy 3277 AAAAAATTTTTGTAGACACTGGGTCTTACTACGTGGCCAGGCTTGTCTTAAACTCCTG 3336

Db 13145 TTTTAAAAAGCAGAAAGCGGGTTTACCATGGTGGTCAGGCTGGTCTCAAACTCCTG 13204

Qy 3337 GCTTCAAGCAATCCTCTACCTTGGCATCCCAAGTCTGGGATTACAGGGGTGAGCCAC 3396

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Qy 3397 CATGTGCGGCTACTTATTCTTTACAT-----TCCATCTTTCCAATAGAA 3441

Db 13263 CGCACCAGCCTGCATCAGCTTTCATGTGCCTACCTCCAGACCCCTTGTGTGACAAAC 13322

Qy 3442 TGTAAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCTTTTCTTTTGTAGACAGAG 3501

Db 13323 AGAAACTCCTTAGTTTTTAGTTGTTGGTTTTTTTGTGTTTTTTTTTTTGTAGATGGAG 13382

Qy 3502 TCTCACTTCATCACTCAACCTCCGT-----TCAGTCACTGCAACCTCTG 3547

Db 13383 TCTCGCTCTGTCCGCCAGGCTGGAGTGCAGTGGCATGATCTGAGCTCACTGCAACCTCCG 13442

Qy 3548 CCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGT 3607

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Qy 3608 GCACCACCATGCTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGGTTTTTACCATGTTG 3667

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Qy	3728	CTGGAATTATAGGCGTGAGTCAC	TGTGCTGGCCGATTACTGTCATTTTCTTTATGCT	3787
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Qy	3788	ATATCCCCAGATCTAGAGCAGTGTCTG	ACATATAGTGGTGTCAATAAATTAATTGATGA	3847
Db	13682	TTCTTTTTTTTGGAGA-CAGGGTTTCA	CTCCTGTTGCCAGGTGGAGTGCATGGTGC	13740
Qy	3848	ATGCACAGCCTAGATATAAACTTTTCT	TTTTTTTAAACAATCTTGACAACTTTGC	3907
Db	13741	AATCTTGGCTCA---CCACAACCTCC	ACCTCTCAGGTTCAAGCGATTCTCCTGCCTCAGC	13797
Qy	3908	AGAATAAATACAACTCTTGCAATTCTG	CTTTTTCACCTTATCACCTTGTATTAGACTTTTTCAT	3967
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Db	13918	ACCCACCTCAGCCTCCCAAAGTGTGG	GATTACAGATGTGAGCCACCATGCCCGGCCAAC	13977
Qy	4088	TGATGAAAGCTATGAACCCCTCTC	CCCCAGAGAAATACACACACACACACTCACACAC	4147
Db	13978	TCCTTAGTTTTTAATCACCTCCACC	ACCACACATATTTCTAAAATAAGAGAACCTTG	14037
Qy	4148	AGTTTTTTTTTAATGTTTGCAACTA	AGACAAGAAACCTGCATTAGAGGATGTTTGTTCAT	4207
Db	14038	TATCTTTAGACTGAAAGTACATTTCT	GTCCTATAGTCTTTATAGTATGTCTTCACCTTTAA	14097
Qy	4208	ATTAATTAATAAATAACTCAGTTGG	GCACAGTCAAGCCTGAACCAACAGTACTTTGG	4267
Db	14098	GACATATTTTGTGGAAGTTACTGAA	TTTCAAGAATGATAATCAGAATCCCAGCACTTTGG	14157
Qy	4268	AAGTCCAAGTGGGTGGATCACTTG	AGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGG	4327
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Qy	4328	TGAACCCCTATCTCTACTAAAAAT	ACAAAAATTAGCTGGGTGTAGTGATGCCTGTA	4387
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Qy	4448	CAGTGAGCCGAGATCCCACCACCTG	CACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTC	4507
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

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14833.946 Million cell updates/sec

Title: SEQ1-4500-9500-7328G
Perfect score: 4997.8
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9312410 seqs, 2039259788 residues

Total number of hits satisfying chosen parameters: 18624820

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Published Applications NA_New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	419	8.4	180531	18	US-11-114-798-57
4	417.6	8.4	154548	17	US-11-121-086-33
5	416.6	8.3	179892	17	US-11-112-908-39
6	413.6	8.3	215974	11	US-10-330-773-500
7	406.2	8.1	348101	11	US-10-330-773-122
8	400.8	8.0	46878	10	US-10-995-561-13276
9	393.8	7.9	175416	17	US-11-121-086-43
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Sequence 33, Appl					
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Sequence 50, Appl					
Sequence 58, Appl					
Sequence 14, Appl					
Sequence 33, Appl					
Sequence 12, Appl					

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18	373.8	7.5	180654	17	US-11-121-086-58	Sequence 58, Appl
19	372.6	7.5	167891	17	US-11-121-086-14	Sequence 14, Appl
20	369.6	7.4	55826	10	US-10-995-561-13256	Sequence 13256, A
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22	367.8	7.4	35770	10	US-10-995-561-13296	Sequence 13296, A
23	364	7.3	141121	10	US-10-995-561-13262	Sequence 13262, A
24	362.4	7.3	171427	17	US-11-112-908-60	Sequence 60, Appl
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RESULT 2

US-10-960-414-12

; Sequence 12, Application US/10960414

; Publication No. US20060074565A1

; GENERAL INFORMATION:

; APPLICANT: MILLER, LANCE D.

; APPLICANT: GEORGE, JOSH

; APPLICANT: VEGA, VINSENIUS B.

; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,

; TITLE OF INVENTION: PROGNOSIS, AND DIAGNOSIS OF CANCERS

; FILE REFERENCE: 38271-76067

; CURRENT APPLICATION NUMBER: US/10/960,414

; CURRENT FILING DATE: 2004-10-06

; NUMBER OF SEQ ID NOS: 500

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 12

; LENGTH: 159440

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-960-414-12

Query Match 8.5%; Score 424; DB 13; Length 159440;

Best Local Similarity 60.7%; Pred. No. 33;

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RESULT 4
US-11-121-086-33
; Sequence 33, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 154548
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-33

Query Match 8.4%; Score 417.6; DB 17; Length 154548;

Best Local Similarity 59.5%; Pred. No. 39;

Matches 908; Conservative 2; Mismatches 536; Indels 80; Gaps 9;

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QY 3224 GCCTCCCAAGTAGTGGGACTACGAGCGTGCAACACACGCTTGCTTAACCTCCTGGCTCAA 3283
Db 25143 GCCTCCAGAGTAGCTGGGACTACAGGCGTGCAACCAAYGCCTAGCTAATT-TTCATATT 25201
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Db 25202 TTTAGTAGAGACGGGTTTCACCATGTTGGTCAGGCTGGTCTTTGAACCTCCTGACCTCAG 25261
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Db 25442 GTCTCAGCTCCGTTGCCAGGCTGGAGTGACGTGATGCAATCATAGGTCACTGTAACCTC 25501
QY 3546 TGCCTCCCGGGTTCAAGYGATTCTCCTGCCT-AAGCCTCCTGAGTAGCTGGAATTACAAG 3604
Db 25502 AACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAAGCCTTCCAAGTAGCTGGGACTACAGG 25561

Db 84299 TCACCCAGGCTGGAGTACAGTGGTGAATCTCAGCTCACTGCAACCTCTGCCCTCCTGGGT 84240

QY 2944 GTGTTAATTTCTTGGTTCTGGGCACTGTCTCCTTTAATCCTCAGAACAACTATGGGA 3003

Db 84239 TCAAACGATTCTCCTGCCTAGCCTCTTAAGTACCTTGGGATTACAGGCGTGCACTGCTACG 84180

QY 3004 TAGGTACAATTATCCTCACTTAAACAGATAAGAAAACTGAGGCTCAGAAGCTGAG----- 3058

Db 84179 CCCAGCTAATTTTTTTGTATTTTGTATTTTAGTAGACAGCGGGTTTCGCCATGTTGGCCAGACTGG 84120

QY 3059 -----CTATTTGCCCAAGATCACACAGCTTGT 3085

Db 84119 TCTTGGATTCTTGACCTCAGGTGATCCACCTGTCTTGGCCTCTCAAAGTGTGGGAATTAC 84060

QY 3086 AAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTTGTGTTTAGAGACAGGGTCTTGTCTGTCA 3145

Db 84059 AGGCGTGAGCCACTGCGCCCGGCCCTCTTTATTTTGTGAACAGGGTCTCGCTCTGTG 84000

QY 3146 CCCAGGCATGAGCACAGTGGTGCAACATAGGTCACTGCAGCTCAACCTCCTGAGCTCA 3205

Db 83999 CCCAGGCTGGAGTGCACTGGTATGATCTTGGATCACTGCAACCTCTGCCTCCTGGGCTCA 83940

QY 3206 AGGGATCTGTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCAACCACCGCC 3265

Db 83939 GGCAGTCT-CTCACCTCAGCCTCCTGAGTAGCTGGGACTACAGGCACATGCCACTATGTC 83881

QY 3266 TGGCTAATTAANAANAATTTTTTTGTAGAGACTGGGTCTTTACTACGTTGGCCAGGCTTGTG 3325

Db 83880 CTGCTAATTTTGTATTTTTT--GAGAAACAGGGTTCTACCACTTACCCAGGCTGGTC 83824

QY 3326 TTAAACTCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAG 3385

Db 83823 TCCAACTCTGGGCTCAAGTGATCCACCTGCCTCGGCCCTCCCAAAGTCTGGGACTACAG 83764

QY 3386 GGGTGAGCCACCATGTGCGGCTACTTANTTCTTTACATTCCAATTTCCAATAGAAATGTA 3445

Db 83763 CAGTGAGC-----CTGCTTTTCTTTTAAAGTAAACTTTATTCAAATACATTTAA 83716

QY 3446 AGATCCACAGAACAGGGATTACTGCCTATTCTTCTCCTTTCTTTT---TGAGACAGAG 3501

Db 83715 GTAAATATTAAATAGGTATTTTGTGTTCTTTCTTTCTTTTCTTTTCTTTCTGAGACAGAG 83656

QY 3502 TCTCACTTCATCACCTCAACCT-----CCGTTCACTCACTGCAACCTCT 3546

Db 83655 TTTTGTCTCTGTTGCCCAGGCTGGAGTGCAATGGCGTATCTTGGCTCACCAACCTCT 83596

QY 3547 GCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCG 3606

Db 83595 GCCTCCTGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCAGAGTAGCTGGGATTACAGGCA 83536

QY 3607 TGCACCACCATGCTTGGCTAATTTTTTGTATTTTGTAGCAGAGATGGGGTTTTTACCATGTT 3666

Db 83535 TGTGCCACCACGCCCGGCTAA--TTTGTATTTTAGTAGAGACGGGGTTTCTCTATGTT 83478

QY 3667 GCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTGCTCAGTCTCCC-AAAG 3725

Db 83477 GGTCAAGGCTGGTCTCAAACTCCCAACCTCAGATGATCTGCCCGCTCAGCCTCCCAAAAG 83418

QY 3726 TGCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTCTAT-----TTTC 3778

Db 83417 TGCTGGGATTACAGCGGTGAGCCACCAGGCCAGCCTGTTTCTTCTTCTTCTTCTGTTTT 83358

QY 3779 TTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAAT 3838

Db 83357 TTTTGAGACAAAAGTCTCACTCTTGTGCCCAGGCTATAGTGCAGTGGTGCCATCTTGGCT 83298

QY 3839 AATTGATGAATGCACAGCCTTAGATATAAACTTTCTTTTCTTTTAAAAACAATCTTGA 3898

Db 83297 CACAGCAACCTCCACCTCCTAGGGTCAAGTGATTCTCTTGTGTGACGCTCCCAAG-TAGC 83239

QY 3899 CAACTTTGCAGAATAAAATACAATCTTGCAATCTGCTTTTTCACATTATCACCTTGTATTGA 3958

Db 83238 TGGGATTACAGGCACCCGCCCAACACGCCCGGCTAAATTTTGTATTTTAGTAGGATGGGG 83179

QY 3959 CTTTTTCATATTGCC---TCAAACCTTTTATTGTACTGTTTTTTTCATTGTTACTATTTTA 4015

Db 83178 TTTTTCATGTTGGCCAGGCTGGTCTCAAACCTCCCAACATCAGGTGATCCACCACCTGC 83119

QY 4016 GTCACCTGAATAATATGGCTTAATTTGCTTATACATCTCCTGCTCCACTTTTAGAAGGCCA 4075

Db 83118 CTCGGCCTCCAAAGTGTCTGGGATTACAGGAGTGAGCCACCGCGCCCGGCAATAAGTAT 83059

QY 4076 AATTTACAAAATCTGATGAAAGCTATGAACCTCTCCCCCAGAGAAAATACACACACACAC 4135

Db 83058 TTTTAAAAAGCCATAAGAACTAATAAGTGAATTTAGCAAGCCTGTAAAAATAGAGGTTAC 82999

QY 4136 ACACTCACACACAGTTTTTTTTTAAATGTTTGCACATAAGACAAGAAACCTGCATTAGAGG 4195

Db 82998 TATACAAAAGCACGTTCTTATCTATTAGTAGCAAAACAATTGGAATA-----TTA 82950

QY 4196 ATGTTTGTTCATATTAAATTAATAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACC 4255

Db 82949 AAATTTTAAATTTTATTAAATAGCATCA-----CAGGCCGGGTGCCTGTAATC 82899

QY 4256 ACAGTACTTTTGAAGTCCAAGGTGGTGGATCACTTGAGGTGAGAAGTTTCGAGACCAGCC 4315

Db 82898 CTTGCATTTTGGAGGCCAAGGTAGCGGATCACTGAGGTCAGGGTTCCAGACCAGCC 82839

QY 4316 TGGTCAATATGGTGAAACCCCTATCTCTACTAAATAACAAAAATTAGCTGGGTGTAGTGA 4375

Db 82838 TGGCCAAACACGGTGAATCCCATCTTTACTACAAACACAAAAAATCAGTAGGTCGTGGTG 82779

QY 4376 TGCATGCCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTTGAACCTGGG 4435

Db 82778 CGTATGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAAATCGCTTGAAACCAGG 82719

QY 4436 AGGCAGAGGTTGCAGTGAGCCGAGATCCCACCCTGCACTCCAGCTCCAGCTGGCGACACAGCG 4495

Db 82718 AGCGGAGGTTGCAGTGAGCTGGTATTTCGCCCACTGTACTCCAGCTGGGCAACAGAGTG 82659

QY 4496 AGACTCTATCTCAAAAAATAATAATAATAATAAATAAAGGATCGGAGAGAAACAAACTAAT 4555

Db 82658 AGATTCGCTCTCGAAATAAATAATAATAATAATAATAATAATAATAATAATAATAA 82599

QY 4556 AAGATTCTCTGAAGGTAAGCAGAGATACGTAAATTATATGTAAATAAGTTTAAA 4608

Db 82598 TAAATAATAAAATAGCATCACAAAAAATACACATTTAGATAAATTTAACA 82546

RESULT 6

US-10-330-773-500/c

; Sequence 500, Application US/10330773

; Publication No. US20060040262A1

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001300

; CURRENT APPLICATION NUMBER: US/10/330,773

; CURRENT FILING DATE: 2002-12-27

; NUMBER OF SEQ ID NOS: 981

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 500

; LENGTH: 215974

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(215974)

; OTHER INFORMATION: n = A,T,C or G

US-10-330-773-500

Query Match 8.3%; Score 413.6; DB 11; Length 215974;

Best Local Similarity 59.6%; Pred. No. 33;

Matches 847; Conservative 0; Mismatches 529; Indels 46; Gaps 7;

Db 97561 AATGCCGTGACTT---GTGATCCCCTCCCATGGCCTCCCAAAGTGTGGATTACAGTCA 97616
Qy 3389 TGAGCCACCATGTGCGGCTACTTATTCTTTTACATTCCATCTTTCCAAATAGAATGTAAGA 3448
Db 97617 TGAGCCACCACCTGGCCGTTTTTTGTGTTTTTTTTTTTTT----- 97660
Qy 3449 TCCACAGAACAGGGATTACTGCCTATTTTCTTCTCTTTTGTGAGACAGAGTCTCACT 3508
Db 97661 -----TTTGTAGACAAAGTTTGCTCTTGTGCGGAGGCTGGAGTGCAATG 97706
Qy 3509 TCATCACCTCAACCTCCGTTTCAGTCACTGCAACCTCTGCCCTCCGGGTTCAAGYGATTC 3568
Db 97707 GTGTGATCTTGA-----CTCACTGCAACCTCTGCCCTCCGGGTTCAAGCGATTC 97755
Qy 3569 TCCTGCCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCAACCATGCTTGGCTAAT 3628
Db 97756 TCCTGCCCTCAGCCTCCGAGTAGCTGTGATTACAGGTGCCCTGCCACCATGCCCTGGCTAAT 97815
Qy 3629 TTTTGTATTTTGTAGCAGAGATGGGGTTTACCATTGTTGCCAGGCTGGTCTCAAACTCC 3688
Db 97816 TTTTGTATTTTAGTAAAGACAGGGTTTCACCATTTTGGCCAGACTGTCTTGAACCTC 97875
Qy 3689 TGACCTCAAGTGATCTGCCCTGCCCTCAGTCTCCCAAAGTCTGGAATTATAGGCGTGATC 3748
Db 97876 TGACCTCAGGTGATCCACCCCTGCTCGGCCCTCCCAAAGTGTGGGATTACAGGCGTGAGCC 97935
Qy 3749 ACTGTGCCCTGGCCGATTACTGTCTATT--TTCTTTATTGCTATATCCCCAGATCTAGAGC 3806
Db 97936 ACTGTGCCCTGGCCACCAATTACTTTTAAATAGGATAAAAATTTTATTCTCAAAAGTAACA 97995
Qy 3807 AGTGCTGACATATAGTAGGTGCTCAATAAATAAATTGATGAATGCACAGCCTAGATATAA 3866
Db 97996 ATTGAAAAACAGAGGCAAGTGAAAAATGGAAAAAAATCATTTTATGGCAACTAATATAA 98055
Qy 3867 ACTTCTTTTTCTTTTTTAAACAATCTTGACAACTT-----TGCAGAATAAAATACA 3919
Db 98056 TTTTGTGCATCATTTTAAACATCTTTTACAAAGTTGTACTTCTAGCATACATGTAAG 98115
Qy 3920 ATCTTGCAATCTGCTTTTTCACCTTATCACCTTGTTATGACTTTTTCATATTGCCCTCAAAC 3979
Db 98116 TTTTATGATCTGTAGGTTTTTAATGATCTCCTAGACATTGTTTGTGGTGGTTTTTAGCAT 98175
Qy 3980 CTTTATTGTACTGTTTTTTCATTGTGTACTATTTTAGTCACGTGAATAATATGGCTTAAAT 4039
Db 98176 AAAGTGAACATAATTAAATTTGCTCTTTTCTGCTAGGTGGTAAATAATAATAGAAATGAA 98235
Qy 4040 TGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTA 4099
Db 98236 AGCTAACATTTATTCAATTCAGGCTCTTTGTAGGCTCAGGGGGCAAAAGTCAAGAACAAAA 98295
Qy 4100 TGAACCCCTC-----CCAGAGAAAAATACACACACACACACTCACACAGTTTTT 4154
Db 98296 CAACCATGATCTCTGTCTCAGTTTCTCAGGGAAAGACAGACAATAGAGGGAGAAAGGAA 98355
Qy 4155 TTTTAATGTTTGCAACTAAGACAAGAAACCTGTCAT--TAGAGGATGTTTGTTCATATTAA 4212
Db 98356 ATGGGATGTTAGAAGGTGATGAATGCATGAGGGAGGCAGGAAGTGAAGTGGGAAGGCTCG 98415
Qy 4213 TTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCCACAGTACTTTTGGAAAGTC 4272
Db 98416 CTTAGGAGTGAGGATTTGGGCAAGGTGACTCAGCCTGTAATCCAGCACCTTTAGAAATC 98475
Qy 4273 CAAGGTGGGTGGATCACTTGAGGTGAGAGTTTCGAGACCAGCCTGGTCAATATGGTGAAA 4332
Db 98476 TGAGACAGGTGGATCACTTGAGCCCAAGGAGTTTCGAGGCCAGCCTGGGCAACATGGTGAAA 98535
Qy 4333 CCCTATCTCTACTAAAAAATACAAAAATTAGCTGGGTGATGATGCATGCCTGTAGTCCC 4392
Db 98536 CTCAGTCTCTACTATAAATAACAAAAATTAGCTGGGCAATGATGGTGCATGCCTGTGATCCC 98595
Qy 4393 AGCTACTCGGAGGCTGAGGCAAGAGAAATTGCTTTGAACCTGGGAGGCAGAGGTTGCAGTG 4452
Db 98596 AGCTACTGGGAGGCTGAGGTGGGAGGATCACCTGAGCCCCAGGACCCAGAGGTTGCAGTG 98655

Qy 4453 AGCCGAGATCCCACTGCACTCCAGCTCCAGCCTGGGGACACAGCGAGACTCTATCTCAAAA 4512
Db 98656 AGCTGAGATCACACCCCTTCACTCCAGCCTGGGCAAGAGAGTGAGACCCCTGTCTCAAAAC 98715
Qy 4513 AATAAATAAATAAATAAAGGATCGGAGAGAAACAAA 4549
Db 98716 AAACAAACAAAAACAGAAAGAAAGAAAAAGAAAGAA 98752

RESULT 8
US-10-995-561-13276/c
; Sequence 13276, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13276
; LENGTH: 46878
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13276

Query Match 8.0%; Score 400.8; DB 10; Length 46878;
Best Local Similarity 49.9%; Pred. No. 1.3e+02;
Matches 1922; Conservative 13; Mismatches 1670; Indels 247; Gaps 28;

Qy 802 TATTATTCTTATTATTATTGAGACAGAGTCTTGCTTTGTGCGCAAGGCTGGAGTACAGTG 861
Db 34282 TTTTKTTTTTTTTTTTTTTGAGATGGAGTCTTGTGTTGCCAGGCTGGAGTGCAGTG 34223
Qy 862 GTGCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGTTTACGCCATTCTCCGCTCAG 921
Db 34222 GCAGATCTCGGCTCACTGCAAGCTCTGCCCTCCYGGTTTACGCCATTCTCCTGCCTCAG 34163
Qy 922 CCTCCCCAGTAGCTGGGACTAAAGGCGCCTGCCACCAACGCCCGCTAAATTTTTTTGTA-- 979
Db 34162 CCTCCCAAGTAGCTGGGACTACAGGTGCTGCCACCAACGCCCTGGCTAAATTTTTTATATT 34103
Qy 980 TTTTAAATAAAGACGGGTTTTCATCGTGTGTAGCCAGGATGGTCTCGATCTCATGACCTTG 1039
Db 34102 TTTTGTAGTAGAGCTGGGTTTACCATGTTAGCCAGGATGGTCTTGATCTCCTGACCTCA 34043
Qy 1040 TGATCCGCCTGCCCTCGCCTCCCAAAGTGTCTGGATTACAGGCATGAGCCACCGTGCCCG 1099
Db 34042 TGATCTGCCRCCTCAGCTTCCCAAAGTSTGGGATTACAGGCGTAAGCCACTGCACCCG 33983
Qy 1100 GCCTTATCACATTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 1159
Db 33982 GCC----AGGATTTTTTTTTTTTTTTTTTTTGTAGACAGGGTCTCACTCTGTGGCCAGCC 33927
Qy 1160 TTAGAGATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 1219
Db 33926 TGGAGTGCCATGGCTCAGTCATAGCTTACTGCTCAACCTCCCGGCTCAAGCGATCCTCC 33867
Qy 1220 CACTGCTGATCTCTAGCTCCTAGGACAGAGCCTTGAACATATCTGACCTAGGGAGGCTGAGCAGG 1279
Db 33866 CACCCAGCCTCCCGAGTAGCTGGGAC-TACATGTGGGCACCAACACACCTTGGCTAATTT 33808
Qy 1280 TTCACTGGATAAACAGTGCAGATAGTTTTAAAACTATCTGACCTAGGGAGGCTGAGCAGG 1339
Db 33807 TTTTTTTTTTTTTTTTTTTTGAGGKGGAGTTTTCGCTCTCTTTGCCCAGGCTGGAGTGCAATG 33748
Qy 1340 AGAATGGCGTG-----AAACCCGGGAAGCAGAGTTTGCAGTGAGCTGAAATCGTGTC 1390
Db 33747 GTATGATCTCGGCTCAATGCAACCTCTGCCTCCAGGTTCAAGTGATTCTCCTGCCTCAG 33688

Db	31632	-----TTGGCTCACTGCAACCTCTGCCTCCCAAGTTCAAGTGATTTCTTGTGCCTCAGC	31580
QY	3581	CTCCTGAGTAGCTGGAATTACAAGCGGTGCACCACCATTGCTTGGCTAAATTTTGTGATTTT	3640
Db	31579	CTCCCAAGTAGCTGGGATTATATGCAATGTGCCACCACGCCAGCTAA-TTTTTGTGTTTC	31521
QY	3641	TAGCAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTG	3700
Db	31520	TTGTAGAGACAGGGTTTCGCCATGTTGGCCAGACTAGTCTCAAACTCCTGTCTCAAGTG	31461
QY	3701	ATCTGCCTGCCTCAGTCTCCCCAAAGTGTGGAATTATAGGCGTGAGTCACTGTGCCCTGGC	3760
Db	31460	AGTCGCCTGCCTYGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACTGYGCCTGGA	31401
QY	3761	CGATTACTGCTAT-----TTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGA	3815
Db	31400	CAAGAAATTTCTATTATTATTTTCTCTCAACAAATTATCAACATCTGTTACATCTYGA	31341
QY	3816	CATATAGTAGTGCTCAATAAATAATTGATGAATGCACAGCCTAGAT-----	3862
Db	31340	CAGGCAACAGATAAGCATGAATAAGGACATGGGTCACCAATCTCACTGGGGACAGATGA	31281
QY	3863	-----ATAAACTTTCTTTTCTTTTTTTTAAACAAATCTTGACAACTTTG	3906
Db	31280	CAAAGTAGGAACAACAAACAGCCTGGCATGTGGCTTGTGCTATATAATCCAGCTACTTGG	31221
QY	3907	CAGAAATA-----ATACAATCTTGCAATCTGCTTTTTCATTTATCACCTTGTTATGACT	3960
Db	31220	GAGGCTGAGGTGGGAGGATCACTTGAACCCAGGAGTTCAAGGCTGCAGTGAGGTATGATT	31161
QY	3961	TTTTTCATATTGCCTCA-----AACCCTTATTGTTACTGT	3994
Db	31160	GCATCATGSGACTCCAGCATTTGGCGACACAGCAAGGCTCCGCTCTTTGAAAAAAAAG	31101
QY	3995	TTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTC	4054
Db	31100	TGAGAAGTGCTATATATCATATCACTGATAGACAGAGTAACACTAGGGCATGGGTACTT	31041
QY	4055	CTGCTCCACT--TTAGAAGGCCAAATTACAAATCTGATGAAGCTATGAACCTCTCCC	4112
Db	31040	CAGCTGGGCTGAGGGGAATGGGATTGTTAGGGACATGACATTTACACTGAGGTCTGAAGG	30981
QY	4113	CAGAGAAATACACACACA-----CACACACACTCACACACAGTTTTTTTTTAATGT	4163
Db	30980	ATGAGAAAGAGCCAGAAATGTTTGTGGGAAAGCACTTTCAGACAGAGGGAACAGCAATGT	30921
QY	4164	TTGCAACTAAGACAAGAAACCTGCAATTAGAGGATGTTTGTTCATATTAAATTAATAAC	4223
Db	30920	AAAGGCCCGAGCAGGAATGAGCTTGTGTTGTAGGAACCA--CAAGAAAGCCAGTG	30864
QY	4224	TCAGTTGGGCACAGTGACTCAAGCCTGTAACCACACAGTACTTTGGAAGTCCAAGTGGTG	4283
Db	30863	TGGGCTGGGCGGTGGCTCATGCCCTGTAATCCCAGCATTTTGGGAGGCTGAGGCGGGTG	30804
QY	4284	GATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCATCTCTA	4343
Db	30803	GATCACCT---TTCAGGAGTTTGAGACCAGCCTGGCCAATGTGTGAAACCCCGTCTCTA	30747
QY	4344	CTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCCTGAGTCCCAGCTACTCGGG	4403
Db	30746	CTAAAAATACAAAAATTAGCTGGGCTTGGTGGCGCCTGTAATCCCAGCTAGTCTGG	30687
QY	4404	AGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCC	4463
Db	30686	AGGCTGGGGCAGGAGAAACGCTTGAACCGGAGGTGGAGGTTGCAGTGAGGTGTC	30627
QY	4464	---CACCACTGCACCTCCAGCCTGGCGAC-ACAGCGAGACTCTATCTCAAAAAATAAA	4518
Db	30626	AGTAAGCCATTGCACTCCAGCCTGGGCAACAAGAGTGAAACTCCATCTCAAAACAACAC	
QY	4519	TAAATAAAATAA 4530	

Db	30566	AACAAAAAGAAA	30555
RESULT 9			
US-11-121-086-43/c			
; Sequence 43, Application US/11121086			
; Publication No. US20050266459A1			
; GENERAL INFORMATION:			
; APPLICANT: POULSEN, TIM S.			
; APPLICANT: NIELSEN, KIRSTEN V.			
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES			
; FILE REFERENCE: 09138.6000-00000			
; CURRENT APPLICATION NUMBER: US/11/121,086			
; CURRENT FILING DATE: 2005-05-04			
; PRIOR APPLICATION NUMBER: 60/567,570			
; PRIOR FILING DATE: 2004-05-04			
; NUMBER OF SEQ ID NOS: 107			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 43			
; LENGTH: 175416			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-121-086-43			
Query Match 7.9%; Score 393.8; DB 17; Length 175416;			
Best Local Similarity 52.2%; Pred. No. 57;			
Matches 1210; Conservative 4; Mismatches 986; Indels 117; Gaps 11;			
QY	2276	TTAAAAATCGCTTTCAGGCCAGGCGGTGGCTCATCGCTGTAATCCCAGCACCTTTGGGA	2335
Db	99774	TTAAAAAAAATGCGCCAGGCCCGTGGCTACGCCCTATAATCCCAGCACCTTGAGA	99715
QY	2336	GGCCGAGGCGGGGATCACTTGAGGTCAGGATCGAGACCAGCCTGGCCACATGGTG	2395
Db	99714	GGCCGAGGTGCGCAGATCACCTGAGGTCAGAAAGTT--TGACCAGCCTGGCCACATGGCG	99657
QY	2396	AAACCCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGGAGCGCCTGTAA	2455
Db	99656	AAACTCCCGTCTCTACTAAAAAGTGCAAGAAATTAGCTGGGTGTGGTGGCGCACGCTGTCA	99597
QY	2456	CCCAGCTACTTGGGAGACTGA-----GTTGGAGGTTTCA	2490
Db	99596	TCCCAGCTACTCTGGAGGCTGAGGCAAAAAATAATCGCTTGAACCTGGGAGCGGAGTTCA	99537
QY	2491	GTGAGCCAAAGTCTGTCACTGTGTCCAGCCTGGGTAACAGAGCAACTCTGTCTCAAAA	2550
Db	99536	GTGAGCCGAGATCTCGTACTGAACTCCAGCCTGGACAACAGAGCAAGACTCTGTCTCCA	99477
QY	2551	AAAAAAAATGCTTTCAATAAATATATGATAAAAGGACTTATATTTTTCAAGCCATAGGA	2610
Db	99476	AAAAAAACCCAAAAAACAAGAACAAACAACAACACTGAAATGAAACTCTGTACCCATCAA	99417
QY	2611	TCATTTCTCCTGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCTCTGAGAGTGGGCAGGT	2670
Db	99416	ACAATAATTCT-----CCCCCTGCCCTCCTACTCAAGTCCCTGGCAACCACTTCCACTCT	99362
QY	2671	GAGGCTGACCTATTGCTCTGCACCTTACTCTCTATCTCAGCTGTCCCTCCCACCTTCCAGG	2730
Db	99361	TTGATTCTATGAATTTGACTATTTTTRTCATAGATACCGCATACAAGTGAATCGTGACT	99302
QY	2731	TGCTGCCAGACACATGACAACTGCTAYGACCAGGCCAAGAAAGCTGGACAGCTGTAAATTT	2790
Db	99301	CTTTGCCTTTCTGTGTCTGGCTTATTTCACCTTAGCATCGTGTCTTCCAGGTTTCATCAATG	99242
QY	2791	CTGCTGGACAMMCCGTACACCCACACCTATTTCATACTCGTGTCTGTGGCTCGGCAATCACC	2850
Db	99241	TTGGAGCATGTGTCGGAATTTCTCTCTTTTAA-AGCTGAATGTTCCATTGTATGTACG	99183
QY	2851	TGTAGCAGTAGGTTTATCCCTTCTCTTGACCTATGAATTTCTAG-----TTGGTTCTCAGTA	2905
Db	99182	CACTACATTTTGTTTTATTCAATTCATGAATGGAAGAAACAAGGGCGCTTGAGTTGCTTCT	99123
QY	2906	GGCCGGGGGAAATAATAGTAACAACAGCCATGATTTAGTTGTTAAATTTTCTTGGTTCTGG	2965

Db	99122	ATCCTTTGGCTATTGTGAGTAGTACTACTATGAACATAGGAGTACAAGATTGGCACATT	99063
Qy	2966	GCAGTGTCTCCTTTAATCCTCAGAACACACTATGGGATAGGTACAATTATCCTCACTTA	3025
Db	99062	ACTTTTAAACACTTAAAAAATGATAGACGCTGTCTGAAGACTGAAACATGTTCAATTA	99003
Qy	3026	ACAGATAAGAAAACTGAGGCTCAGAAGGCTGAGCTATTTTGCCCAAGATCACACAGCTTGT	3085
Db	99002	CTTTTCAGTTTCACAAGGACCTTTTGGAAATATCTTTGTCCAGGTCTAATCCTAATCAAG	98943
Qy	3086	AAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTTTAGAGACAGGGTCTTGGCTGTGTC	3145
Db	98942	ATTTCTACCCATTTTCTTTTMTTTTATT-----TTTTGAGATAAAAGTCTTGGCTCTGTCG	98887
Qy	3146	CCCAGGATGAGCACAGTGGTGCAACCATAGGTCACTGCGCTCAACCTCCTGAGCTCA	3205
Db	98886	CCCAGGCTGGAGTGTAGTACACAATCTTGGCTCACTGCAACCCCTGCCTCCCAGGTTCA	98827
Qy	3206	AGGGATCTGTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCGCC	3265
Db	98826	AGCAATTCTTTGCTCAGCCTCCGAGTAGCTGGAATTACAGGCACGTGCTACCCATGCC	98767
Qy	3266	TGGCTAATTAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTC	3325
Db	98766	CGGCCAAATTTTGTATTTTGTAGTACAGACAGGGTTTCACCATGTTACCCAGGATGGTC	98707
Qy	3326	TTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTCTGGGATTACAG	3385
Db	98706	TCGATTTCTGT--ATCTCGTATCCACTCACTTCAGCCTCCCAAGTGTAGGGATTACAG	98649
Qy	3386	GGTGAGCCACCATGTGCGGTACTTATTTCTTTACATTCATCTTCCAATAGATGTA	3445
Db	98648	GCATGAGCCACCGCGCCAGGCCCAFTTCTTTATTAGAGAGAGTCTCAATCCATCATC	98589
Qy	3446	AGATCCACAGAACAGGGATTACTGCTATTTTCTTCCTTCTTTTGTGACAGAGTCTC	3505
Db	98588	CAGGCTGGAGTGCAGAGGCACGATCTT-----	98562
Qy	3506	ACTTCATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGA	3565
Db	98561	-----GGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGTGA	98526
Qy	3566	TTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCT	3625
Db	98525	TTCTCGTAGTCAGCCTCTCTAGTAGCTGGATTATAGGCGTGTGCAACCAGGCCTGGCT	98466
Qy	3626	AATTTTTGTATTTTACGACAGATGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAA	3685
Db	98465	AATTTTTGTATTCTTATTAGAGACGGGCTTTCGCCAGKTTCGCCAGGTTGGTTTTGAAC	98406
Qy	3686	TCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAGTGTGGAATTATAGGCGTGA	3745
Db	98405	TCCTGGCCTCATGCGATCCCCCACCCTTGGCCTCCCAAGAGCTGGGATTACAGGSCATGA	98346
Qy	3746	GTCACTGTGCCCTGGCCGATTACTGTCTATTT-----TCTTTATTGCTATATCCCC	3795
Db	98345	ACTATTGCACCCAGCCTCTACCCATTTTCATGAAGACCAAGTTATATAGCTGTGATTAG	98286
Qy	3796	AGATCTAGACGAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAG	3855
Db	98285	CATCTCAATATAGCACCTTTTATTACCCAGATCCAATATGCAATGGTTAAAAAATTACTGAG	98226
Qy	3856	CCTAGATATAAACTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTGCAGAAATAA	3915
Db	98225	TGATTTGGGGGCAGCATTTGCAGTATGGCCATGATATTTCTCAACTTCCCTCTCCCTT	98166
Qy	3916	TACAATCTGCATTCTGCTTTTCACTTATCACCTTGTATGACTTTTTTCATATTGCTC	3975
Db	98165	GCCRGTTGCAGACTCAGCCCTTGATCACAAGAGGTAGGCACGTGGTGAAGCTAATGCAAT	98106
Qy	3976	AAACCTTTATTGTTACTGTTTTTTCATTGTTTACTATTTTAGTCACTGAATAATATGCTT	4035

Db	98105	CAGATTACTTTTCTCTGGGAATTTGAATAAATCATTTGGATAGCAAGATCCCCAACAGAAGT	98046
Qy	4036	AATTTGCTTATACATCCTCTCTGCTCCACTTTTAGAAGGCCAAATTTTACAAATCTGATGAAA	4095
Db	98045	TTCTTACAGGCCTCTGCCACTGTGATTCACAGACCTGTCTGGTTCCCTGCTTTAATTTT	97986
Qy	4096	GCTATGAACCCCTCTCCCCCAGAGAAATACACACACACACACACTCACACACAGTTTTTT	4155
Db	97985	GTGAGCTTCTCAGTGTCAATTGAAAACAACCTTTTTTTGGCTTACATTTCAATGAGTCAATTTCT	97926
Qy	4156	TTTAATGTTT----GCAACTAAGACAAAGAACTGTCATTAGAGGATGTTTGTTCATATT	4210
Db	97925	ATTGCTTCTATCACAGAACTTCAACTGATACAATTCAMAGCTGATGCTCGAATTTCTT	97866
Qy	4211	AATTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTTGAAG	4270
Db	97865	CAAGAAATAT-AGGAGGCCGGGCACGGTGGCTCACGCCTGTAATCCGAACACTTTGGGAG	97807
Qy	4271	TCCAAGGTGGGTGATCACTTGAGGTGAGAAGTTTCGAGACCAGCCCTGGTCAATATGGTGA	4330
Db	97806	GCCGAGGCAGGTGGATCACTTGATGTCAGGAGTTCAAGACCAGGCTGGCCAACATGGTGA	97747
Qy	4331	AACCTATCTCTACTAAAAATACAAAAAATTAGTGGGTGTAGTGATGCATGCTGTAGTC	4390
Db	97746	AACACCGCCTCTACTAAAAATACAAAAATTAGCTTGGTAGGTGGCACGCGTCTGTAATT	97687
Qy	4391	CCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAG	4450
Db	97686	CTAGCTACTCGGCAGGCTGAGGCAGGAGAAATTGCTTGAACCCGGGAGGTGGAGGTTGCAG	97627
Qy	4451	TGAGCCGAGATCCCAACCACTGCACCTCCAGCCTCGGCGCACACAGCGAGACTCTATCTCAA	4510
Db	97626	TGAGCCAAGATCACACCACTGCACCTCTAGCCTGGGTGACAGAGCAAAACTTCATCTCAA	97567
Qy	4511	AAAAATAAATAAATAAAGGATCGGAGAGAAACA	4547
Db	97566	AAAAAAAATATATATATATATAKAGAGAGAGAGAGA	97530

RESULT 10
US-11-114-798-50
; Sequence 50, Application US/11114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 0618.011.0004
; CURRENT APPLICATION NUMBER: US/11/114,798
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 50
; LENGTH: 92199
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-50

Query Match	7.8%;	Score 387.6;	DB 18;	Length 92199;
Best Local Similarity	53.6%;	Pred. No.1e+02;		
Matches 1252;	Conservative 3;	Mismatches 937;	Indels 144;	Gaps 16;
Qy	2273	ATGTTAAAAATCGCTTTCAGGCCAGGCGGGTGCCTCATGCCCTGTAATCCAGCACCTTTG	2332	
Db	26807	ATTTTAATAGTTATCTGTGGCCAGGCATGGTGGCTTGTGCCTATAATCCAGCACTTAG	26866	

Qy	2333	GGAGCCGAGCGGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAACATG	2392
Db	26867	AGAGCCCAAGACAGCGGGATCACCTGAGGTCAGGAGTTCGAGACTAGCCTGACCAACATG	26926
Qy	2393	GTGAAACCCGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCAGCGCCTG	2452
Db	26927	GAGAAACCCCTCTCTACTAAAA--TACAAAAATTAGCCGGCGTAGTGGCACATGCTTG	26984
Qy	2453	TAACCCAGCTACTTGGGAGACT-----GAGTTGGAGGT	2486
Db	26985	TAATCCTAGCTACTCGGGAGGCTGAGCGAGGAGAATCGCTTGAACCCGGGAGTCAGAGGT	27044
Qy	2487	TTCAGTGAGCAAGGTCGTGTCACTGTCTCCAGCCTGGGTAAAC-AGAGCAACTCTGTCT	2545
Db	27045	TGCTGTGAGCGGAGATCAGGCCATTGCACCTCCAGCCTGGGCAACAAGAGCAAACTCCGT	27104
Qy	2546	CAAAAAAANAATGCTTTCAATAAATATATGATAAAAGGACTTATATTTTCAAGCCA	2605
Db	27105	CTCAAAAAAAGAAAAGAAAACACTGATTTAGACCAACTGCCTCGTTTACAGATAGA	27164
Qy	2606	TAGGATCATTTCTCCTGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCCTGAGAGTGGG	2665
Db	27165	GAGGGTGACGCTAGAGAAGGTCAGCTCCAGGTCATCCAGGAGGTAGACTCTTTCTCTCC	27224
Qy	2666	CAGGTGAGGCTGACCTATTGCTCTGCACCTTACTCTATCTCAGCTGTCCCTCCCACCTT	2725
Db	27225	AGCTCAGAGCTTTTCAAACTTTAAATGTGCATACAAATCACTTGGCAGTTCTTGTTAATGT	27284
Qy	2726	CCAGGTGCTGCC-----AGACACATGACAAACTGCTAYGACCAGGCCCAAGAGCTGGACA	2779
Db	27285	GCAGATTCTGATTTGGTAGGTTGCAGGAAGCCTGCGATTTGTATTTCTTGTGTTCTT	27344
Qy	2780	GCTGTAAATTTCTGCTGGACAMMCCGTACACCCACACCTATTTCATACTCGTCTCTGCT	2839
Db	27345	TGTTTGAGATGGAATTTCACTCTTTGTTGCCAGGCTGGAGTGAATGGCACTATCTCGSC	27404
Qy	2840	CGGCAATCACCTGTAGCAGTAGGTTTAT-----CCCTTCCTTGACCT	2881
Db	27405	TCACTGCAACCTCTGCCTTCGGTTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGC	27464
Qy	2882	ATGAATTCATGTTGGTTCTCAGTAGCGCGGGGGGAAATAATAGTAACAACAGCCATGATT	2941
Db	27465	TGGGATTACAGGCATGTGCCACTATGCTTGGCTAAATTTTGTATTTTGTAGTAGAGA-CAGG	27523
Qy	2942	TAGTGTTAAATTTCTGGTCTCGGGCAGTGTCTCCTTTAATCCTCAGAAACAACACTATGG	3001
Db	27524	GTTTCTCCATGTTGGTCAGGCTGGTCTTGAACCTCCTGACCTCAGGTGATCTGCCACCTC	27583
Qy	3002	GATAGGTACAATTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGGCTGAGCTA	3061
Db	27584	AGCCTCCCAAAGTCTGGGATGACAGGGGTGAGCCACTCGCGCCAGCCGAGATTTGTCTAT	27643
Qy	3062	TTTGCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGG-----GTTTT	3107
Db	27644	TCTTAACAAAGCTCCCAGGGGATGCCAATACTGTCAAGTTGGGACCACACTTGATTTTTTTT	27703
Qy	3108	TTTTTGTGTTGTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGCACAGTGGTG	3167
Db	27704	GTTTTTTGTTTTTTTGAGACAGGGGTCTCACTCTGTCTTCCAGGCTGGAGTGCAGTGGA	27763
Qy	3168	CAACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGCCT	3227
Db	27764	GGTTCTCGGCTCAATGCAACCTCCGCCTCCTGGGTTCAAGTGAATCTTGTGCCTCAGCCT	27823
Qy	3228	CCCAAGTAGTGGGACTACGAGCGGTGCACCACCGCCTGGCTGAATTAATAAAAAATTTTT	3287
Db	27824	CCCGAGTAGTGGGATTACAGGCTTGAGTTACCATTGCCTGGCTAAATTTTTTATATTTTA	27883
Qy	3288	TGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAA	3347
Db	27884	-GTAGAGACGAGGTTTCACCATGTTGCCGAGACTGGTCTCCAACTCCTGGCCTCAATTGA	27942

Qy	3348	TCCTCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATTGTGCGGCT	3407
Db	27943	TCCACATACCTCAACTT--CATAGTGTGGGATTACAGGTGTAAAGCCACTGTGCTGTCT	28000
Qy	3408	ACTTATTTCTTTACATTCCCATCTTTCCAATAGAATGTAAAGATCCACAGAACAGGGAATTAC	3467
Db	28001	TGTTTTTATATATTTT-----ATTTT	28022
Qy	3468	TGCCTATTTTCTTCCTTTCTTTTGTGACACAGAGTCTCACTTCAACCTCAACCTCCGT	3527
Db	28023	TTATTTTGGATAGGGTCTCACTGTTGCCAGGCTGGAGTGAATGGCACATC-----	28077
Qy	3528	TCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGA	3587
Db	28078	ATGGCTCCCTGCAGCCTCAAACCTCCTGGGATCAAGTGATCCTCCCACCTCAGCCTTCCAA	28137
Qy	3588	GTAGCTGGAATTACAAGCGTGCAACCATTGCTTGGCTAAATTTT--TGTATTTTAGCA	3645
Db	28138	GTAGCTGGGACTACAGATGGGAAACACCACGCTCTGCTAAATTTTAAAAAATGTTTTGTA	28197
Qy	3646	GAGATGGGTTTTACCATGTTGCCAGGCTGCTCAAACTCCTGACCTCAAGTGATCTG	3705
Db	28198	GAGATGGGTCCTCCTATGTTGCCAGGCTGGTCTTAAACTACTGACCTCAAGTGATCCT	28257
Qy	3706	CCTGCCTCAGTCTCCAAAAGTGCTGGAATTAPAGCGTGAGTCACCTGTGCCTGGC----	3760
Db	28258	CTTGCCTTGGCCTCCCAAAGTACTAGGATTTCACTTGTGAGCCACCATACCCAGCTGGGA	28317
Qy	3761	---CGATTACTGTCTATTTTCTTTATTGCTATATATCCCAGATCTAGAGCAGTGTCTGACA	3817
Db	28318	CCACACTGAATAGCAAGGCTCCTGTAACTCCTTCAGCAGACACATTTCTCCCTCATACCA	28377
Qy	3818	TATAGTAGGTGCTCAATAAATAATTTGATGAATGCACAGCCTAGATATAAACTTTCTTTT	3877
Db	28378	CCTGGTAAGTGATCACTGTAAACTTCTCAATGGCAAGGACAGGCTCTTGTTCAATTATGT	28437
Qy	3878	CTTTTTTTAAAAACAATCTTTGACAACTTTTGCAG--AATAAATACAATCTTGCAATTCTGCTT	3935
Db	28438	GCCCTCAACCCACTACCTTACCACAGTTCCCGGCACACAGTGAGGGCTTAATTAACACCC	28497
Qy	3936	TTTCACTTATCACCTTGTATGACTTTTTTCATPATTCCTCAAACTTTTATTTGTTACTGTT	3995
Db	28498	ACTGACTCTAGGTGTTTCAGGTTCTTAGCAAGTGGCAACACACCTTGAGCAAAAAAATT	28557
Qy	3996	TTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTTATACATCCTCC	4055
Db	28558	GTTCAAGGCTGGSCACAGTAGCTCATGCCCTATGATCCAGCACTTTGGAAGGCTGAGGTG	28617
Qy	4056	TGCTCCACTTTTAGRAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCTCCAG	4115
Db	28618	GGAGGACTGCTTGAGCCCAGGAGTTTGAGACCTG-----CCTGGGTGA	28660
Qy	4116	AGAAATACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCACACTAAGA	4175
Db	28661	CATAGTAAGACTGCATCTCTACAAAAACAACCAACCTTATTCAAAAACATTTCTGCAATGC	28720
Qy	4176	CAAGAAACCTGCAATTAGAGGATGTTTGTTCATATTAATTAATAATACTCAGTTGGGCAC	4235
Db	28721	TTCTTTGTGACAGACACTGGAGAAAGCACTTTTCATAAAATGAGTTTGTGGGCCAGATGT	28780
Qy	4236	AGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGG	4295
Db	28781	GGTGGCTCATGCCCTGTAATCACAGCACTTTTGGGAGGCCGAGGCGGATCACCTGAGG	28840
Qy	4296	TGAGAAAGTTCGAGACACAGCCTGGTCAATATGTTGAAACCTCTATCTCTACTAAAAATACAA	4355
Db	28841	TCAGGAGTTCGAGACCAGCTTGGCCAACATGATAAAACCCCGTCTCTACTAAAAATAC-A	28899
Qy	4356	AAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAA	4415
Db	28900	AAATTAGCTGGACATGGTGACACACGCTGTAAATCCCAGCTACTCGGGAGGCTGAGGCAG	28959
Qy	4416	GAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGTCAGTGAGCCGAGATCCCACCACCTGCACT	4475

Db 28960 GAGAAATGCTTGAACCTGGGAGCGGAGGCTACAGTGAGCCAAGATCATGCCACTGCACT 29019
Qy 4476 CCAGCCTGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAAATAAA 4531
Db 29020 CCACCCTGGGTGACAGAGTGAGACTGTGTCTCAAAAAATAAATAAAATAAA 29075

RESULT 11
US-11-114-798-58
; Sequence 58, Application US/11114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 0618.011.0004
; CURRENT APPLICATION NUMBER: US/11/114,798
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 58
; LENGTH: 318488
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-58

Query Match 7.8%; Score 387.6; DB 18; Length 318488;
Best Local Similarity 53.6%; Pred. No. 42;
Matches 1252; Conservative 3; Mismatches 937; Indels 144; Gaps 16;
Qy 2273 ATGTTAAAAATCGCTTTCAGGCCAGCGCGGTGGCTCATGCTGTAAATCCCAGCACTTG 2332
Db 84122 ATTTTAAATAGTTATCTGTTGGCCAGGCATGGTGGCTTGGCTATAATCCCAGCACTAG 84181
Qy 2333 GGAGCGCGAGCGGGGATCACTTGAGGTCAGGAGTTCAGACCAGCCTGGCCAAACATG 2392
Db 84182 AGAGCCAAAGACAGGCGGATCACTGAGGTCAGGAGTTCAGACTAGCCTGACCAACATG 84241
Qy 2393 GTGAAACCCCTGTCTCTACTAAAAATAACAAAAATTAGCCGACATGGTGGCGAGCGCTG 2452
Db 84242 GAGAAACCCCTCTCTACTAAAAA--TACAAAAATTAGCCGGCGTAGTGGCACATGCTTG 84299
Qy 2453 TAACCCACAGCTACTTGGGAGACT-----GAGTTGGAGGT 2486
Db 84300 TAATCCTAGCTACTCGGGAGGCTGAGGCAGGAGAAATCGCTTGAACCCGGGAGTCAGAGGT 84359
Qy 2487 TTCAGTGAGCCAAAGGTCGTGTCACTGTCTCCAGCCTGGGTAAC-AGAGCAAACCTCTGTCT 2545
Db 84360 TGCTGTGAGCCGAGATCAGGCCATTGCACCTCCAGCCTGGGCAACAAGACAAACTCCGT 84419
Qy 2546 CAAAAAANAANAATGCTTTCAATAAATATATGATAAAAGGACTTATATTTTTCAGCCCA 2605
Db 84420 CTCAAAAANAAGAAAGAAACACTGATTTAGACCAACTGCCTCGTTTACAGATAGA 84479
Qy 2606 TAGGATCATTTCTCCTGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCCTGAGAGTGGG 2665
Db 84480 GAGGTGCAGCCTAGAGAAGGTCAGTCCAGGTCAATCCAGGAGGTAGACTCTTTTCCTCC 84539
Qy 2666 CAGGTGAGGCTGACCTATTGCTCTGCACCTTACTCCTATCTCAGCTGTCCCTCCCACTTT 2725
Db 84540 AGCTCAGAGCTTTTCAAACTTTAATGTGCATACAAATCACTTGGCAGTTCTTGTTAATGT 84599
Qy 2726 CCAGGTGCTGCC-----AGACACATGACAACTGCTAYGACCAGGCCCAAGAAGCTGGACA 2779

Db 84600 GCAGATTCTGATTTGGTAGGTTGCAGGAAGCCTGCGATTTGTTATTCTTGTGTTTCTT 84659
Qy 2780 GCTGTAAATTTCTGCTGGACAMMCCTGTACACCCACACCTATTTCATATCTCGTCTCTGGCT 2839
Db 84660 TGTTTGAGATGGAATTTCACTCTTGTGTGCCAGGCTGGAGTGCAAATGGCACTATCTCGGC 84719
Qy 2840 CGGCAATCACCTGTAGCAGTAGGTTTAT-----CCCTTCCTTGACCT 2881
Db 84720 TCACTGCAACCTCTGCCTTCGGTTTCAAGCGATTTCTCCTGCCTCAGCCTCCGAGTAGC 84779
Qy 2882 ATGAATTCTAGTTGGTTCTCAGTAGCGCGGGGAAATAATAGTAACAACAGCCATGATT 2941
Db 84780 TGGGATTACAGGCATGTGCCACTATGCCCTGGCTAAATTTTGTATTTTGTAGAGA-CAGG 84838
Qy 2942 TAGTGTTAATTTTCTTGGTTCTGGGCAGTGTCTCCTTTAATCCTCAGAAACAACACTATGG 3001
Db 84839 GTTTCCTCATGTTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGTGATCTGCCACCTC 84898
Qy 3002 GATAGGTACAATTTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGGCTGAGCTA 3061
Db 84899 AGCCTCCCAAAGTGTGGGATGACAGGCGTGAGCCACTGCGCCAGCGAGATTTGTCTAT 84958
Qy 3062 TTTGCCCCAAGATCACACAGCTTGTAAGTGGTGACAGTTTG-----GTTTT 3107
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Qy 3108 TTTTGTGTTGTTTAGAGACAGGGTCTTGTCTGTCAACCCAGGCATGAGCACAGTGGTG 3167
Db 85019 GTTTTTTGTTTTTTGAGACAGGGTCTCACTCTGTCTTCCAGGCTGGAGTGCAAGTGCA 85078
Qy 3168 CAACCATAGGTCACTCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCT 3227
Db 85079 GGTTCCTGGCTCAATGCAACCTCCGCCCTCCTGGGTCAAGTGATTCTTGTGCTCAGCCT 85138
Qy 3228 CCCAAGTAGCTGGGACTACGAGCGTGCCACCACCGCCTGGCTAATTAAAAAATTTTT 3287
Db 85139 CCCGAGTAGCTGGGATTACAGGCTTGAGTTACCATGCCTGGCTAATTTTTTTTATTTTA 85198
Qy 3288 TGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTGTCTTAAACTCCTGGCTTCAAGCAA 3347
Db 85199 -GTAGAGACGAGGTTTCACCATGTTGCCGAGACTGGTCTCCAACCTCCTGGCCTCAATTGA 85257
Qy 3348 TCCTCTACCTTGGCATCCCAAAGTGTCTGGGATPACAGGGGTGAGCCACCATGTGCGGT 3407
Db 85258 TCCACATACCTCAACTT--CATAGTCTGGGATTACAGGTGTAAAGCCACTGTGCTTGCT 85315
Qy 3408 ACTTATTCTTTACATTCATCTTTCCAATAGATGTAAGATCCACAGAACAGGGATTAC 3467
Db 85316 TGTTTTTTTATTATTTTT-----ATTTT 85337
Qy 3468 TGCCTATTTTCTTCCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGT 3527
Db 85338 TTATTTTGGATAGGGTCTCACTGTTGCCCAGGCTGGAGTGCAATGGCACAAATC----- 85392
Qy 3528 TCAGCTCACTGCAAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGA 3587
Db 85393 ATGGCTCCCTGCAGCTCAAACTCCTGGGATCAAGTGATCCTCCCACCTCAGCCTTCCAA 85452
Qy 3588 GTAGCTGGAATTACAAGCGTGCAACCATGCTTGGCTAATTTTT--TGATTTTTTAGCA 3645
Db 85453 GTAGCTGGGACTACAGATGGGAAACACCACCGTCTGCTAATTTTTTAAAAAATGTTTTGTA 85512
Qy 3646 GAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTG 3705
Db 85513 GAGATGGGTTCTCCCTATGTTGCCAGGCTGGTCTTAAACTACTGACCTCAAGTGATCCT 85572
Qy 3706 CCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGAGTCACCTGTGCCTGGC----- 3760
Db 85573 CTTGCCTTGGCCTCCCAAAGTACTAGGATTTTCAAGTGTGAGCCACCATACCCAGCTGGGA 85632
Qy 3761 --CGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACA 3817
Db 85633 CCACACTGAATAGCAAGGCTCCTGCTAACTCCTTTCAGCAGACACATTTCTCCCTCATACCA 85692

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QY 3818 TATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCGCTAGATATAAACTTTCTTTTT 3877
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Db 85693 CCTGGTAAGTGATCACGTGTAACCTTCTCAATGGCAAGGACAGGCTCTTGTTCAATTTATGT 85752

QY 3878 CTTTTTTTAAAAAATCTTTGACAACTTTGCAG--AATAAATAACAATCTTGCATTTCTGCTT 3935
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Db 85753 GCCCJCAACCACCTACCTACCACAGTTCCTCCGGCACACAGTGAGGGCTTAATTAACACCC 85812

QY 3936 TTTCACTTATCACCTTGTATGACTTTTTTTCATATTGCCCTCAAACTTTATTGTTACTGTT 3995
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Db 85813 ACTGACTCTAGGTGTTTCAGGTTCCCTAGCAAAAGTGCCAAACACCTTGAGCAAAAAAAT 85872

QY 3996 TTTTCATTGTTACTATTTTAGTCACCTGAATAATATGGCTTAATTGCTTTATACATCCTCC 4055
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Db 85873 GTTCAAGGCTGGGCACAGTAGCTCATGCTATGATCCCAGCACCTTGGAAAGCTGAGGTG 85932

QY 4056 TGCTCCACTTTAGAAGGCCAAAATTTACAAAATCTGATGAAAGCTATGAACCCCTCTCCCCAG 4115
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Db 85933 GGAGGACTGCTTGAGCCCAGGAGTTTGAGACCTG-----CCTGGGTGA 85975

QY 4116 AGAAATACACACACACACACACTCACACAGTTTTTTTTTTAATGTTTGCAACTAAGA 4175
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Db 85976 CATAGTAAGACTGCATCTCTACAAAAACAAAAAACCTTATTCAAAAAACATTTCTGCTATGC 86035

QY 4176 CAAGAAAACCTGCATTAGAGGATGTTTGTTTCATATTAAATTAATAAATAAATCAGTTGGGCAC 4235
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Db 86036 TTCCTTTGTGACAGACACTGGAGAAAGCACTTTTCATAAATGAGTTTGTGGCCAGATGT 86095

QY 4236 AGTGACTCAAGCCTGTAACCCACAGTACTTTTGAAGTCCAAGGTGGGTGATCACTTGAGG 4295
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Db 86096 GGTGGCTCATGCTGTAATCACAGCACTTTGGAGGCCGAGGCGGATCACCTGAGG 86155

QY 4296 TGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATACAA 4355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86156 TCAGGAGITCGAGACCAGCTTGGCCAAACATGATAAAACCCCGTCTCTACTAAAAATAC-A 86214

QY 4356 AAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAA 4415
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Db 86215 AAATTAGCTGGACATGGTGACACACGCGCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAG 86274

QY 4416 GAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACCTGCACT 4475
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86275 GAGAAATGGCTTGAACCTGGGAGCGGAGGCTACAGTGAGCCAAAGATCATGCCACTGCACT 86334

QY 4476 CCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAAA 4531
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Db 86335 CCACCCTGGGTGACAGAGTGAGACTGTGTCTCAAAAAATAAATAAATAAATAAAA 86390
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RESULT 12
US-11-121-086-14/c
; Sequence 14, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 167891
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-14
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Query Match          7.7%; Score 384.8; DB 17; Length 167891;
Best Local Similarity 53.8%; Pred. No. 71;
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Matches 1239; Conservative 3; Mismatches 910; Indels 150; Gaps 16;

QY 2292 GGCCAGGCGGTGGCTCATGCTGTAAATCCCAGCACTTTGGGAGGCCGAGGCGGCGGA 2351
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Db 61654 GCCCAGACGCGTGGCTCACCCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGCGAGA 61595

QY 2352 TCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTCTACT 2411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61594 TCACCTGAGGTCGAGTTCGAGACCAGCCTGACCAACATGGAGAAACCCCTGTATCTACT 61535

QY 2412 AAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTAAACCCAGCTACTTGGGA 2471
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Db 61534 AAAAA--TACAAAAATTAGCCAGGCATAGTGTACATGCCTGTAACTCCAGCTACTTGGGA 61477

QY 2472 GACTGAGT-TGGAGTMTTCAGTGAGCCAAAGGTCGTCTCACTGTGCCAGCCTGGGTAAC 2530
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Db 61476 GGCTGAGTCAGGAGAATTGCTTGAACCTGGGAGGAGAGGTTTCGGTGAGCCGAGATTGC 61417

QY 2531 AGAGCAACTCTGTCTCAAAAAAATAAATGCTTTCAATAAAATATATGATAAAGGACTTA 2590
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Db 61416 GCCATTGCACCTCCAGCCTGGGCAACAAGAGC-AAAACTCCGTCTCAAAAAAATAAATAA 61358

QY 2591 TATTTTTTCAAGCCATAGGATCATTTTCTCCTGAAGCATCTTGGCGAAGTCATCCCCACCT 2650
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Db 61357 AAAAAACACAGATGGGAGGAAGGAGTGATGAAGAGAGGTTGATTAATGAGTACAAATA 61298

QY 2651 GTTCCTGAGAGTGGCAGGCTGAGGCTGACCTATTGCTCTGCACCTTACTCCTATCTCAGC 2710
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Db 61297 TATTTTGATACAAGAAGTAAGACCACCTTACTGTTCATATAGATCAGTAGGATGATTATAGT 61238

QY 2711 TGTCCCTCCCACTTTTCCAGGTGCTGCCAGACACATGACAACACTGCTAYGACCAGGCCAAGA 2770
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Db 61237 TATCATTAATTGATGGTGCAATCCAAATTAGTAGAAAAAATAAATTTGAAATATCCAAACA 61178

QY 2771 AGCTGGACAGCTGFAAATTTTCTGCTGGACAMMCCGTACACCCACACCTATTATCACTCGT 2830
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Db 61177 TAAAGAAAAAGATAAATATTTTCAGGT-GATGGATATTCCAATTACCCTGATTGATTATAT 61119

QY 2831 GCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCCTTGACCTATGAATTCT 2890
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Db 61118 GAATGTATCAAAATTTATCACATGTACCGTCCAAAAATATG-----TACATCA 61074

QY 2891 AGTTGGTTCTCAGTAGGCCGGGGGAAATAATAGTAACAACAGCCATGATTAGTGTTAA 2950
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Db 61073 AATTTGTATCAACAAAAATAAATGAATAAATAAATAGGACACAGATGAACCCACAGATG 61014

QY 2951 TTTTCTTGTTCTGGCAGTGTCTCCTTTAATCCTCAGAACAAACACTATGGSATAGGTAC 3010
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Db 61013 AAGTACGTGGGGGAGGTCTGAAAGGGTAGGTGATCAACATA-----GGAGCTTC 60964

QY 3011 AATTATCCTCACTTAAACAGATAAGAAAACTGAGGCTCAGAAAGGCTGAGCTATTTGCCCAA 3070
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Db 60963 TGTCTTCATGGAGATGAAGTGTGCCACTCTCTCGCCATGGAGGCTTTTACTCAGCTCAT 60904

QY 3071 GATCACACAGCTTGAAGTGGTGACAGTTTGGGTTTTTTTTTTGTTGTTGTTTAGAGACAG 3130
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Db 60903 CAAGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGTTTTTTTGTGTTTGTGAGACGG 60844

QY 3131 GGTCTTGCTCTGTACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTC 3190
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Db 60843 AGTCTCACTCTGTGCGCCAGGCTGGAGTGCAATGSCACGATCTCCGCTTACTGCAACCTG 60784

QY 3191 AACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGC 3250
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Db 60783 CACCTCCCAGGTTCAACCGATTCTCCTCGCCTCAGCTCCAGAGTAGCTGGGATTACAGGC 60724

QY 3251 GTGCACCACCACGCTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 3310
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Db 60723 ACCCACTACCAACGCCCGCACTAATTTTGTACTTTTA--GTAGAGACGGGGTTTCACCATG 60666

QY 3311 TTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAA 3370
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Db 60665 TTGGTCAGACTGGTCTTGAACCTCCTGACCTCAAGCATTCACACCTGCCTCGGCCCTCCCAA 60606
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Qy	3371	GTGCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTCTTTTACATTCATCT	3430
Db	60605	GTGCTGGGATTACAGGCATGAGCCACCGTGCCGGCTTTTCTTTCTTTGAGAT--	60548
Qy	3431	TTCCAATAGAATGTAAGATCCACAGAACAGGGATTACTGCTATTTTCTTCCTTTCTTTT	3490
Db	60547	-----GGAGTCTCACTC	60536
Qy	3491	TTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTCAGCTCACTGCAACCTCTGCCT	3550
Db	60535	TGTTGCCCAGGCTGGAGTGCAGTGGTGCAATCTCG-----GCTCACTGCAACCTCTGCCT	60481
Qy	3551	CCCGGGTTCAAGYGATTCTCTCGCTAAGCCCTCCTGAGTAGCTGGAATTACAAGCGTGC	3610
Db	60480	CCGGGTTCAAGCGGATTCTCTCGCTCAGCCTCCCAAGTAGCAGGGATTGCAGAGTGC	60421
Qy	3611	CCACCATGCTTGGCTAATTTTGTATTTTAGCAGAGATGGGTTTACCATGTGCCCC	3670
Db	60420	CCACCACGACGAGCTAA-TTTTGTATTTTATTAGACGGGATTTACCATGTGTGCC	60362
Qy	3671	AGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGCTG	3730
Db	60361	AGGCTGGTCTCTAACTCTTGACCTCAGGTGATCTCCCACTTAACCTCCCATAGTGCTG	60302
Qy	3731	GAATTATA-----GGCGTGAGTCACTGTGCTGCCTGGCCGATTAAGTCTC	3771
Db	60301	GAATTACAGGTGTGAGCTGGGATTACAGGTGTGAGCCACCGCACCGGCCCATCAAGTGT	60242
Qy	3772	TATTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGA-----	3815
Db	60241	TGTTCAACAGGTTTATTAGAGGCTTTGGCCAGGCGGTGGCTCATGCCTGTAAACCCGAAC	60182
Qy	3816	-----CATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGAT	3862
Db	60181	ACTTTGAGAGGCTCATGTAGGAGATCACTTGAGCACAGGAGTTCAAGACCAGCCTGGGC	60122
Qy	3863	ATAAACTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTGCAGAATAAAATACAATC	3922
Db	60121	ATATACTGAGACCCCATCTCTACAAAAACCCCTTTATTAAATTTAAAAAAATTTT	60062
Qy	3923	TGCAATTCTGCTTT-TTCATTATCACCTTGTTATGACTTTTTCATATTGCTCAACCT	3981
Db	60061	TTTTTTTGGAGTGGAGTCTGCTCTGTTGCCAAACTGGAATGCAATGGCGCATCTC	60002
Qy	3982	TTATTGTTACTGTTTTTCAATGTTTACTATTTTAGTCACTGAATAATATGGCTTAATTTG	4041
Db	60001	AGCTCACTGCAACTTCTGCCTCCCGGTTTCAAGCAATTTCTCTCAGCCTCCTTAGTAGC	59942
Qy	4042	CTTATACATCTCTCTGCTCCACTTTAGAAAGGCCAAATTTACAAATCTGATGAAG----	4096
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Qy	4097	-----CTATGAACCCCTCTCCCCAGAGAAATACACACACACACACACTCACACACAGT	4150
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Db	59821	ATCCTCCCAACTTGCTGGGATTACAGGCGTGAGTCACGTACTGGTCCCTAAAAATTTT	59762
Qy	4211	AATTA-AAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACAGTACTTTGGAA	4269
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Qy	4270	GTCAAAGGTGGGTGGATCACTTGAGGTGAGAAGTTTCGAGACCAGCCTGGTCAATATGGTG	4329
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Qy	4330	AAACCTATCTCTACTAAAAATACAAAAAATTAGCTGGGTGATGATGCATGCCCTGTAGT	4389
Db	59641	AAACCTGTCTCTAC-AAAAAACAAAAAATTAGCTGGGTATGATGGCGGATACCTGTAAT	59583

Qy	4390	CCAGCTACTCGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCA	4449
Db	59582	TCCAGCTACTCGGAAGGTTGAAGCAGGAGAAATCGCTTGAACCCAGGAAGCAGAGGTTGCA	59523
Qy	4450	GTGAGCCGAGATCCACCACTGCCTCCAGCTCCAGCTGGGCGACACAGCGAGACTTATCTCAA	4509
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Qy	4510	AAAAATAAATAAATAAATAA 4531	
Db	59462	CAACAACAACAAGNAATAAAAA 59441	
RESULT 13			
US-11-121-086-33/c			
; Sequence 33, Application US/11121086			
; Publication No. US20050266459A1			
; GENERAL INFORMATION:			
; APPLICANT: POULSEN, TIM S.			
; APPLICANT: NIELSEN, KIRSTEN V.			
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES			
; FILE REFERENCE: 09138.6000-00000			
; CURRENT APPLICATION NUMBER: US/11/121,086			
; CURRENT FILING DATE: 2005-05-04			
; PRIOR APPLICATION NUMBER: 60/567,570			
; PRIOR FILING DATE: 2004-05-04			
; NUMBER OF SEQ ID NOS: 107			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 33			
; LENGTH: 154548			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-121-086-33			
Query Match 7.7%; Score 384.2; DB 17; Length 154548;			
Best Local Similarity 59.4%; Pred. No. 76;			
Matches 861; Conservative 1; Mismatches 524; Indels 63; Gaps 10;			
Qy	3085	TAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTTTGTAGAGACAGGGTCTTGCTC-TGT	3143
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Qy	3144	CACCCAGGCATGAGCACAGTGGTGCAACCATAGTCACTGCAGCCTCAACCTCCTGAGCT	3203
Db	71946	CACCCAGGCTGGAGTGCAGTGGTGCAATCTCGGCTCACTGCAACCTCTGCCTCCTGGGT	71887
Qy	3204	CAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGTGGGACTACGAGCGTGCACCACACG	3263
Db	71886	CAAGCAATTCTCCTGCCTCAGCCTCCCAAGTAATCGGATTAAGGCGTGCACCACACA	71827
Qy	3264	CCTGGCTAATTAATAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTG	3323
Db	71826	CCCGG--GCTAATTTTGTATTATTGTAGAGACGGAGTTTACCATTGTCGGCCAGTCTGG	71769
Qy	3324	TCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTAC	3383
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Db	71624	AGCTGGAGTACAGTGGCGTGATCTCAGCTCACTGCAGCCTCCATCTCTCCAGACTTAGGC	71565
Qy	3564	GATTCTCCTGACCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGG	3623
Db	71564	GATTCTCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACGCGCCACCGCCAG	71505

Qy 3945 TCACCTTGTTATGACTTTTTCATATTTGCCTCAAAACCTTTTATTGTTACTGTTTTCATTG 4004
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Qy 4065 TTAGAGGCCCAAAATTTACAAATCTGATGAAGCTATGAACCTCTCCCCAGAGAAATACA 4124
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Qy 4125 CACACACACACACTCACACAGATTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACC 4184
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Qy 4185 TGCATTAGAGGATGTTTGTTCATATT-----AATTAAAAATAAATCACTCAGTTGGGCACAG 4237
Db 71502 TTTTTTTTTTTTTTTTTTTTACATTATAGAGAAATTTTAAACATAGAGGCTGGCGCAG 71443
Qy 4238 TGACTCAAGCCTGTAACACACAGTACTTTTGAAGTCCAAGTGGGTGGATCACCTTGAGGTG 4297
Db 71442 TGGCTTGTGCCTGTAATCCCAGCACTTTGGGGGGCCGAGGCGGTAGATCACCTTGAGGTC 71383
Qy 4298 AGAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATACAAAA 4357
Db 71382 AGGAGTTCGAGACCAGTCTGGCCAAACATGGTGAATCACCGTCTCTACTAAAAATACAAAA 71323
Qy 4358 ATTAGTGGGTGTAGTGATGCTGCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGA 4417
Db 71322 ATTAGTGGGTATGGTGGTGACACACTGTAGTCCCAGCTACTCAGGAGGCTGAGGTGGGA 71263
Qy 4418 GAATTGCTTGAACCTGGAGGCAGAGGTGTCAGTGAGCCGAGATCCCACCACCTGCATCC 4477
Db 71262 GAATTGCTTGAACCTGGAGGCGGAGGTGTCAGTGAGCTGAGATCGGGCCATTGCACCTCC 71203
Qy 4478 AGCCTGGCGCACACAGCGGAGACTCTATCTCAAAAAATAAATAAATAAAGGATCG 4537
Db 71202 AGCCTGGGCAACAGAGTGAGACTCTGTTTCAAAAAACCCAAATAACAACAACAAAAA 71143
Qy 4538 GAGAGAAACAAACTAATAAGATTCTCTG-----AAGGTAAGCAGAGATACGTAA 4586
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Qy 4587 ATTATATGTAATAAGTTTAAATGCAATTTTAACTGTAATCTTATTGTTTATTTTGGTTAT 4646
Db 71082 ATACTGCTGGGCATGGTGGCTCAAGCCTGTGATCCTAGCACTTTGGAAGGCCAAGGCTGG 71023
Qy 4647 AAAAGTAAACAAGCCAA-----AAGTAATGCAACTTCAAAACKTACATAAAATATCTAT 4699
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Qy 4700 TATGAAAAGTGAAGGCATCTATAATCCTACTACCCAAAGATAAACCAGTTACATATTCCT 4759
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Qy 4760 CCAGATTTTGGGGCATACACTAGCTTTTATTTTGGGAAAAATTTCCATGTGCAGGCAT 4819
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Qy 4820 ACCTAATTTTCTAAATGTCTATGTAGTATTCCATTTTAAGGATGTTCCATAATTTTAAA 4879
Db 70842 ATGAGATTGTGCCACCTTACTCCAGCCTGGAGTCTGTATCAAAAAATAACACAGCTAGA 70783
Qy 4880 ATACATGCTTTAAAGTAGAGAAACTAGGTTGGGCAATGGTGGCTCACGCCT-GTATCCAG 4938
Db 70782 GTCTGTATCAAAAAAATAAAAAAAGAGGCTGGTCAACGGTGGCTCATGCTGGAATCCAC 70723
Qy 4939 CACTTTGGGAGCCGAGGCAAAATGGATCACTTGAGGTCCGGAGTTTGAGACCAGCCTGGA 4998
Db 70722 CACTTTGGAAGCCGAGGCGGGTGGATCACCTGAGGTTCGGAGTTGGAGACCAGCCTGAC 70663

Qy 4999 CAA 5001
Db 70662 CAA 70660
RESULT 15
US-10-960-414-490
; Sequence 490, Application US/10960414
; Publication No. US20060074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSH
; APPLICANT: VEGA, VINSENIUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; TITLE OF INVENTION: PROGNOSIS, AND DIAGNOSIS OF CANCERS
; FILE REFERENCE: 38271-76067
; CURRENT APPLICATION NUMBER: US/10/960,414
; CURRENT FILING DATE: 2004-10-06
; NUMBER OF SEQ ID NOS: 500
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 490
; LENGTH: 174009
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-960-414-490
Query Match 7.6%; Score 377.8; DB 13; Length 174009;
Best Local Similarity 58.7%; Pred. No. 79;
Matches 837; Conservative 1; Mismatches 493; Indels 94; Gaps 7;
Qy 3105 TTTTTTTTGTGTTGTAGAGACAGGGTCTTGCTGTCTGTCACCCAGGCATGAGCACAGTG 3164
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Qy 3165 GTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAG 3224
Db 121001 GCGAGATCTCAGCTCACAGCAGCCTCTGCTCCCGGTGGAAGCGATTTTCTGCTCAG 121060
Qy 3225 CCTCCCAAGTAGTGGGACTACGAGCGTGCACCAACGCGCTGGCTAATTAATAAAATTT 3284
Db 121061 CTTCTGATTAGCTGGGACCACAGGCATCAGCCACCATGCCAGCTAATTTTGTGTA--TT 121118
Qy 3285 TTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCAAG 3344
Db 121119 TTTAGTAGAGACAGGGGTTCACTATATTGGCCAGGCTGGTCTCAAACTCCTGACCTCAA 121178
Qy 3345 CAATCCTCCTACCTTGGCATCCCAAAGTGTGCGGATTACAGGGGTGAGCCACCATGTGCG 3404
Db 121179 AGATCCGCCACCTTGGCCTCCCAAAGTCTCTGGGATTGCGGCGTGCAGCCCGTGCCTG 121238
Qy 3405 GCTACTTATTTCTTTACATTCATCTTTTCCAAATAGAATGTAAGATCCACAGAACAGGGAT 3464
Db 121239 GC-----CTGAACTTTTAATTTTAAATTTGATTTTAACCTTTTTT 121281
Qy 3465 TACTGCCTATTTTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCTC 3524
Db 121282 TTTTTTTTTTTGTGAGACAGAGTCTCGCTCTGTCCGCCAGGCTGGAGTGCAGTGGTGCA 121341
Qy 3525 CGTTCAGCTCACTGCAACCTCTGCTCCCGGTTCAAGYGATTTCTCTGCTAAGCCTCC 3584
Db 121342 ATCTCGGCTCACTGCAAGCTCTGCTCCCAAGTTTACACCATTTCTCTACCTCAGCCTCC 121401
Qy 3585 TGAGTAGCTGGAATTACAAGCGTGCACCACTGCTGGCTAA--TTTTTTGTATTTTA 3642
Db 121402 CGAGTAGCTGGGACTACAGGCGCTGCCACCACGCTGGCTAATTTTGTGATTTTA 121461
Qy 3643 GCAGAGATGGGGTTTACCATGTTGCCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTGAT 3702
Db 121462 GTAGAGACGGGGTTTACGTTGTTAGCCAGGATGATCTTGATCTACTGACCTC--GTGAT 121519
Qy 3703 CTGCCTGCCTCAGTCTCCCAAAGTGTGGAAATTATAGGCGTGAGTCACTGTGCTGGCCG 3762
Db 121520 CTGCCTGCCTCGGCCTCCCAAAGTGTGGGAATTACAGGCGTGAGCCACCGTGCC----- 121573


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QY 3763 ATTACTGTCATATTTCTTTATTGCTATATCCCAGATCTAGAGCAGTGTCTGACATATAG 3822
Db 121574 -----CAGCTTAAAAATTTGATT 121590

QY 3823 TAGTGCTCAATAAATAAATGATGAATGCACAGCCTAGATATAAACAATTTCTTTTCTTTT 3882
Db 121591 TAAATAACCATATTTGTATTGAACAGCACAATTTTCATACCTTAAAGTTTATTATTGTAATGA 121650

QY 3883 TTTAAAAACAATCTTGACAACCTTTGCAGAAATAAATAACAATCTTGCAATCTGCTTTTTCAC 3942
Db 121651 TTCAAAGTGAGGCTAATGGGTTTTTATTGTTAGATTCAAAAAACAAGTTTATTATTGTTAG 121710

QY 3943 TATCACCTTGTATGACTTTTTTCATATTGCCCTCAAACCTTTATTGTTACTGTTTTTTTCAT 4002
Db 121711 ATTCAAAGTGAGGCTAATGGGACAAGAATTATTCAGCAGCAGTTTGGAGGATATTGTGGCT 121770

QY 4003 TGTTACTATTTTAGTCACTGAATAATATATGGCTTAATTTTGCTTATACATCCTCCTGCTCCA 4062
Db 121771 GAAAGGAAAAATTCAGAGCACAAACTGTCAATACGTTTGTCAAGAGTACATGAAAAAGCCA 121830

QY 4063 CTTTAGAAGGCCAAAATTTTACAAATCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAAATA 4122
Db 121831 CTTCACTGTGACCAGCATTCATATGT-----ATAAGACATGCAATATATTAGCATA 121882

QY 4123 CACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAAGAAA 4182
Db 121883 CATGGACATATGTGAAAAATCAAAAAGAAATGCTTCCAATGTTATGAGCTAAAGGGAAAAA 121942

QY 4183 CCTGCATTAGAGGATGTTTGTTCATATTAAATAAATAAATCACTCAGTTGGGCACAGTGACT 4242
Db 121943 AGACATTCAG-----TAAAAATATAACAGCTGTTGGCCAGGCACAGTGGCT 121988

QY 4243 CAAGCCTGTAAACCACAGTACTTTTGGAACTCCAAGGTGGTGGATCACTTGAGGTGAGAAG 4302
Db 121989 CATGCCCTGCAATACCAGCACCTTTGGAGGCTGAAGAGGGCAGATCACCTGAGGTCAGGAG 122048

QY 4303 TTCGAGACCAGCCTGGTCAATATGTTGAAACCCCTATCTCTACTAAAAATACAAAAATTAG 4362
Db 122049 TTCGAAACCAGCCTGGCCAACATGGCGAAACCCCTGTCTCTACTAAAAATACCAAATTAG 122108

QY 4363 CTGGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATT 4422
Db 122109 CCGGGCGCAGTGGTGGCGCCTGTAAATCCCAGCGACTCGGGAGCCTGAGGCAGGAGAATC 122168

QY 4423 GCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCAACCACTGCACCTCCAGCCT 4482
Db 122169 ACTTGAACCTAGGAGCGGAGTCTACAGTGAGCTGAGATTGTGTCAATTACACTCCAGCCT 122228

QY 4483 GGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAAAA 4527
Db 122229 GGGTGACAGAGTGAGACTCTATCTCAAAAAAATATATATATAA 122273
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RESULT 16
US-10-995-561-13303
; Sequence 13303, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13303
; LENGTH: 201990
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (1)...(201990)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-4)
US-10-995-561-13303
```

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Query Match 7.5%; Score 376.8; DB 10; Length 201990;
Best Local Similarity 59.5%; Pred. No. 72;
Matches 842; Conservative 4; Mismatches 501; Indels 67; Gaps 10;
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QY 3104 TTTTNTTTTGTGTTGTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCGATGAGCACAGT 3163
Db 33667 TATTATTATTATTATTTTGRACGGAGTCTCGCTCTGTGGCCAGGCTGGAGTGCAGT 33726

QY 3164 GGTGCAACCATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 3223
Db 33727 GCGGTGATCTTGGCTCAGTCAACCTCCGCCCTCCTGGGTTTAAGCAATTCTCTG-CCTCA 33785

QY 3224 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCCACCGCCTGGCTAATTAAAAAATT 3283
Db 33786 TCCTCCCGAGTAGCAGGGATTACAGGCATGTGCCACCGCCAGCTAATTTTGTGA--T 33843

QY 3284 TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAA 3343
Db 33844 TTTTAGTAGAGACGGGGTTTCAACCATCTTGGCCAAGCTGGTCTTTGAACCTTCTGACCTC-- 33901

QY 3344 GCAATCCTCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTAGCCACCATGTGC 3403
Db 33902 GTGATCCAACCTGCCTCGSCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCACCATGCCT 33961

QY 3404 GGCTACTTATTCTTTTACATTCCTCTTCCAAATAGAAATGTAAGATCCACAGAACAGGGA 3463
Db 33962 GGC--CTATTTATTATTATTTTATTTTGTAGTTGAAGTTTGTCTCTTGTGGCCAGGC 34019

QY 3464 TTAATGCCTATTTTCTTCTTTTGTAGACAGAGTCTCACTTTCATCACCTCAACCT 3523
Db 34020 TGGAGTGCAATGGTGTGCTTT----- 34041

QY 3524 CCGTTCAGCTCAGTGCACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAAGCCTC 3583
Db 34042 -----GGCTCAGTGCACCTCCGCCCTCCAGGTTCAAGCGATTCTCCTGCCTCAGTCTC 34095

QY 3584 CTGAGTAGCTGGAATTAACAAGCGTGACCCACCATGCTTGGCTAATTTTTTGTATTTTAG 3643
Db 34096 CCAAGTAGCTGAGATTACAGGCATGCGCCACCAACGCGCGGCTAA-TTTTGTATTTTCA 34154

QY 3644 CAGAGATGGGGTTTTACCATGTTGCCAGGCTGTCTCAAACTCCTGACCTCAAGTGATC 3703
Db 34155 TAGAGGTGGGGTTTACCATGTTGGCCAGGCTGATCTAGAACTCCTGATCTCAGGTGATC 34214

QY 3704 TGCCTGCCTCAGTCTCCCAAAGTGTGGAATTAAGGCGTGAGTCACTGTGCCCTGGCCGA 3763
Db 34215 CACCCACCTCAGCTTCCCAAAGTGTAGGATTACAGTGTAGCGTGAGCCACCATGCCTGGCCAC 34274

QY 3764 TTAATGCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGT 3823
Db 34275 ACCCCGGTTTATTGCAAT--TTGCTTCTAATAGAGAAATCAACCCAGTAAACAAATGAATT 34332

QY 3824 AGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACCCTTTCTTTTCTTTT 3883
Db 34333 ATTGTTAGCAAAACTGGGGGTGGGTTGGGAAAGGAAAGTAGTTCTCTCTATAATAAAGAAC 34392

QY 3884 TTAACAACAATCTTGACAACTTTGCAGAAATAAATACAATCTTGCAATTTCTGCTTTTTCAC 3943
Db 34393 TTGCTGATATTTCGTTGAAAGTCATTTGTCTTACTCATCTTGTATAGATAAGTACACACA 34452

QY 3944 ATCACCTTGTATGACTTTTTCATATTGCTCAACCTTAAACCTTTATTGTTACTGTTTTCATT 4003
Db 34453 ATGAGTGGTATCAGGGTTGAGGGGTTTCCGCCCTGTGAGGACACRATGGGATGAACCGTGT 34512

QY 4004 GTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCAC 4063
Db 34513 GTGGGATGGTCTGTTAAAGAAAAAACAAGAGCCATGTG--TTGAAACAACCTAAGTAT 34569
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Db      18942 TGTGTGTTGTTGT-----TGTTTTTTT 18962
QY      3481 CCTTCTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTTCAGCTCACTGCA 3540
Db      18963 TGAGGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGCAGTGAATCTCAGCTCACTGAA 19022
QY      3541 ACCTCTGCCCTCCGGGTTCAAGYGATTCCTCTGCCCTAAGCCTCCTGAGTAGCTGGAATTA 3600
Db      19023 ACCTCTGCCCTCCTGGGTTCAAGTGATTTCTCATATCTCAGCCTCCTAAATAGCTGGCATT 19082
QY      3601 CAAGCGTGCACCAACCATGCTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGTTTAC 3660
Db      19083 CAGGCTCCCAACCAACGACGCTGGCTAA-TTTTGTATTTTGTAGAGACAGGATTTAC 19141
QY      3661 CATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTGCCTCAGTCTCC 3720
Db      19142 CATGTTGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCTGCCACCTTGGCCTCC 19201
QY      3721 CAAAGTGCTGGAATTATAGCGGTGAGTCACTGTGCTTGCCTGGCCGATTACTGTCTATTTTCTT 3780
Db      19202 CAAAGCGCTGGGATTACAGGTGCGTGCCACCAACACCTGGCCCCCAGCAGTATTACITTATA 19261
QY      3781 TATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATATAGTGGTCTCAATAAATAA 3840
Db      19262 AGCCTCTAGTGCATACTGGGGCCCTCTCTGGGACAATCTT-----CTTA 19303
QY      3841 TTGATGAATGCACAGCCTTAGATATAAACTTTCTTTTCTTTTCTTTTAAACAATCTTGACA 3900
Db      19304 TTCCCAACAACAGCTCACACTCATGACACTTCTGAGCCTTTTCTAGGCTGGACACCTG 19363
QY      3901 ACTTTGCAGATAAATAACAATCTTGCAATCTGCTTTTTCATTCATCACCTTGTTATGACT 3960
Db      19364 GCCTGGAAGGTCTCTCTGCCGCTCCCAACCGCACCTCACCCCCACGACCTATGAGCTTC 19423
QY      3961 TTTTTCATATTGCCCTCAAAACCTTTATTGTACTGTTTTTTTTCATTGTACTATTTTAGTC-- 4018
Db      19424 CCCATCTGSGAAGCCTGCCCCTGCTTTGAAGCCAAGAACACTGTGGAAGGAGTTTCTCCCA 19483
QY      4019 -ACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCCAA 4077
Db      19484 GCCCTAAGGATGGGTCTAAGAAAGGAGGTGCCTTAGGAGAGGTCCCCACAGGCAGGAGGCC 19543
QY      4078 TTTACAAATCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAATAACACACACACACAC 4137
Db      19544 TGCAGCACCCAGACTCAGCTGGGCTCCTGTAAACCA-----TTTCAGAAATACAGAT 19596
QY      4138 ACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAAGAAACCTGCAATTAGAGGAT 4197
Db      19597 TTTTAGAAAAGTTTGTTTTCTCTTAACATATAAAAGTGACACA-----TGC 19644
QY      4198 GTTGTGTTCAATTAATAAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCAC 4257
Db      19645 TTGTGGTTTAAAAAATAAAAAAAGCAAGCGCATGGCTCACACCTGTAATACC 19704
QY      4258 AGTACTTTGGAAGTCCAAGGTGGTGGATCACTTGAGGTGAGAAGTTCGAGACCCAGCCTG 4317
Db      19705 AGCACTTTGGAGGCTGAGGTGAGTGGATCAC--GAGGTCAGGAGATTGAGACCATCCTG 19762
QY      4318 GTCAATATGTTGAAACCCCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGAT 4376
Db      19763 GCCAACATGTTGAACCCCATCTCTACTAAAGTACAAAAAATTAGCCGGGTGTAGTGGC 19822
QY      4377 GCATGCCCTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGA 4436
Db      19823 GGGCGCCTGTAGTCCCAGCTACTCAGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGA 19882
QY      4437 GGCAGAGTTGCAGTGAGCCGAGATCCCAACCACTGCATCCAGCTGGGCGACACAGCGA 4496
Db      19883 GGTGAGGTTGCAGTGAGCCGAGATTGTGCCACTGCACCTCCAGCCT-AGCGATGGAGTGA 19941
QY      4497 GACTCTATCTCAAAAAAATAAATAATAAAAA 4527
Db      19942 GACTCCATCTCAAAAAAATAAATAAAAAAA 19972
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RESULT 18
US-11-121-086-58
; Sequence 58, Application US/11121086
; Publication No. US2005026645A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 180654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-58
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Query Match      7.5%; Score 373.8; DB 17; Length 180654;
Best Local Similarity 60.5%; Pred. No. 84;
Matches 861; Conservative 1; Mismatches 483; Indels 78; Gaps 12;

QY      3104 TTTTTTTTTTGTGTGTTTAGAGACAGGGTCTTGGCTC-TGTCACCCAGGCAATGAGCACAG 3162
Db      153715 TTTTTTTTTTGTGTGTTTAGAGACGAAAGTTTCGCTCTTGTGCCAGGCTGGAGTGCAA 153774
QY      3163 TGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC 3222
Db      153775 TGGTGCAATCTCAGCTTACAGCAACCTCTGCCCTCTGGGTTCAAGCGATTCTCCTGCCTC 153834
QY      3223 AGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACGCTGGCTAATTAAAAAAAT 3282
Db      153835 AGCCTCCCAAGTAGCTGGGATTATAGGCATGTGCCACACGCTGGCTAATTTTGTGA--- 153891
QY      3283 TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCA 3342
Db      153892 TTTTAGTAGAAAACAGGCTTTCTCCACGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCA 153951
QY      3343 AGCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTG 3402
Db      153952 GGTGATCCGCCCAACCTCGGCCCTCCCAAAGTGTGGGATTACAGGTGTGAGCCACTGTGCC 154011
QY      3403 CGGCTACTTATTTCTTTACATCTCCATCTTTCCATAGAATGTAAGATCCACAGAACAGGG 3462
Db      154012 CAGACCTTTTTTTTTTTTTTTTTTGA----- 154036
QY      3463 ATTACTGCCTATTTTCTTCCTTTCTTTTGTAGACAGAGTCTCACTTTCATCACCTCAACC 3522
Db      154037 -----GACAGAGTCTCACTCTGTTGCCAGGCTGGAGTGCAGTGGCGTGATC----- 154083
QY      3523 TCCGTTCACTCACTGCAACCTCTGCTCCCGGTTCAAGYGATTCTCCTGCCTCAAGCCT 3582
Db      154084 -----TCAGCTCACTGCAACCTCCACCTCCCGGTTCAAGCGATTCTCCTGCCTCAGCCT 154138
QY      3583 CCTGAGTAGCTGGAAATTAAGAAGTGCACCAACCATGCTTGGCTAATTTTTTTGTATTTTA 3642
Db      154139 CCAAAGTAGCTGGGATTACAGGCATCGCCACCATGCCAGCTAA-TTTTTCTATTGTTA 154197
QY      3643 GCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGAT 3702
Db      154198 GTAGAGACGGGTTTACCATGTTGGCCAGGCTGTTTGAACCTCCTGACCTCAGGTGAT 154257
QY      3703 CTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGAGTCACTGTGCCTGGCCG 3762
Db      154258 CCACCCACCTCGGCCCTCCCAAAGTGTCTGGGATTATAAGCGTGAGCCACTGCCGCCAGGCTG 154317
QY      3763 ATTACTGTCTATTTTCTTTATTGCTATATATATATATATATATATATATATATATATATAT 3822
Db      154317 ATTACTGTCTATTTTCTTTATTGCTATATATATATATATATATATATATATATATATATATAT
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Db 154318 ACAGTGGTATTTTCTAAATAGCTTATTTCTGTACATATTTCTCCAGCCTCATAACAAAGTT 154377
Qy 3823 TAGGTGCTCAATAAAATAATTGATGAAT--GCACAGCCTAGATATAAAACTTTCTTTTCTT 3880
Db 154378 TACTATTTTAAGCTGTGCTCTTTGGTTCAGCTGAGCATGGTGATGAAAAGCCCTTCCCA 154437
Qy 3881 TTTTAAACA-ATCTTGACAACTTTGCAGAAATAATACAATCTTGCATTCTGCTTTTC 3939
Db 154438 TGAAGAAGTTACATGGAGAACTCTTGAAGCCCTTAGGCAAGCACTAACCCAGACCTCAT 154497
Qy 3940 ACTTATCACCTTGTATGACTTTTTTCATATTGCCTCAAACTTTATTGTTACTGTTTTT 3999
Db 154498 GGTAAAGCCCAACAATGCATATGGATGAACTGTTAGTTACAGCTGGACTGACAGTTCCAA 154557
Qy 4000 CATTTGTACTATTTTAGTCACCTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCT 4059
Db 154558 AGCTG-CAGAGCAGTCTAGATCACAGATCACCTTTGCGTGGATTAGAAAAGGTGCCCT 154616
Qy 4060 CCACITTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCTCCAGAGAA 4119
Db 154617 TCTCTGAGTGACACACAGTTCCACACCAGGTACTCATCTTGGTAAGTGGAGTACAGAAATAG 154676
Qy 4120 ATACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAG 4179
Db 154677 ATTTCCACCCTCACTTGCCACCCTGAAACAGGTATCCTTT--TGCTGGTGCAATCTCTAT 154734
Qy 4180 AAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATACTCAGTTGGGCACAGTG 4239
Db 154735 GGTCTACACAGCAGCACCGT-----TAAGAAGTGTACCGCCAGGCACCGCT 154782
Qy 4240 ACTCAAGCCTGTAACCACAGTACTTTGGAAGTCCAAGGTGGGTGGGATCACTTGAGGTGAG 4299
Db 154783 GTTCAAGCGGTAAATCCCAACACTTTGGAAGCCGAGGCAGGCTGATCAC-AGAGGTICAG 154841
Qy 4300 AAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCTATCTCTACTAAAAATACAAAAAT 4359
Db 154842 GAGTTTGAGACCAGCCTGGCCAAACATGGTGAAACCCCGTCTCTACTAAAAATATGAAAT 154901
Qy 4360 TAGCTGGGTGTAGTGATGCATGCCGTGTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGA 4419
Db 154902 TATCCGGGCATGGTGGCAGGCACCTGTAATCCAGCTACTCGAGAGGCTGAGGCAGGAGA 154961
Qy 4420 ATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACCTGCACCTCCAG 4479
Db 154962 ATCGCTTGAACCTGGGAGGTGGAGGCTGAGGCTGAGCCGAGATTCGCGCCACTGCACCTCCAG 155021
Qy 4480 CCTGGGCGAC-ACAGCGAGACTCTATCTCAAAAAATAAATAA 4521
Db 155022 CCTGGGCAACAAGAGCGAAACTCTGTCTCAAAAAAGAAAA 155064

RESULT 19
US-11-121-086-14
; Sequence 14, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 167891
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-14

Query Match 7.5%; Score 372.6; DB 17; Length 167891;

Best Local Similarity 60.7%; Pred. No. 90;
Matches 866; Conservative 1; Mismatches 440; Indels 120; Gaps 11;
Qy 3174 TAGGTCACCTGCAGCCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAG 3233
Db 52286 TTGCCAGCCTGGTCTCAAAACCCCTGACCTCAAGTATCAACCCACCTCGGCCTCCCTAA 52345
Qy 3234 TAGCTGGGACTACGAGCGTGCACCACCACCGCCTGGCTAATTAAAAAAATTTTTTTGTAGA 3293
Db 52346 GTGCTGGGATTACAGGCATGAGCCACTGGGCCCCAGCCTATTTTTTTA--TTTTTTGTAGA 52403
Qy 3294 GACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAACTCCTGGCTTCAAGCAATCCTCC 3353
Db 52404 GACAGGGTCTCGCTATGTTGCCCAGGTTGGTCTTGAACTCCTGAGCCAGGCAGTCTCTCC 52463
Qy 3354 TACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTAT 3413
Db 52464 CAACTTGGCTTCCCAAAGTTTGGGATTACAGGCATCAGCTGCTGTTGGCTGTTATTG 52523
Qy 3414 TTCTTTACATTCCATCTTTTCCAATAGAAATGTAAGATCCACAGAACAGGGATTACTGCCTA 3473
Db 52524 TATTGTCCA-----AAATTTAACTTTCCAACTACTCAAAGTTGTTGAACTTTTACTTT 52577
Qy 3474 TTTTCTTCCTTTCTTTTGTAGACAGAGTCTCACCTTTCATCACCT-----CAA 3520
Db 52578 TTTTTTTTTTTTTTTTGTAGACAGTTTCCCTCTTGTGCCCCAGGTTGGAGTGCAATGG 52637
Qy 3521 CCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCCTCGCTAAGC 3580
Db 52638 CACGATCTTGGCTCACTGCAACCTCCGCTCCTGGGTTCAAGCGATTCTCCTGTCTCGGC 52697
Qy 3581 CTCCTGAGTAGCTGGAATTAAGCGTGCACCACCACTGCTTGGCTAAATTTTTTGTATTTT 3640
Db 52698 CTCCTGAGTAGCTGGGATTACAGGCATGTGCCACCACGCGCGGCTAA--TTTTTATATTTT 52756
Qy 3641 TAGCAGAGATGGGTTTTTACCATGTTGCCCAGGCTGCTCAAACTCCTGACCTCAAGTG 3700
Db 52757 TAGTAGAGACGGGGTTTCTCCATGTGGGTGAGGCTGCTCGAACTCCCGACCTCATGTG 52816
Qy 3701 ATCTGCCCTCAGTCTCCCAAAGTGTGGAATATAGGCGTGAGTCACGTGTGCCCTGSC 3760
Db 52817 ATCAGCCCACTCGGTCTCTAAAGTGTCTGGGATTACAGGCGTGAGCCACCATGCCCGC 52876
Qy 3761 CGATTACTGTCTATTTTCTTTATGCTATATATCCCAGATCTAGAGCAGTGTCTGACATAT 3820
Db 52877 -----CTGAACCTTCTACTTTTATGTAATATCTTCAGTCCT-----T 52912
Qy 3821 AGTAGGTGCTCAATAAAATAATTGATGAATGCACAGCTAGATATAAACTTTCTTTTCTT 3880
Db 52913 AGTAAAGTATCCTCTACATTTGGGATAAATGTTGTCTTTAGTTTTCAACTACTTTTCTTT 52972
Qy 3881 TTTTTA-AAACAATCTTGACAACTTTTGAGAAATAAATAACAATCTTGCAATCTGCTTTTTC 3939
Db 52973 GGCTTATTCTCTCTCTCTCCCTCCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 53032
Qy 3940 ACTTATCACCTTGTATGACTTTTTCATATTGCTTCAAACTTTTATTTGTTACTGTTTTT 3999
Db 53033 GTGTGTGTGTGTGTATTTCATGTTTTTCTTAATCTATCTGAATTGTTGTGTCGTTTTT 53092
Qy 4000 CATTTGTACTATTTTGTACTGAAATAATATGGCTTAATTTGCTTATACATCCTCCTGCT 4059
Db 53093 CCATGCGAATTTCCAGTTACCTCCACAGTATTCGTT-----TCAGAAATGCT 53138
Qy 4060 CCACCTTTAGAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCCCCAGAGAA 4119
Db 53139 TCCTTTTGGTGCTACTTTTIGATATCTATTTTCTCATATAGTAAACATCGGTTTCTGGTA 53198
Qy 4120 ATACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGAACATAAGACAAG 4179
Db 53199 AAACACACACACACACACTCAGATATAACACA----- 53230
Qy 4180 AAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATAAATACTCAGTTGGGCAGTG 4239


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Qy 3639 TTTAGCAGAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAG 3698
Db 14911 TTTAGTAGCGATACGGTTTCACAAATGTTAGCCAGGATGGTTCGATCTCCTGACCTCR-- 14854

Qy 3699 TGATCTGCCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGGCGTGAGTCACTGTGCGCTG 3758
Db 14853 TGA TCTGCCACCTTGGCCTCCCTAAGTCTGGAATTACAGCAAGAGCCACCCCTGCCAG 14794

Qy 3759 GCCG-----ATTACTGTCTATTTTCTTTATGTCTATATCCCCAGATCTAG 3803
Db 14793 GCCCCTACTATGTTTAAACATAGTTGAACCTGAACTTTCAGCTTTAGATAAGGATAATTAA 14734

Qy 3804 AGCAGTGTCTGACATATAGTAGTGCTCAATAAATAAATTGATGAATGCACAGCCCTAGATA 3863
Db 14733 CATAGGPACATGCATTTTCATTGTGTPAACATTTATTTTACAAATCTACCATTAAATGAAC 14674

Qy 3864 TAACTTTCTTTTCTTTTAAAAACAATCTTGACAACCTTTGCAGAATAAATAACAATCT 3923
Db 14673 TATAATTACATGATCAAAAAATTTAAGAAATTATTTTAAACAACAACATCATCTATCAAAATGCA 14614

Qy 3924 TGCATCTGCTTTTTCACCTTATCACTTGTGTATGACTTTTTCATATTGCCCTCAAACTTT 3983
Db 14613 TCAATCTCATATTTTACTAAAAACTACTGTATAAAACATTTAGTCTCCCTCATTTTCAG 14554

Qy 3984 ATTTGTACTGTTTTTTCATTGTGTACTATTTTAGTCACTGAAATAATATGGCTTAATTGCT 4043
Db 14553 TACCTAAATAAAGTTTCATTCTTGGAGATTCTACAGTAAATTACTAATGGTGAAAGGAAAT 14494

Qy 4044 TATACATCTCCTGCTCCACTTTAGAAGGCCAAATTTTACAAATCTGATGAAGCTATGAA 4103
Db 14493 TTTAGTCCCTAGAACACAGTTAATTATTTATTTTAAAAAAGAGATCTCACTATGTTGCCAG 14434

Qy 4104 CC----CTCTCCCCAGAGAAATACACACACACACACACTACACACAGTTTTTTTTTTA 4159
Db 14433 GCTGGACTTGAACCTCAGGGCTCAAGGGATCTTCCCTGCCTCAGCCTCCCGAGCAGCTAGA 14374

Qy 4160 ATGTTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTGTTTCATATTAATTAATAA 4219
Db 14373 ACTACAGAAACATGACACTGTGCCAGCTCCCTAGAACATTTATTTCTTTTAAACATGTA 14314

Qy 4220 TAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAAAGTCCAGGTG 4279
Db 14313 T--GTCAGTCAAGCATGGTGGCTCACACCTGTAATCCCAGCAGTTTGGGAGGCCGAGGTG 14256

Qy 4280 GGTGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCCTATC 4339
Db 14255 GGTGACTGCTTGAGGCTGGGAGTTCGAGACCAGCCTGACCAATACGGTGAAACCTCGTC 14196

Qy 4340 TCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGATGCCTGTAGTCCCAGCTACT 4399
Db 14195 TCTACTAAAAATACAAAAATTAGC-CAGCATGGTGGTGTGTGTACCTGTAGTCCCTAGCTAAT 14137

Qy 4400 CGGGAGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAG 4459
Db 14136 CAGGACACTGAGGCATGAGAATCGCTTGAACCCAGGAAGTAGAGCCTGCAGTGAGCCAAG 14077

Qy 4460 ATCCCACCACTG-CACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAA 4518
Db 14076 ACCATGCCACTGCCACTCCAGTCTGGGTAACAGAGCAAGACTCTGTCTCCAAAAATAAAA 14017

Qy 4519 TAAATAAAAT 4528
Db 14016 ATAAAAAAAT 14007
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RESULT 21
US-11-121-086-18
; Sequence 18, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.

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; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 18  
; LENGTH: 175023  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-11-121-086-18
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Query Match 7.4%; Score 368.4; DB 17; Length 175023;  
Best Local Similarity 50.6%; Pred. No. 95;  
Matches 1534; Conservative 2; Mismatches 1298; Indels 198; Gaps 19;  
  
Qy 780 TTTCTTACTTATCACATTTATTATTATTCTTATTATTATTGAGACAGAGTCTTGCTTTG 839  
Db 113485 TTGATTTACTATTTTGGCTGTAACTTTTGTTCTCTTTTGTGAGACAGAGTCTCTCTG 113544  
  
Qy 840 TCGCCAAGGCTGGAGTACAGTGGTGCATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 899  
Db 113545 TCGCCCAGGCTGCAGTGGGTGGTGCATCTCGGCTCACTGCAA-CTCTGCTCTCCGGGC 113603  
  
Qy 900 TCACGCCATTCTCCGCTCAGCCTCCCAAGTAGCTGGGACTAAAGGCGCTGCCACCAC 959  
Db 113604 TCACGCCATTCTCCTGCTTAGCCTCCCAAGTAGCTGGGACTACAGGCACCTGCCACCAT 113663  
  
Qy 960 GCCCGCTAATTTTTTGTATTTTAAATAAGACGGGTTTCATCGTGTAGCCAGGATG 1019  
Db 113664 GCCCGCTAATTTTTTGTATTTTGGTAGACGGAGTTTCACCGCATTAGCCAGGATG 113723  
  
Qy 1020 GTCTCGATCTCATGACCTTGTGATCCGCTGCCTCGGCTCCCAAGTCTCGGATTACA 1079  
Db 113724 GTCTTGATTTTCTGACCTTGTGATCCGCCACCTCGGCTCCGAAAGTCTGGAATTACA 113783  
  
Qy 1080 GGCATGAGCCACCCTGCCGCTTATCACATTTATTATTATTGTTTTCTCTCCCAC 1139  
Db 113784 GGCCTGATCCACCATGCCAGCCT-----CTTTTTTTTTTCCCATTTAAAA 113832  
  
Qy 1140 AGTTTGTAAAGCTCCATGAGGTTAGAGATTATTATTATTATTATTATTATTATTA 1199  
Db 113833 AATATTTTGTGTCAGGCACGGTGGCTCATGCTATAATCCAGCACTTTGGGAGGCTGAG 113892  
  
Qy 1200 TTATTATTATTATCTGTTCACTGCTGTATCTCTAGCTCCTAGACAGAGCCTGGCACA 1259  
Db 113893 GTGGCAGATCACCTGAGGTCAGGAGTTCAAACCAGCCTGGCCAACATGGCAAAATCCT 113952  
  
Qy 1260 TAGTAAGTGTCAATAAATATTCACTGGATAAACAGTGCAGATAGTTTAAACTATCTGA 1319  
Db 113953 GTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGTGGCACACACCTGTATTCACACT 114012  
  
Qy 1320 CCTAGGGAGGCTGAGCAGGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGAGCT 1379  
Db 114013 ACTTGGGAAGCTGAGCAGGAGAAATCACTTGAACCTGGGAGCGGAAGCTGCAGTGAGCT 114072  
  
Qy 1380 GAAATCGTGTCACTGCACCTCCAACCTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAA 1439  
Db 114073 GAGATCATGCCACTGAACCCCACTGTGGGCAACAGAAATATGACTCCGTCTCAAAAAAAA 114132  
  
Qy 1440 AAAAAAATATCAGGCTAGCTGGGTGGCACAATGCTGTAAATCCTAGCTGAGGCGGTAGG 1499  
Db 114133 ATATATATATATATATATATATATATATATATATATGTGTGTGTGTGTGTGTGTG 114192  
  
Qy 1500 GTCCCAGAAGAAGAAGAAAAAGAAAGATATATATATATATATATATATATACACACAA 1559  
Db 114193 T-----GTGTTGTGTGTATTTATTATTATT 114223  
  
Qy 1560 AGATATAAACTTTATATATATAAAGTTTTCATTAATAAAAAAACCCTCTACCCACT 1619  
Db 114224 TTATAAAAAATAGACAGGGGTCTCACTATGTTTCCCAGGCTGATCTTGAAGTGGCTCA 114283
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QY	1620	TTCACTTTTACCAGGTTTCCTGGGTCCAA	CGGTCTT	CAGAGGAGGCAGCTGGCAGGGGT	CAG	1679
Db	114284	AGCTATCCTCTCTGCTTCCGGCTTCCCAAAGTGCT	---	GGGATTACAGGTGTGAACCACTCG		114340
QY	1680	GGAGGACGCTGGGACCCGAGGGAGCAGGA	AGGCAGTGTGTCCCGGGGTGCTGGCAGAC		1739	
Db	114341	GCCAACTTCTGCTTCTTAAACATCCTTA	CCCTGAAGTCATTAGGAGTTCAAGTCTTCA		114400	
QY	1740	CGATTTGAACCTCTGGCTATGCTTCTTTC	GCAGTGGCGCGCCGCMCAGCGGCATCAGCCCT		1799	
Db	114401	GCATTAGTTTGTCTGCCAGTTCTCTTGCCT	TGGCACCAGGCAATAAATGCCTCACCTCCG		114460	
QY	1800	CGGGCCGTGTGGCAGTTCCGC	CAAAATGATCAAGTGCCTGATCCCGGGAGTGACCCCTTY		1859	
Db	114461	CTTGTCTTAAATCCCAGCGTC	--AGTGTTTGTGTTTGTGTTTTCCTGTGTGCTGCGTAA		114518	
QY	1860	TTGGAATACAACTACGGCTGCTACTGTG	GGCTTGGGGGCTCAGGCACCCCGTGGAT		1919	
Db	114519	GCAGACCCAAAGTTCAGTTGGGTAA	CAGCTAGGATCTAAAGTTAAGGAAGCAAGTGAA		114578	
QY	1920	GAACTGGACAAGTAAGTGATCGCCTGC	AGGAAATTTGGAGTGCCTGCCGGGGGGGGT		1979	
Db	114579	CTTTGTGTTGGCTTTTCCCACTAC	CCAGAGATAAACCGATACAGGAGTAAAGTCCCA		114638	
QY	1980	GGGGCACAGCCCAAGGATCTCACGAGGC	ATACAAAGGGGACTTGCATATCTGCTAAGGAT		2039	
Db	114639	TTTTTACAGGCTGTATATGAGAGGAC	CTGTGTGAGTGCAGAGCAGTGTCTCCGGGT		114698	
QY	2040	AACATATTTTCACTCTTGTCAAAATA	AAACAAATATGTTCCAAGAGGACCTGTAGCGAAC		2099	
Db	114699	AGAAAGTCTTGCTTAAAGATCAAA	CAATCAGTATGT-----		114735	
QY	2100	GCACCCCTTAGAGATGGAACA	CAATGACCGACGTGCAAAAACAGTGGCGGATGCTGCCCTC		2159	
Db	114736	-----	-----CACTATGAGTTCTCTTGACCC		114757	
QY	2160	CAGTGGCAGAAATGTAGCAACAGTA	AAACATCACAGCAACTATCCACGTGTCAATTTTCTAGC		2219	
Db	114758	AAGAGCTCTGCAGGCCTGGAGGAA	CATCTGTCCCAGAGTGGTCTTTATGGAGAATTTCT		114817	
QY	2220	AGTGGTTGTCACTGCACCTTCTCT	GAAATACAGGATTTTACTGTATTTCTTGCAACCATGTTAA		2279	
Db	114818	TAGGGTTGTGTCATTAGGGA	AAATGTCCCCAAGGAACATTTGATTCTTACCTATATAAGAA		114877	
QY	2280	AAATCGCTTTCAGGCCAGGCGGTGG	CTCATGCTGTAAATCCACGACATTTGGGAGGCC		2339	
Db	114878	TACATACACCCAGGCCGGCGTGGT	GGCTCACGCTGTAATCCACGACATTTGGGAGGCC		114937	
QY	2340	GAGCGGGCGGATCACTTGAGTFCAG	GAGTTCGAGACCAGCCTGGCCAAACATGGTGAAAC		2399	
Db	114938	AAGCGGGCGGATCAC--GAGT	CAGGAGATCGAGACCATCCTGGCTAAACACGGTGAAAG		114995	
QY	2400	CCTGTCTCTACTAAAAAATACAAAA	AATTAGCCGGACATGGTGGCGAGCGCCTGTAAACCC		2459	
Db	114996	CCTGTCTCTACTAAAAAATACAAAA	AATTAGCTGGCATGGTGGCGAGCACCTATAGTCCC		115055	
QY	2460	AGCTACTTGGGAGACT-----	-----GAGTTGGAGGTTTTCAGTG		2493	
Db	115056	AGCTACTTGGGAGGCTGAGGCAGG	AGAAATGGCGTGAACCTGGGAGGCGGAGCTTGCAGTG		115115	
QY	2494	AGCCAAGGTGCTGCTCACTGCTGT	CCAGCCTGGGTAAACAGA--GCAACTCTGTCTCAAAA		2551	
Db	115116	AGCCGAGACTGCGCCACTGCACT	CCAGCCTGGGTGACAGAGTGAGACTCTGTCTCAAAA		115175	
QY	2552	AAAAAATGCTTTCAATAAATATAT	ATATATAAAGGACTTATATTTTTTCAAGCCATAGGAT		2611	
Db	115176	AAAAA	AAAAAAGAAATATATACCTCACTCCCCCATTTTTTGTGAGACCTGAGAAAGCAG		115235	
QY	2612	CATTTCTCTGAAGCATCTTGGCG	AAGTCAATCCCACTGTTTCTCTGAGAGTGGCAGGTG		2671	
Db	115236	TAAGGACAGTAATGACGATGA	ATAGTGACTTCTTTTATTTCTACTATGCAAGCTCTGTG		115295	

QY	2672	AGGGCTGACCTATTGCTCTGCACCTTATCCTCTATCTCAGCTGTCCTCCCACATTTCCAGGT	2731
Db	115296		
QY	2732	GCTGCCAGACACA---TGACAACCTGCTAYGACCAGGCCAAGAAGCTGGACAGCTGTAAA	2787
Db	115356		
QY	2788	TTTCTGCTGGACAMMCCGTACACCCACACCTATTTCATCTCGTCTCTGGCTCGGCAATC	2847
Db	115416		
QY	2848	ACCTGTAGCAGTAGGTTTATCCCTTCCCTTGACCTATGAATTCCTAGTTGGTTCTCAGTAGG	2907
Db	115476		
QY	2908	CCGGGGGAAATAATAGTAAACAACAGCCATGATTTAGTGTAAATTTCTTGGTTCTGGGC	2967
Db	115536		
QY	2968	AGTGTCTCCTTTAATCCTCAGAACACACTATGGATAGGTACAAATATCCTCACATTA--	3025
Db	115596	ATTGCCTTCCCAATCCTGCTTGGACTGACTCTCAGAT-GCTACAGTGACACTGCTTCAGA	115654
QY	3026	-----ACAGATAAGAAAACTGAGGCTCAGAAAGGCTGAGCTATTTGCCCAAGATCA	3075
Db	115655		
QY	3076	CACAGCTTGTAAAGGTGACAGTTTGGGTTTTTTTTTGTGTTGTTTAGAGACAGGGTCT	3135
Db	115715		
QY	3136	TGCTCTGTCAACCCAGGCATGAGCACAGTGGTGCAACCATAGGTCACCTGCAGCCTCAACCT	3195
Db	115775		
QY	3196	CCTGAGCTCAAGGGATCTGTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCA	3255
Db	115835	TCTGGATTCAAGTGATTCTCCTGCCTCAGCCTCTCGAGTAGCTGGGACTACAGCCATGGC	115894
QY	3256	CCACCACGCCCTGGCTAAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGC	3315
Db	115895		
QY	3316	CAGGCTTGCTTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCT	3375
Db	115953		
QY	3376	GGGATTACAGGGGTGAGCCACCATTGTGGGCTACTTATTTTCTTTACATTCCATCTTTCCA	3435
Db	116011		
QY	3436	ATAGAAATGTAAGATCCACAGAACAGGGAATTACTGCCTATTTTCTTCTTTTGTAG	3495
Db	116066		
QY	3496	ACAGAGTCTCACTTCATCACCTCAACCTCCGTTTCAGCTCAGTCGCAACCTCTGCTCCCGG	3555
Db	116126		
QY	3556	GTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACC	3615
Db	116159		
QY	3616	ATGCTTGGCTAAAT-----TTTTGTATTTTAGCAGAGATGGGGTTTTTACCATGTTGCC	3669
Db	116219		
QY	3670	CAGGCTGGTCTCAAACTCCTGACCTCAAGTGAATCTGCCTGCCTCAGTCTCCCCAAAGTGCT	3729
Db	116279		
QY	3730	GGAATTATAGGCGTGAGTCACTGTGCCTGGCC	3761

Db 116338 GAGATT-CAGGCATGAGCCACTGCACCTGGCC 116368

RESULT 22

US-10-995-561-13296

; Sequence 13296, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 13296

; LENGTH: 35770

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(35770)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-995-561-13296

Query Match 7.4%; Score 367.8; DB 10; Length 35770;

Best Local Similarity 53.2%; Pred. No. 3.1e+02;

Matches 1223; Conservative 11; Mismatches 914; Indels 153; Gaps 16;

Qy 2292 GGCAGGCGGTGGCTCATGCTTAATCCCAGCACCTTTGGAGGCCGAGGCGGGCGGA 2351

Db 11031 GGCTGGCGTGGTGGCTCACACCTGTAATCCCAGCACCTTTGGAGGCCGAGGCGGTGGA 11090

Qy 2352 TCACCTGAGGTGAGGATTCGAGACCAAGCTGGCCAAACATGTTGAAACCCCTGCTCTACT 2411

Db 11091 TCAC--GAGGTGAGGAGATCGAGACCATCCTTGCCCAACATGGTGAACCCCATCTCTACT 11148

Qy 2412 AAAAAATACAAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTAACCCAGCTACTTGGGA 2471

Db 11149 -AAAAATACAAAAAATTAGCTGGCATGGTGGCATGHCCTTTAGTCCAGCTGCTCGGA 11207

Qy 2472 GACTGAGTTGGAGTTTCAGTGAGCAAGGTGCTGTCACTGCTGTCCAGCCTGGTAACA 2531

Db 11208 GGCTGAG--GCAGGAGAAATGCTTGAACCCCTGGAGCGGAGGTGTCAGTGAGCAGAGATT 11265

Qy 2532 GAGCAACTCTGTCTCAAAAAAATAATGCTTTCAATAAATATATATGATAAAGGACTTAT 2591

Db 11266 GCGCACTGCACCTCCAAGCCTGGGTGACAGAGCGAGTCTCCGTCTCAAAAAAATAA 11325

Qy 2592 ATTTTTCAGCCATAGGATCATTTCTCCTGAAGCATCTTTGGCGAAGTCATCCCCCCTG 2651

Db 11326 ATTCATTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGGTATCAG 11385

Qy 2652 TTCCTGAGAGTGGCAGGTGAGGCTGACCTATTGCTCTGCACTTACTCCTATCTCAGCT 2711

Db 11386 AGACTGACTCCACCCAGAGCTGTGAGCTCCAAAACCTC-----CTAGAGTT 11431

Qy 2712 GTCCCTCCACTTTCAGGTGCTGCCAGACACATGACAACTGCTPAYGACCGCCAGAA 2771

Db 11432 GGGAGCACAGCTCCCTCACCTCTGCCAAAACCCCTGATCKCTCCCTTCATTTCTCCCT 11491

Qy 2772 GCTGGACAGCTGTAAATTCTGCTGGACAMMCCGTACACCCACACCTATTTCATACTCGTG 2831

Db 11492 GCTAGAAATCTATGACAAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACAC 11551

Qy 2832 CTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTTGTGACCTATGAATCTA 2891

Db 11552 ATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCGGGCAGAGCTGYGCT 11611

Qy 2892 GTTGGTTCTCAGTAGGCGGGGGAATAATAGTAACAACAGCCATGATTAGTGTAAAT 2951

Db 11612 GCTGAGGCTCAAGTTAAAAAGTGGAGCAGCACGTGAGCTGTACCAGGTGAGGACATGAGC 11671

Qy 2952 TTTCTTGGTTCTGGCAGTGTCTCCTTTAATCCTCAGAAACAACACTATGGGATAGGTACA 3011

Db 11672 CAGAAAGGAAGGTCAGGCGATGGGCTGGAGAGGGTGAGCTGTGACCAAGGGGGTGCTGTG 11731

Qy 3012 ATTATCCTCACTTTAACAGATAAGAAAAACTGAGGCTCAGAAGGCTGAGCTATTTCGCCAAG 3071

Db 11732 GGTGGCTGGTTACAAGGTCACCTAGATGGTCCCTGAARGATAG-----AAG 11779

Qy 3072 ATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTTAGACACAGG 3131

Db 11780 AACACAAACCATAACAATCCTAGAAACKCTTTTTTTTTTTTTT-----GAGACAGT 11828

Qy 3132 GTCTTGTCTGTACCCAGGCATGAGCACAGTGTGCAACCATAGGTCACTGAGCCTCA 3191

Db 11829 GTCTCACTCTGT-TGCCAAGCTGGAGTGCAGTGCAGTGTATGACCTCAGCTCACTGCAATCTCC 11887

Qy 3192 ACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTAGAGCG 3251

Db 11888 GCCTCCTGGGTTCCAGTGATTCTCCTGCCTCAGCTCCCAAGTAGCTGGGATTACAGGTG 11947

Qy 3252 TGCACCACCACGCTTGGCTAATAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGT 3311

Db 11948 TGGCCACCACGCCCAGCTAATTTTTTGTA--TTTTGGTAGAGATGGGGTTTTTACCATGT 12005

Qy 3312 TGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCTACCTTGGCATCCCAAG 3371

Db 12006 TGGCCAGGATGGTCTCGATCTCTGACCTC--GTGATCCACCTGCTCGGTCTCCCAAG 12063

Qy 3372 TGCTGGGATTACAGGGTGAGCCACCATGTGCGGCTACTTATTCTTTACATTCCTCTT 3431

Db 12064 TGCTCAGATTACAGGCTGAGCCACTGCGCTGGCTCTTTTTTTTTTTTTT----- 12116

Qy 3432 TCCAATAGAATGTAAAGATCCACAGAACAGGGAATTACTGCCTATTATTCTTCTCTTCTTTT 3491

Db 12117 -----TTTTTGAGATGGAGTCTT 12134

Qy 3492 TGAGACAGAGTCTCACTTTCATCACCTCAACCTCCGTTCAGCTCACTGCAACCTCTGCCTC 3551

Db 12135 GCTCTGTGCGCCCGGCTGGAGTACAATGGGGTGATCTCGGCTCACTGCAACCTCCGCTC 12194

Qy 3552 CCGGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTCAGTAGCTGGAATTACAAGCGTGCAC 3611

Db 12195 CTGGGTTCAAGTGATTCTCCTGCCTCAGCCACCCGAGTAGCTGGGATTACAGGCAATGTC 12254

Qy 3612 CACCATGCTTGGCTAATTTTTTGTATTATTTTAGCAGAGATGGGGTTTTTACCATGTTGCCCA 3671

Db 12255 CAACACGCTGGGCTAA-TTTTTGTATTTTTTAGTAGACAGAGTTTTTATCATGTTGCCCA 12313

Qy 3672 GGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCTGCCTCAGTCTCCCAAGTCTGG 3731

Db 12314 GGCTGTCTCAAACTCCTGCTCCCTCAAGTGATTCTCCTACCTGAGCCTCCAGAGTCTGG 12373

Qy 3732 AATTATAGGCGTGAGTCACTGTGCTGCTGGCCGAT-----TACTGTCTATTTTCTTATTGC 3786

Db 12374 GATTACAGGTGTGAGCCACTGCACCCGGAACCTAGAGCACTTTTAAATGTTTCAGACTCTT 12433

Qy 3787 TATATCCCCAGATCTAGAGCAGTGTCTGCATATATAGTGGTCTCAATAAATAATTGATG 3846

Db 12434 TGCATCCTAGGATGTTAAACACTTAGAAGGCTGGAATCTTAGGAGTTGGACTCTTTAAGG 12493

Qy 3847 AATGCACAGCCTAGATATAAACTTTCT-----TTTTCTTTTTTTTAAACAATCTTG 3897

Db 12494 ACACAGGATTCTTGAAAGTTGGAATCTCTGAAAGGTTGGGGCTCTAGAAATCATTTCTGT 12553

Qy 3898 ACAACTTTGCAGATAAATAACAATCTTGCATT-----CTGCTTTTTCACCTTA 3944

Db 12554 CCAATATGACAGCCACTAGTCACATTAGCTTGATTAATAATTTAAATTTGTTAAAAATAA 12613

Qy 3945 TCACCTTGTATGACTTTTTTCATATTGCTCCTCAAACTTTTATTGTTACTGTTTTTCA--- 4001

Db	114879	TGCCTGTAATCCAGCACATTGGGAGCCGAGGAGGATGGATCACCTGAGGTCAGGAGTT	114820
Qy	4305	CGAGACCAGCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAATACAAAAA-TTAGC	4363
Db	114819	CGAGACCAGCTGGCCAAACATGGTGAGACCCCATCTCTACTAAAACTACAAAAATTTAGC	114760
Qy	4364	TGGGTGTAGTGATGCATGCCGTGTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAATTG	4423
Db	114759	CAGGTGTGGTGACGTGTCTGTAGTCCAGCTACTCAGAAAGGCTAAGGCAGGAAAAATCA	114700
Qy	4424	CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCCACACTGCACTCCAGCCTG	4483
Db	114699	TTTGAACCCGGAAGTGGAGGTTGCAGTGAGCTGAAATCACACCA-----CTCCAACCTG	114645
Qy	4484	GGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAATAA 4525	
Db	114644	GGCGACAGAGCAAGACGTTGTCTCAACAACAACAACAATA 114603	
RESULT 25			
US-10-995-561-13274/c			
; Sequence 13274, Application US/109955561			
; Publication No. US20050272054A1			
; GENERAL INFORMATION:			
; APPLICANT: CARGILL, Michele et al.			
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH			
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF			
; TITLE OF INVENTION: DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001559			
; CURRENT APPLICATION NUMBER: US/10/995,561			
; CURRENT FILING DATE: 2004-11-24			
; NUMBER OF SEQ ID NOS: 85702			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 13274			
; LENGTH: 415117			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (1)..(415117)			
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-			
US-10-995-561-13274			
Query Match 7.2%; Score 362.2; DB 10; Length 415117;			
Best Local Similarity 56.4%; Pred. No. 57;			
Matches 825; Conservative 2; Mismatches 605; Indels 31; Gaps 7;			
Qy	3098	TTTGGGTTTTTTTTTGGTTGTTTGTAGACAGGGTCTTGCTCTGTCACCCAGGCATGAG	3157
Db	326605	TGTTGTTGTTAAATTTTTTTTTTCCAGACAGGGTCTCACATGTCACCCAGGCTGGG	326546
Qy	3158	CACAGTGGTGAACCATAGGTCACTGCAACCTCAACCTCCTGAGTCAAGGGATCTGCTG	3217
Db	326545	TGCAGTGACACGATCTCGGTTCACTGCAACCTCCACCTCCAGGTTTAAGTGATTCTCCT	326486
Qy	3218	ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACCAAGCCTGGCTAATTAAA	3277
Db	326485	GCCTCAGCCTCCCAAGTAGCTGGGATGACAGGTGTGCACCAACCATGCCAGCTAATTTT	326426
Qy	3278	AAAAATTTTTTGTAGAGACTGGGTCCTTACTACGTTGGCCAGGCTGTCTTAAACTCCTGG	3337
Db	326425	GTA--TTTTTAGTAGAGATGGGGTTTTTACCATGTTGTCTGAGCTTAAGTGATGCACCTGC	326368
Qy	3338	CTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGGTGAGCCACC	3397
Db	326367	CT-----AAGCCTCCCAACTGGGCTT-----ACAGCATGAGCCACCATGCCAGCAAAA	326319
Qy	3398	ATGTGGGGTACTATTCTTTTACATTCCATCTTTTCCCAATAGAAATGAATCCACAGAA	3457
Db	326318	AAAAACCGTTTATTCTATTTCATTTTATTATTATTATTATTATTATTATTATTATT	326259
Qy	3458	CAGGGATTACTGCCTATTTTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACCT	3517

Db	326258	CTTACTTATTTTATTTTGTGAGGCAGAGTCTCACTCTGTTGCCAGGCTGGAATGCA	326199
Qy	3518	CAACCTCCGTTCAAGTCACTGCAACCTCTGCCCTCCGGGTTCAAGYGATTCTCTGCTCA	3577
Db	326198	GTGGCACGATCTCGCTCATTTGCAACCTCTGCCCTCTCAAGTTCAAGCGATTCTCTGCTC	326139
Qy	3578	AGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCAACCATGCTTGGCTAATTTTTTGTAT	3637
Db	326138	AGCTTCCCAAGTAGCTGAGATTACAGGCACACACCAACACACCTGGCTAA-TTTTTTCTAT	326080
Qy	3638	TTTTAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAA	3697
Db	326079	TTTTAGTAGAGATGGGTTTTCGCCATGTTGGCCAGGCTGGTTTCGAACCTCCTGACCTCAG	326020
Qy	3698	GTGATCTGCCCTGCCTCAGTCTCCCCAAAGTCTGGGAATTATAGGCGTGAGTCACGTGCTT	3757
Db	326019	GTGATCTGCCCGCCTCGGCCTCCCAAGTGCAGGATTACAGGCATGAGCCACGAAGCCC	325960
Qy	3758	GGCCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACA	3817
Db	325959	GGCCCCCCCCCAAAATTTTTAAATG-----AGGACTTTGGGACGGGATGCTCA	325909
Qy	3818	TATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCCTAGATATAAACTTCTTTT	3877
Db	325908	CTCAACTGTCACTTATTATTATCTCATTTAAAAAATCTAAATCTTTATAAATGAAACTTA	325849
Qy	3878	CTTTTTTAAAAACAATCTTGACAACTTTGCAGAAFAAATACAATCTTGCAATCTGCTTTT	3937
Db	325848	GGTGGCAAGCATACTTGTTCAGAATAATACACCTAGTAAAAAATGAGGAAGGCTGTG	325789
Qy	3938	TCACTTATCACCTTGTATGACTTTTTTCATATTGCTCAAACTTTATTGTTACTGTTTT	3997
Db	325788	AAAGTAATTGCAGAGGAAGAATATTTTGGGCTTCACAACCTGACCAGAGAGGAGGAGGT	325729
Qy	3998	TTCATTGTTACTATTTTAGTCACCTGAATAATATGGCTTAATTTTGCTTATACATCCTCTG	4057
Db	325728	TAGAGGGAAAAAACAARAATAATGCCATATAGTGTACTCTTAGGTTACTAGGGGCATA	325669
Qy	4058	CTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCTCCCAGAG	4117
Db	325668	GAGCATTTCTGTATGTGAAATACTAAAAAAC-----GACCCATGTGAAGGTGTCTAGAA	325609
Qy	4118	AAATACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACA	4177
Db	325608	GAGCATTTCTGTATGTGAAATACTAAAAAAC-----GACCCATGTGAAGGTGTCTAGAA	325556
Qy	4178	AGAAACCTGCATTAGAGGATGTTTGTTCATATTAAATAAATAAATACTCAGTTGGGCACAG	4237
Db	325555	GGGCCCTCACACAAAAAGATTCAATGCTGGGATAGAGATATAGATTTGGGCCAGGCGTGG	325496
Qy	4238	TGACTCAAGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACTTGAGGTG	4297
Db	325495	TGGCTCACACCTGTAAATCCCAGCACTTTGGGAGGCCGAGACAGGCAGATCACCTGAGGTC	325436
Qy	4298	AGAAGTTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAAATACAAA	4357
Db	325435	AGGAGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCGTCTCTACTAAAAAATACAAA	325376
Qy	4358	ATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCCAAGA	4417
Db	325375	ATTAGCCATGTGTGTGGCATGCACCTGTAGTCCCAGCTACTTTGGGAGGCTGAGGCAGGA	325316
Qy	4418	GAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCA-CCACTGCACTC	4476
Db	325315	GAACCACTTGAACCTTGGGAGGTGGAGACTGCACTGAGCCAAGATCGACCCCACTGCACTC	325256
Qy	4477	CAGCCTGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAATAAAGGATC	4536
Db	325255	CAGCCTGGGAGACAGAGCGAGACTCCATCTCAAAAAAATAAATAAATAAATAAATAA	325196
Qy	4537	GGAGAGAAAACAAAACTAATAAGA 4559	

Db	325195	CAAAACAACCAACAAAAA	325173
RESULT 26			
US-11-121-086-4/c			
; Sequence 4, Application US/11121086			
; Publication No. US20050266459A1			
; GENERAL INFORMATION:			
; APPLICANT: POULSEN, TIM S.			
; APPLICANT: NIELSEN, KIRSTEN V.			
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES			
; FILE REFERENCE: 09138.6000-00000			
; CURRENT APPLICATION NUMBER: US/11/121,086			
; CURRENT FILING DATE: 2005-05-04			
; PRIOR APPLICATION NUMBER: 60/567,570			
; PRIOR FILING DATE: 2004-05-04			
; NUMBER OF SEQ ID NOS: 107			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 4			
; LENGTH: 164810			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-121-086-4			
Query Match 7.2%; Score 362; DB 17; Length 164810;			
Best Local Similarity 57.5%; Pred. No. 1.1e+02;			
Matches 858; Conservative 1; Mismatches 566; Indels 67; Gaps 9;			
Qy	3097	GTTTGGGTTTTTTTTTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGA	3156
Db	122909	GTTATCTTGTATTATTTTATTATTTTATAGACCGGGTCTGACTGTCTCCCAGGCTGGA	122850
Qy	3157	GCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCTGTAGCTCAAGGGATCTGCT	3216
Db	122849	TTGCAACGGCGCATTCACAGCCCACTGCAGCCTCAACCTCCTGGGCTCCAGTGATCCTCC	122790
Qy	3217	GACCTCAGCCTCCCAAGTAGTGGGACTACGAGCGTGCAACACCACGCCTGGCTAATTAA	3276
Db	122789	TGCCTCAGCCTCTGGTGTAGCTAGGACTACAGGTGCATACCACAATGTGTGGCTAATTT	122730
Qy	3277	AAAAAT-----TTTTTTGTAGAGACTGGGTCTTTACTACGTTGGCCAGGCTTGTCTTAAA	3330
Db	122729	TCTTTTCTTTTCTTTTTTTGTAGAGATGGTGTCTCTCTATGTGCAAGGCTGGGCTTGAA	122670
Qy	3331	CTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAAGTGTGGATTACAGGGGTG	3390
Db	122669	TACCTGGCCTTAAGCGAATCTCCTGTCTCAGCCTCCTAAAGCGCT-GGATTACAGGTGTC	122611
Qy	3391	AGCCACCATGTGCGGCTACTTATTTTCTTTTACATTCCATCTTTCCAATAGAATGTAAGATC	3450
Db	122610	AGACACTGCACCTGGCTGCCACTCTTTCCTCTTTTATTATTATTTTAT-----	122557
Qy	3451	CACAGAACAGGGATTACTGCGCTAATTTTCTCTCTTTCTTTTGTGAGACAGAGTCTCACTTC	3510
Db	122556	-----TTATTGTTTGAGATGGAGTTTTTGCTCTTGTCAACCCAGGCTGCAGTGC	122510
Qy	3511	ATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCTCCCGGGTTCAAGYGATTCCTC	3570
Db	122509	AATGGCGCAATC-----TCAGCTCACTGCAACCTCCACCTCCCGGGTTCAAGCAATTCTC	122455
Qy	3571	CTGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACACCACCATGCTTGGCTAATTT	3630
Db	122454	CTGCCTCAGCCTCCTGAATAGCCAGGATTACAGGCAACAGCCACCGCCTGGCTAA--T	122397
Qy	3631	TTTGTATTTTTCAGCAGAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTG	3690
Db	122396	TGTATATTTTTCAGCAGAGATGGGGTTTTTACCAT--TTGGCCAGGCTGGTCTCTAACTCCTG	122338
Qy	3691	ACCTCAAGTGAATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGAGTCAC	3750
Db	122337	ACCTCAGGGGATCCGCTTGCCCTCCCAAAGTGTGGGATTACAGGCATGAGCCAC	122278
Qy	3751	TGTGCTGGC--CGATTACTGTCTATTTTCTTTTATTGCTATATCCCCAGATCTAGAGCAG	3808

Db	122277	CGAGCCCGCCTCCATTGTTTAAAGACCCCTTAGGCCAGCTGTGGTGCATGCCTA	122218
Qy	3809	TGTCTGACATATAGTAGTGTCTCAATAAATAAATTGATGAATGCACAGCCTAGATATAAAC	3868
Db	122217	TAATCCCAACACTTTGCAAAAGCTAAGGCAGGAGAATTGCTTGAGCCCAGGAGGTCGAGGC	122158
Qy	3869	TTTCTTTTCTTTTAAAAACAATCTTGACAACCTTTCAGAAATAAATAACAATCTTGCAT	3928
Db	122157	TGCAGTGAACCTGTGATTGCATTGTTGCACTCCAGCCTGGGTAACAGAGTGAACCCCTTA	122098
Qy	3929	TCTGCTTTTTCACTTATCACCTTGTTAAG-----ACTTTTTCAT	3967
Db	122097	TCTATTTGAAAAATAAAGCCGGGTGCGGTGAGTCCAGCCTGTAATCCAGCACTTTGG	122038
Qy	3968	ATTGCTTCAAAACCTTTATTTGTTACTGTTTTTTCATTTGTTACTATTTTAGTCACTGAATAA	4027
Db	122037	GAGGCCGAGGCGGGTGGATCACGAGGTCAAGGATCAGGACCATCCTGGCCAAACATGGTG	121978
Qy	4028	TATGGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATC	4087
Db	121977	AAACCCGGTCTTTTACTGAAATAACAAAAAGCAGGTCAATGTTGGCGCATGCCTGTAATCCC	121918
Qy	4088	TGATGAAAGCTATGAACCTCTCCCCAGAGAAATACACACACACACACACTCACACAC	4147
Db	121917	TGCTACTTGGAGGCTGAGGCAGGAGAGTGCGTGAACCCGGGAGGGAGGTGCGAGTG	121858
Qy	4148	AGTTTTTTTTTAATGTTTGCAACTAAG-----ACAAGAAACCTGCATTAGAGGAT	4197
Db	121857	AGCTGAGATCGTGCCACTGCACCTCCAGCCTGGGGACAGAGAGACTCCATCTCAGAAA	121798
Qy	4198	GTTTGTTCATATTAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	4257
Db	121797	ATAAAAAATAAAGTAATAAATAAATAAAGAGCTGGGCACAGTGGCTCACGCCTGTAATCCT	121738
Qy	4258	AGTACTTTGGAAGTCCAAAGGTGGTGGATCACTTGAGGTGAGAAGTTTCGAGACCAAGCCTG	4317
Db	121737	AACACTTCGGAAGSCCGAGCAGGAGGATCACCTGAGGTCAAGAGTTCAAGACCAAGCCTG	121678
Qy	4318	GTCAATATGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATG	4377
Db	121677	GCCAAACATGGCAAAACCCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGTG	121618
Qy	4378	CATGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAG	4437
Db	121617	CGCGCCTGTAATCCAGCTACTGGGGAGGCTGAGGTGGAAGAAATCACTTGAACCCGGAG	121558
Qy	4438	GCAGAGGTTGCAGTGAGCCGAGATCCCACCCTGCACTCCAGCTGGGCGACACAGCGAG	4497
Db	121557	GCAGAGGTTGCAGTGAGCCAAAGATTGCATATTGCACTCCAGCTGGGTGACAGAGCGAG	121498
Qy	4498	ACTCTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAA	4549
Db	121497	GCTCCGCTCTCAAAACATAAAATTTAAAAAATACAAAAATAAAAAATAAAAA	121446

RESULT 27

US-10-775-169-234/c

; Sequence 234, Application US/10775169

; Publication No. US20050287532A9

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Burczynski, Michael

; APPLICANT: Twine, Natalie

; APPLICANT: Dörner, Andrew

; APPLICANT: Trepicchio, William

; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo

; FILE REFERENCE: AM101080 (031896-013000)

; CURRENT APPLICATION NUMBER: US/10/775,169

; CURRENT FILING DATE: 2004-02-11

; NUMBER OF SEQ ID NOS: 5278

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 234


```

; LENGTH: 35962
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-234

      Query Match      7.2%; Score 361.6; DB 10; Length 35962;
Best Local Similarity 58.9%; Pred. No. 3.5e+02;
Matches 844; Conservative 1; Mismatches 460; Indels 127; Gaps 8;

QY 3104 TTTTNTTTTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCAGGCATGAGCACAGT 3163
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33142 TTTTNTTTTGTGTTGTTTAGAGACAGAGTCTCATTTCTGTTACCCAGGCTGAAGTGCAGT 33083

QY 3164 GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 3223
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33082 GGTGCGATCTCAGGTCACTGC AACCTCTTCCCCCGGGGCTCAAGATATTCTCCTGCCTCA 33023

QY 3224 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACCAACGCTGGCTAATTA AAAAATT 3283
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33022 GCCTCCTGAGTAGCTGAGATTACAGTGCATGCCACCACGCGCATCTAATTTTGTGA--T 32965

QY 3284 TTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCAA 3343
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32964 TTTTAGTACAGACGGGGTTTTCATCAGTTGGCCAGGCCAGTTTCGAACACTACTGACCTCAA 32905

QY 3344 GCAATCCTCCTACCTTGGCATCCCAAAGTGTCTGGGATTACAGGGTGAGCCACCATGTGC 3403
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32904 GTGATCCGCTGCCTCATCTCTCCCAAAGTGTGGGATTACAGSCGTGAGCCACCAACCC 32845

QY 3404 GGCTACTTATTTCTTTTACATTCCTATCTTCCAAATAGAATGTAAGATCCACAGAACAGGA 3463
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32844 AGCCAGGAATTCTTTTNTTTTGTGACAAAG----- 32809

QY 3464 TTACTGCTATTTTCTTCTCTTTTGTGAGACAGAGTCTCATTCTACCTCAACCT 3523
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32808 --TTTCGCTCTGTGTGCCAGGCTGGAGTGCAATGGTGTGATCTCGTCTCAATGCAACCT 32751

QY 3524 CCGTTACGCTCACTGCAACCTCTGCCTCCCGGTTTCAAGYGATTTCTCTGCCTAAGCCTC 3583
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32750 CCG-----CTCCGGGGTTTCAAGCAATTTCTCCTGCCTCAGCCTC 32713

QY 3584 CTGAGTAGTGGGAATTACAAGCGTGCACCACCATGCTTGGTGAATTTTGTATTTTAG 3643
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32712 CTGAGTAGTGGGATTAGAGGCATGTGCCACCACGCCCCGGCTAATTTT--TACTTTTGG 32655

QY 3644 CAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC 3703
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32654 TAGAGACAGGGTTTCTCCATGTTAGTCAGGCTGGTCTCTGAACTCCCGACCTCAGGTGATC 32595

QY 3704 TGCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGGCGTGAGTCACTGTGCCGCGCA 3763
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32594 TGCCCACTTCGGCCTCCCAAAGTCTGGGATTACAGGCGTGAGCCACTGTGCCCGGC--- 32538

QY 3764 TTACTGCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGT 3823
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32537 -----CTAGCCAGGAATTTCTTTAAAGGCT 32514

QY 3824 AGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTT 3883
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32513 GGCTGCCTTTAAGAAACTCTACCAATGAACTGTAT-----TTTTTNTTTT 32468

QY 3884 TTA AAACAACTTTGCAGAAATAAATAACAATCTTGCAATCTGCTTTTTCACTT 3943
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32467 TTTACCCCGAGAGACACGGTCTCCCTCTATTGCCCCAAATTGGAATGCAGTGTGTGTTTC 32408

QY 3944 ATCACCTTGTATGACTTTTTCATATTGCTTCAAAACCTTTTATGTACTGTTTTCATT 4003
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32407 ATGGCTCACCGCAGCCTCGACTCTTTGGCTCCAGTGGGAGCTTGGCTAATTTT TAAATT 32348

QY 4004 GTTACTATTTTAGTCACTGAATAATATGGCTTAATTTTGCTTATACATCCTCCTGCTCCAC 4063
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32347 TCTGTAGAGTAAGATCTCACTAGATTGCACAGCTGGGTTTCGAAC-----TCCTGAC 32296
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QY 4064 TTTAGAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCTCCCAGAGAAATAC 4123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32295 CTCAGGTGATCCACCTCGCCTCGGCCCTCCCAAAGTGTGGGATTACAAGCACGAG----- 32242

QY 4124 ACACACACACACACACTCACACACAGTTTTTTTTTTTTAATGTTTGCAACTAAGACAGA AAC 4183
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32241 -----CCACAGCACCTGGCCTCCATTTTGCACTTTGAATGGATCTTTAAACCTGTGCA 32190

QY 4184 CTGCATTAGAGGATGTTTGTTCATATTAAATTAAAAATAACTCAGTTGGGCACAGTGACTC 4243
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32189 TGATTTTATATCATGCATGATCATTTAGAAAAATAATGGTTTGGCTGGGCACCGTGGCTC 32130

QY 4244 AAGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAA GT 4303
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32129 ACACCTGTAATCCAGCATTTTGGGAGGCTGAGGTGGCCAGATCATTTGAAAGTCAGGAGT 32070

QY 4304 TCGAGACCAGCCTGGTCAATATGGTGA AACCCCTATCTCTACTAAAAATACAAAATTATG 4363
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32069 TCAAGACCAGCCTGGCTAAACATGGTGA AACCTCCATCTCTACTAAAAATACAAAATTAT 32010

QY 4364 TGGGTGTAGTGATGCATGCCTGTAGTCCCAGTACTCGGAGGCTGAGGCAAGAGAATTG 4423
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32009 CACTTGTGGTGCATGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCACGAGAATTG 31950

QY 4424 CTTGAACCTGGGAGSCAGAGGTTGCAGTGAGCCGAGATCCCACCCTGCCTCCAGCCTG 4483
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31949 CTTAAACCTGGGAGGTGGAGGTTGTAGTGAGCCGAGATCATGCCACTACACTCCAGCCTA 31890

QY 4484 GCGACACACGCGAGACTCTATCTCAAAAAATAAATAAATAAATAAAGGAT 4535
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31889 GACAAACACAGCAAGACTCTGTGCAAAAAACAACAAAAAAGAAATATTTGAT 31838
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RESULT 28
US-10-995-561-13308/c
; Sequence 13308, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13308
; LENGTH: 148935
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13308
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Query Match      7.2%; Score 360.2; DB 10; Length 148935;
Best Local Similarity 59.1%; Pred. No. 1.3e+02;
Matches 897; Conservative 2; Mismatches 500; Indels 118; Gaps 12;
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QY 3073 TCACACAGCTTGTAAAGTGGTGACAGTTTTGGGTTTTTTTTTGTGTTTAGAGACAGGG 3132
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 44221 TCTTATATATAGCATATAGTAGGATTTGTTTTTGTGTTTTTTTTTTTGTGAGTGGAG 44162

QY 3133 TCTTGCTC-TGTCACCCAGGCATGAGCACAGTGGTGC AACCATAGGTCACTGCAGCCTCA 3191
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 44161 TTTTGTCTCTTGTGTCAGGCTGGAGTGCAATGGTGC AAATCTCAGCTCACTACAACTCT 44102

QY 3192 ACCTCCTGAGCTCAAGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCG 3251
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 44101 GTCACCCAGGTTCAAGCATTTCTCCTGCCTCAGCCTCCTGGGTAGCTGGGATTACAGGCA 44042

QY 3252 TGCACCAACCAACGCTCGCTAAATTA AAAAAATTTTTTGTAGAGACTGGGTCTTACTACGT 3311
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 44041 TGCACCACTACACCCAGCTAATGTTTGTA--TTTTTAGTAGAGTTTGGGTTTACCATGT 43984
```


Db 19925 -----CTGGAGTGCAGTGGCAC 19909

Qy 3524 CCGTTCAGTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCTGCCTAAGCCTC 3583

Db 19908 AATCTCGGTCAGTCAACCTCCACCTCCTGGGTTCAAGTGAATCTCTCGCTCAGCCTC 19849

Qy 3584 CTGAGTAGCTGGAATTACAAGCGTGCACACCACCATGCTTGGCTAATTTTTTGTATTTTAG 3643

Db 19848 CTGAGTAGCTGGGACTACAGGCGCCGCCACTACACCCGGCTAAATTTTTGTACTTTTAG 19789

Qy 3644 CAGAGATGGGGTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC 3703

Db 19788 TAGAGATGGGGTTTCACCATGTTGCCAGGATGGTCTCAATCTCCTTGACCTC--GTGATC 19731

Qy 3704 TGCCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCCGA 3763

Db 19730 CACTCACCTCAGCCTCCCAAAGTCTGGTATTACAGGTGTGAGCCATCGCGCTTGGCTTT 19671

Qy 3764 TTAAGTGTCTATTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGT 3823

Db 19670 TTTTTTTTTTTTTTTTAAACCACAAGCATGTGTCACTTTTATAGTTAAGAGGAAAAACA 19611

Qy 3824 AGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTT 3883

Db 19610 AACTTTTTCTAAAAAATCTGTATTTCTGAATGTTAGCAGGAGCCCAGCTGAGTCTGGGG 19551

Qy 3884 TTAACAACAATCTTGACAACTTTTGCAGAAATAATACAATCTTGCAATCTGCATTTTTCATT 3943

Db 19550 T-----GCTGCAGGCCTCCTGCCTGTGGGACCTCTCCTAGGCACCTCCTTTCTTAGAC 19497

Qy 3944 ATCACCTTGTTATGACTTTTTTCATATTGCCTCAAAACCTTTATTTGTTACTGTTTTTCAAT 4003

Db 19496 CCATCCTTAGGGCTGGGAGAACTCCTTCCACAGTGTCTCTGGCTTCAAAGCAGGGCAGG 19437

Qy 4004 GTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCTCCAC 4063

Db 19436 CTTCCACAGATGGGGAAGCTCATAGGCTGG-----TGGGGTGAGGTGC 19394

Qy 4064 TTTAGAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAAATAC 4123

Db 19393 GGTGGGAGCGGCAGAGAGACCTTCCAGGCCAGGTGTCCAGCT-----AGAAAAAGGC 19340

Qy 4124 ACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAAC 4183

Db 19339 TCAGAAGTGTGCATGAGTGTGAGCTGTGTTGGGAATAAGAAGATTGTCCCAGGAGGGCC 19280

Qy 4184 CTGCATTTAGAGGATGTTTGTTCATATTAATTAAAAATAACTCAGTTGGGCACAGTGACTC 4243

Db 19279 CAGTAT-----GCACTAGAGGCTTATAAGTAATACTGCTGGGGCCAGGTGTGGTGCCAC 19225

Qy 4244 AAGCCTGTAACCCACAGTACTTTTGGAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGT 4303

Db 19224 GCACCTGTAATCCCAGCGCTTTGGGAGGCCAAGGTGGGCAGATCACCTGAGGTCAAGGAGT 19165

Qy 4304 TCGAGACCAAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAAATACAAAAATTAGC 4363

Db 19164 TCGAGACCAAGCCTGGCCAACATGGTGAATCCTGTCTCTACTAAAAAATACAAAAATTAGC 19105

Qy 4364 TGGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAATTG 4423

Db 19104 CAGGCGTGGTGGGAGCCCTGTATGCCAGCTATTTAGGAGGCTGAGATATGAGAATCA 19045

Qy 4424 CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCCACCAGCTGCCTCCAGCCTG 4483

Db 19044 CTTGAACCCAGGAGGCAGAGGTTTTCAGTGAGCTGAGATTACACTGCTGCCTCCAGCCTG 18985

Qy 4484 GCGCACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAATAA 4531

Db 18984 GGTGACAGAGTGAGACTCTCTCAAAAAAACAACAACAACAACA 18937

RESULT 30

US-10-995-561-13308

; Sequence 13308, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13308

; LENGTH: 148935

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-995-561-13308

Query Match 7.1%; Score 357.2; DB 10; Length 148935;

Best Local Similarity 60.1%; Pred. No. 1.3e+02;

Matches 863; Conservative 3; Mismatches 431; Indels 139; Gaps 11;

Qy 3097 GTTTGGGTTTTTTTTTGTGTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCATGA 3156

Db 68303 KTTGTTGTTGTTGTTGTTGTTGTTGAGAAAGAGTCTCGCTCTGTCACCCAGGCTGGA 68362

Qy 3157 GCACAGTGGTGCAACCATAGGTCACCTGCAGCCCTCAACCTCCTGAGCTCAAGGGATCTGCT 3216

Db 68363 GTGCAGTGGCATGATCTCGGCTTACTGCAACCTCCACCTCCAGGTTCAAGCGATTCTCC 68422

Qy 3217 GACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACACCACCGCTGGCTAATTAA 3276

Db 68423 TGCCTCAGCCTCCTGAGTAGCTGGGATTACAGACGCATGCCACCGCTGGCTAATTTT 68482

Qy 3277 AAAAAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTG 3336

Db 68483 TGTA--TTTTTAGTAGAGACAGGGTTTCACAAATGTTGGTCAGGCTGGTCTTGAACCTCTG 68540

Qy 3337 GCTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTCTGGGATTACAGGGGTGAGCCAC 3396

Db 68541 ACCTC--GTGATCTGCCGCCTTGGCCTCCCAAAATTGTGGGATTACAGGCGTGAGCCAC 68598

Qy 3397 CATGTGCGGCTACTTATTCTTTTACATTCCTATCTTCCAATAGAATGTAAGATCCACAGA 3456

Db 68599 CATGCCTGG----TTTTTTTTTTTGTGTTTTTTTTTTTGAGATGGAGTCTCTAGTATGTCA 68653

Qy 3457 ACAGGGATTACTGCCFATTTTCTTCTTCTTTCTTTTGTGACACAGAGTCTCACTTCATCACC 3516

Db 68654 CCCAGGCTGGAGTGCAGTGTGCAGTGGTGCAATCTGG----- 68690

Qy 3517 TCAACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCT 3576

Db 68691 -----GCTCACTGCAACCTCCACCTCCCGAGTTCAAGCGATTCTCCTGCCT 68736

Qy 3577 AAGCCTCCTGAGTAGTGGAAATTACAAGCGTGCACACCATTGCTTGGCTAA-TTTTTTGT 3635

Db 68737 CAGCCTCCCAAGTAGCTGGGATTACAGGTGCGCACCCACCGCTGGCTAATTTTTTTGT 68796

Qy 3636 ATTTTAGCAGAGATGGGGTTTACCATTGTTGCCAGGCTGGTCTCAAACTCCTGACCTC 3695

Db 68797 ATTTTAGTAGACACAGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGA-CTC 68855

Qy 3696 AAGTGATCTGCCCTGCCCTCAGTCTCCCAAAGTCTCGGAATTATAGGCGTGAGTCACTGTGC 3755

Db 68856 AGGTGATCCGCCAGCCTCGGCCTCCCAAAGTCTGGGGTTACAGGCGTGAACCCCGCGC 68915

Qy 3756 CTGGCCGATTACTGTCTATTTTCTTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGA 3815

Db 68916 CCGCCGCCCACTTGGTTTTTTTTTTTGTGTTTTTGTGTTT-----TTTATTTTCA 68961

Qy 3816 CATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTT 3875

Db 68962 GTTTTCTTTACTTAGCAATATATCTTGGGCAAAATTTCCAAACATCATTAATAATCATGGTAG 69021


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QY 3876 TTCTTTTAAACAATCTTGACAACTTTGCAGAAATAAATACAACTCTTGCATTTCTGCTT 3935
Db | | | | |
69022 GAAATAATTTCTGCTTAAACCAAGATGATAACAGATTATCATCAGAGACAGATTTAGAAA 69081
QY 3936 TTTCACTTATCACCTTGTATGACTTTTTCATATTGCCCTCAAACCTTTTATTGTTACTGTT 3995
Db | | | | |
69082 CTTTAAACAAGCTGTTTAGTTTCAGTTTCYCCCTGTCTTTAAGACAGAGCTTTTGTCTCT 69141
QY 3996 TTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCC 4055
Db | | | | |
69142 TTTTAA-----AATAAACTCCCTGCCTTACCTTCCCTCCGACTCCTCACCC 69184
QY 4056 TGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCTCCAG 4115
Db | | | | |
69185 CCAGACTCTAGACCAGGCC-----CTGTCCTGTTACAGTTCCTTCCA 69225
QY 4116 AGAAATACACACACACACACTCACACAGTTTTCATGTTTAAATGTTTGCAACTAAGA 4175
Db | | | | |
69226 TTCTGAGCTCAGGGGCTCTGACAGGCACCCCTTCTCTTATATAAGCAGAGCCTCACTG- 69284
QY 4176 CAAGAACTGCAATTAGAGGATGTTTGTATATTAATTAATAAATAAATACTCAGTTGGSCAC 4235
Db | | | | |
69285 -----TAGAAATAAACAGTTTTCAGCCAGGCGC 69313
QY 4236 AGTGACTCAAGCCTGTAAACCACA-----GTACTTTGGAAGTCCAAGGTGGGTGGAT 4286
Db | | | | |
69314 AGTGGCTYAYGCCGTGTAATCCAGCACTTTGGGCACCTTTGGAAGGCCGAGGTAGGTGGAT 69373
QY 4287 CACTTGAGGTGAGAAGTTTCGAGACCCTGGTCAATATGGTGAACCCCTATCTCTACTA 4346
Db | | | | |
69374 AACCTGAGGTCAGGAGTTTCAAGGCCAGCCTGGCCAACATGGTGAACCTCCGTCCTACTA 69433
QY 4347 AAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGAGG 4406
Db | | | | |
69434 AAAATACAAAAATTAGCCAGGCATGGTGGTGGCGCCTGTAGTCTCTGGCTACTCGGAGG 69493
QY 4407 CTGAGGCAAGAGAATTGCTTGAACTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCAC 4466
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69494 CTGAGGACGAGAATTGCTTGAACCTGGGAGCGGAGGTTGCAATGAGCCAAGATCACAC 69553
QY 4467 CACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAA 4522
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69554 CACTGCACTCCAGCCTGGGTGACAGACGAAGACTTTCATTTGAAAAAAGAAAGAA 69609

RESULT 31
US-11-121-086-61
; Sequence 61, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 169495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (70072)..(70171)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (139457)..(157244)
; OTHER INFORMATION: a, c, g, t, unknown or other
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US-11-121-086-61
Query Match 7.1%; Score 356.8; DB 17; Length 169495;
Best Local Similarity 58.2%; Pred. No. 1.2e+02;
Matches 884; Conservative 1; Mismatches 513; Indels 120; Gaps 10;

QY 3099 TTGGGTTTTTTTTTTGTTGTTTAGAGACAGGGTCTTGTCTGTCAACCAGGATGAGC 3158
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QY 3159 ACAGTGGTGCAACCATPAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGA 3218
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QY 3219 CCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCAACCACCGCTGGCTAAATAAAA 3278
Db | | | | |
9670 CCTCAGTCTCCCAAGCAGCTGGGGCTGCAGGTGCACGCCACCATGCCTGGCTAATTCTT 9729
QY 3279 AAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGC 3338
Db | | | | |
9730 TTTGTTTTTTGTAGAGATGGTGTCTCACTGTGTGCCCAGGCTAGCGTGGAACCTCTGGA 9789
QY 3339 TTCAAGCAATCCTCTACCTTGGCATCCCAAAGTGCACCATCCAGGGGTGAGCCACCA 3398
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9790 TACAAAGCGATCCTCC-ACCTCGTCTTCCCAAAGTGTGGGATTACAGGCATGAGTCACTG 9848
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Db | | | | |
9849 CGCTGGGCCCTCTGTACTTCTAATTAAATTAATT------ 9882
QY 3459 AGGATTACTGCCATTTTCTTCTCTTTTGAGACAGAGTCTCATTTCATCACCTC 3518
Db | | | | |
9883 ----AATTGACTTTTGGGGGAGACACAGTTTTTACTGTGCCCCCAGGCTGGAGTGCAGG 9938
QY 3519 AACCTCCGTTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAA 3578
Db | | | | |
9939 GCTGTGATCTTGGCTCACTGCAACCTCCGCCCTTCAGATTCAAGCAATTTCTCCTGCCTCA 9998
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10118 TGATCCACCCGCCCTGGCCTCCCAAATGTTGGGATTACTGGCGTAAGCCACCAAGCCCA 10177
QY 3759 GCCGATTACTGTCTATTTTCTTTATTG-----CTATATCCCCAGATCTAGAGCA 3807
Db | | | | |
10178 GCCTCTTCTGTACTTTTAAAAATGTGTCCAGTGGAGTCTATAACAATACCAGTTTGACA 10237
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Db | | | | |
10238 GCTGCCATCTTTTATTATTAGAAAAAATACATGAATAAGCTTTACTCCAGCAGACAAATAT 10297
QY 3860 GATATAAACTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTTGCA-GAATAAATAC 3918
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QY 3919 AATCTTGCAATCTGCTTTTTCATTTATCACCTTATGTTTATGACTTTTT----- 3964
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10358 ATTATTATCTTTTTTTTTTCTTTTTTCTTTTGTGAGATGGAGTTTGTCTGTGGCCTAG 10417
QY 3965 -----CATATTGCCTCAAACCTTTATTGT 3988
Db | | | | |
10418 GCTGGAGTGCAGTGGCAGCATCTCGGCTCACTGCAACCTCTGGCTTCCAGGTTCAAGTGA 10477
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Db	10598	TCTGACCTCAAGTGATCCACCCGCCCTGGCCCTCCCAAAGTGCTGGGACTACAGGCGTGAG	10657
QY	4169	ACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATAATTA	4216
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QY	4217	---AAATAAAGTTCAGTTGGGCACAGTGACTCAAGCCTGTAACCAACAGTACTTTGGAGTCC	4273
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QY	4274	AAGTGGGTGGATCACTTGAGGTGAGAAATTCGAGACCAGCCTGGTCAATATGGTGAAAC	4333
Db	10778	AAGGCAGCAGATTGCCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAAC	10837
QY	4334	CCTATCTCTACTAAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCCTGTAGTCCCA	4393
Db	10838	CCTGTCTCTACTAAAAAATATAAAAAATTAGCCAGTCATGGTGTGTGCCCTGTAAATCCCA	10897
QY	4394	GCTACTCGGAGGCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGA	4453
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QY	4454	GCCGAGATCCCAACCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAA	4513
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RESULT 32

US-11-112-908-57

US 11112508 57 ; Sequence 57, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:

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; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3

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LENGTH: 161994

LENGTH: 1
; TYPE: DNA

ORGANISM: Homo sapiens

US-11-112-908-57

Query Match	7.18;	Score 355.8;	DB 17;	Length 161994;
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Query Match	Score	Pred. No.
Best Local Similarity	57.18	1.3e+02

Sequence	Matches	Conservative	Mismatches	Indels	Gaps
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QY	3167	GCAACCATAGGTCAC	TGAGCTCAAACTCCTGAGCTCAAGGGA	CTGCTGACCTCAGCC	3226
Db	55332	ACAATCTTGGCTCACTACA	AACTCCGCTCCAGGTTCAAGCAAT	TATCCTGCTCAGCT	55391
QY	3227	TCCCAAGTAGCTGGGACTAC	GAGCGTGCACCAACGCTGGCTAAAT	TAAAAAAATTTT	3286
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QY	3287	TTGTAGAGACTGGGTCTT	ACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCA	3346	
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QY	3347	ATCCTCCTACCTTGGCAT	TCCAAAGTCTGGGAT	TACAGGGGTGAGCCACCATGTGCGGC	3406
Db	55512	ATCCACCTGCCTCGGTCT	CAAAAGTACTGGGAT	TACAGGCATGAGCCACCGCGCCAGC	55571
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QY	3467	CTGCCTATTTTCTTCT	TTTCTTTTGGAGACAGAGTCTCACTTTCATCACCTCAACCTCCG	3526	
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Db	55870	CCGCCCGCTTGGCCT	CCCAAAGTCTGGGATTA	CAAAACATGAGCCACCCCTGCCCGGCTA	55929
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QY	3804	AGCAGTGTCTGACAT	ATATAGTAGGTGCTCAATAAATAAT	TGATGAATGCACAGCCTAGATA	3863
Db	55990	AACAAATATGTAC	CCCATATATCTCCACCCCAAGTTAA	TATCATGTTAACATTTTCATTAGTC	56049
QY	3864	TAAACTTTCTTTTCT	TTTTTAAACAATCTTGACAACTTTGCAGAAATAAATACAAATCT	3923	
Db	56050	TGTGAAGTTTTTTA	ATCAAAAAAGAAATAAATTTGGACACCATGTTTCATGCTATTAATCT	56109	
QY	3924	--TGCATTTCTGCT	TTTTTCACTTATCACCTTGTATGACTTTTTTTCATATTTGCCTCAAACTCT	3981	
Db	56110	CAGCCCTTTGAGAG	GCCAATGCAGGAGGATCGCTTGAGCCTAGAAAGTTTGAGACCCAGCCT	56169	
QY	3982	T-----TATTTGTT	ACTGTTTTTTCATTTTACTATTTTAGTCACTGAATAATATGCTTA	4036	
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QY	4037	ATTTGCTTATACAT	CCTCCTGCTCCACTTTTAGAAGGCCAAATTTTACAAAT-----	4086	
Db	56230	AGCTGGAAGTCCAT	CTTTGTTCCCTGGCAAAAGCCAGCCACTTTTAATGAATTCAGCTGGCA	56289	
QY	4087	-----	-----CTGATGAAAGCTATGAACCC	4106	
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QY	4167	CAACTAAGACAA	GAAAACCTTGCATTAGAGGATGTTTTGTTCATATTAATTAATAATAAATAA	CTCA 4226	

Db	56410	GAGTTTGAGACCAGCCTGGGCAACATGGCAAAACCCCTCTCTATAAAAAACACAAAAAAG	56469
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Db	56470	GCCAGGAGCACTGGCTCAGCCCTGTAATCCCATCACTTTGGGAGCCGAGGCGGTGGAT	56529
Qy	4287	CACCTTGAGTGAGAAGTTCGAGACCAAGCCTGGTCAATATGGTGAACCCCTATCTCTACTA	4346
Db	56530	CAC--AAGTTCAGGAGATCGAGACCATCTCTGGCTAACATGGTGAACCCCATCTCTACTA	56587
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Qy	4406	GCTGAGGCAAGAGAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCA	4465
Db	56648	GCTGAGGCAGGAGAAATGGCGTGAACCTGGAAAGCGGAGCTTGCACTGAGCCGAGATCAG	56707
Qy	4466	CCACTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATA	4516
Db	56708	CCACTGCAATCCAGCCTGGGCAACAGAGTGAGACTCCTACTCAAAAAAAA	56758
RESULT 33			
US-10-995-561-13251/c			
; Sequence 13251, Application US/10995561			
; Publication No. US20050272054A1			
; GENERAL INFORMATION:			
; APPLICANT: CARGILL, Michele et al.			
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH			
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF			
; TITLE OF INVENTION: DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001559			
; CURRENT APPLICATION NUMBER: US/10/995,561			
; CURRENT FILING DATE: 2004-11-24			
; NUMBER OF SEQ ID NOS: 85702			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 13251			
; LENGTH: 38023			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-995-561-13251			
Query Match 7.1%; Score 353.2; DB 10; Length 38023;			
Best Local Similarity 52.0%; Pred. No. 4e+02;			
Matches 1199; Conservative 20; Mismatches 968; Indels 117; Gaps 16;			
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Db	32335	AAAAAGAGTGGCAGCCGGGCACAGTGGCTACGCCCTATAATCCTAGCACTTTGGGAGGCC	32276
Qy	2340	GAGGCGGCGGATCACTTGAGGTCAGGATTCGAGACCAGCTGGCCCAACATGGTGAAC	2399
Db	32275	AAGCAGGTGGATCAKCTGAAGTCAGGAGTTCMAGACCAGCCTGGCCAAACATGGTGAAC	32216
Qy	2400	CCTGCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCAGCGCCTGTAAACCCC	2459
Db	32215	TCTATCTCTACTAAAAAATATAAACATTAGGCCAGGTGTGGTGGCAGGTGCCTGTAATCCC	32156
Qy	2460	AGCTACTTGGGAGACTGA-GTTGGAGGTTTCAGTGAGCCAAAGTCGTGTCACTGCTGTCC	2518
Db	32155	AGCTACTCGGAGGCTGAGGCAGGAGAAATCCCTTGAAACCCAGGAGCGGAGGCTGCAGTG	32096
Qy	2519	AGCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAAATGCTTTCAATAAATATATGA	2578
Db	32095	AGCCAAGATCA-----TGCCACTGCATCTCCAGCCTGGGTGACAGAGAGACTC	32047
Qy	2579	TAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTTCTCTGAAAGCATCTTGGCGAAG	2638
Db	32046	CCATCTCAAAAWTTTTTTTTTAAATGCAGAGGTTGGACTGCTACCTATACTCTAATTT	31987
Qy	2639	TCATCCCCACCTGTTCTCTGAGAGTGGGAGGTTGAGGGCTGACCTATTGCTCTGCACTTAC	2698

Db	31986	CTATTCTGGAGTGATTCTCTGGAGAGKCTAGGTAAAGACTGAAAAGGCAYTGTGTACGTCC	31927
Qy	2699	TCCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACACTGCTAYG	2758
Db	31926	ACCTGTCTAT-----CTCACTTGGACAAGAATCCAGGAGAAACTATTGAACCTGAGGTG	31875
Qy	2759	ACCAGGCCAAG---AAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCACA	2815
Db	31874	ACAAAGTTATGATCAATGTGGTGATCTGAGGTGTATTAAAACACTGAGCTCTTTCCAGT	31815
Qy	2816	CCTATTCATACTCTGTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCT	2875
Db	31814	CACAAACACTGCAAGCAGGTGTTTCTAACAAAGCCTTAAGCTGATGTCGACATGCCCCA	31755
Qy	2876	TGACCTATGAATTCFAGTTGGTTCTCAGTAGGCCGACGTCTCCTTTAATCCTCAGAAACAGCC	2935
Db	31754	CAATTCTTGTCACTCACCAAGCAGCATCCCCGCTGCTCCATGCTAGAAGCAGGCAAGGAG	31695
Qy	2936	ATGATTTAGTGTTAATTTTCTTGGTTCTTGGGACGTGTCTCCTTTAATCCTCAGAAACACA	2995
Db	31694	CTGCAGGTGCGTATAYGATGGAGGTGAGGGAGACAGTGGCATGGAATGAATCAACTCAG	31635
Qy	2996	CTATGGGATAGGTACAATTATCCTCACTTAA--CAGATAAGAAAACTGAGGCTCAGAAAG	3053
Db	31634	TTTGGGAGCAGGGAGAACTTTATTGAGGTTATGAATATATTCTACTTGAAAACTGGAAAG	31575
Qy	3054	CTGAGCTATTTGCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTGTG	3113
Db	31574	TAAAGTGTATGAATTTGTGGCTTATGGTAACCTTTGTTAAGCATCTTTCTTTTCTTTT	31515
Qy	3114	TTGTTGTTTAGAGACAGGGTCTTGTCTC-TGTACCCAGGTCATGAGCACAGTGGTGCAACC	3172
Db	31514	TTTTTTTGGTGAGACACAGATTCACTCTTGTCCCCCAGGCTGGAGTGCAATGGCGTGATC	31455
Qy	3173	ATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAA	3232
Db	31454	TCGGCTCACTGCATCCTCTGCCTCCCAAGTTCAAGCGATTCTCGTACCTCAGCCTCCCGA	31395
Qy	3233	GTAGCTGGGACTACGAGCGTGCACCACCACCGCCTGGCTAATTAATAAAATTTTTTTGTAG	3292
Db	31394	GTAGCTGGGATTACAGGCATGTGCCAGCATGCTTGGCTAATTTTGTGTA--TTTTTAGTAG	31338
Qy	3293	AGACTGGGTCTTACTACGTTGGCCAGGCTTGCT-TAAACTCCTGGCTTCAAGCAATCCT	3351
Db	31337	AGATGGGTTTTCACCGTGTGTGCCAAGGCTGATCTCAAAACTCCTGACCTCAGGTGATCTG	31278
Qy	3352	CCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGTGAGCCACCATGTGCGGTACTT	3411
Db	31277	CCCGCCTCAGCCTCCCAAAGTGTGGGATTACAGGCTTGAGCCACTGYGCCCGGCTTTT	31218
Qy	3412	ATTTCTTTACATTCATCTTCCAATAGAAATGTAAGATCCACAGAACAGGGATTACTGCC	3471
Db	31217	TTTTTTTTTTTTTTTTTTTAAATTATTGAGACGGAGCCTTGGCTG-----	31174
Qy	3472	TATTTTCTTCCTTTCTTTTGTAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTTCAG	3531
Db	31173	-----TCACCGAGGCTGGAGTGCACCTGGCACTGTCTYGG	31140
Qy	3532	CTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTTCTCCTGCCTAAGCCTCCTGAGTAG	3591
Db	31139	CTCACTGCAACCTCCGCCTCCCGGTTCAAGCGAATTTCTCTGCCTCAGCCTCCCAAGTAG	31080
Qy	3592	CTGGAATTACAAGCGTGCACCACCATGTCTTGGCTAATTTTTTGTATTTTTTAGCAGAGATG	3651
Db	31079	CTGGGATTACAGGCATGTGCCACCATGCCAGCTAA-TTTTTGTATTTTAGTAGAGGTG	31021
Qy	3652	GGGTTTTACCATGTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTATCTGCCTGCC	3711
Db	31020	AGGTTTCAGCATGTGGCCAGGCTGGTCTTGAACCTCTGACCT--TGTCATCTCCCAACC	30963
Qy	3712	TCAGTCTCCCCAAAGTCTGGAATTATAGGCGTGAGTCACTGTGCCTGGCCGATTACTGTC	3771

Qy	3173	ATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAA	3232
Db	53090	TCGGCTCACTGCATCCTCTGCCCTCCAGGTTCAAGCGATTCTCGTACCTCAGCCTCCCGA	53149
Qy	3233	GTAGCTGGGACTACGAGCGTGCACCACCAGCCTGGCTAATTAAAAAAATTTTGTAG	3292
Db	53150	GTAGCTGGGATTACAGGCATGTGCCAGCATGCTTGGCTAATTGTGA--TTTGTAGTAG	53206
Qy	3293	AGACTGGGTCTTACTACGTTGGCCAGGCTTGCTCT-TAAACTCTGGCTTCAAGCAATCCT	3351
Db	53207	AGATGGGTTTACCGTGTTCCTCAAGGCTGATCTCAAAACTCTGACCTCAGGTGATCTG	53266
Qy	3352	CCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGTGAGCCACCATGTGCCGCTACTT	3411
Db	53267	CCCGCCTCAGCCTCCCAAAGTGTGGGATTACAGGCTTGAGCCACTGYGCCCGCCTTTT	53326
Qy	3412	ATTCTTTTACATTCATCTTTCCAAATAGAAATGTAAGATCCACAGAACAGGATTACTGCC	3471
Db	53327	TTTTTTTTTTTTTTTTTAATTATTGAGACGGAGCCTTGCCTG-----	53370
Qy	3472	TATTTTCTTCTCTTCTTTTTTGTAGACAGAGTCTCACTTTCATCACCTCAACCTCCGTTACG	3531
Db	53371	-----TCACCGAGGCTGGAGTGCACACTGGCACACTGTCTYGG	53404
Qy	3532	CTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCTCGCTTAAGCCTCCTGAGTAG	3591
Db	53405	CTCACTGCAACCTCCGCCCTCCCGGTTCAAGCGATTCTCTCGCTCAGCCTCCCAAAGTAG	53464
Qy	3592	CTGGAATTACAAGCGTGCACCACCATGCTTGGCTAATTTTTTGTATTTTAGCAGAGATG	3651
Db	53465	CTGGGATTACAGGCATGTGCCACCATGCCAGCTAA-TTTTTGTATTTTAGTAGAGGTG	53523
Qy	3652	GGGTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTGCC	3711
Db	53524	AGGTTTCAGCATGTTGCCAGGCTGTCTTTGAACTCCTGACCT--TGTCATCCTCCACC	53581
Qy	3712	TCAGTCTCCCAAAGTCTGGAATTATAGCGGTGAGTCACTGTGCCTGGCCGATTACTGTC	3771
Db	53582	TTGGCTCTCCCAAAGTCTGGGTTTACAGCGYGAGCCACSCGCGCGGTGTTATGTCTCA	53641
Qy	3772	TATTT-----TTCTTTATTGCTATATATATATATATATATATATATATATATATATAT	3808
Db	53642	TCATGGCACTTAAGAGATGCTTTAACAAACCTTTCTCTACAATGTTCTCTCAGATTTTTCAGAG	53701
Qy	3809	TGTCAGACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTTAGATATAAAC	3868
Db	53702	CTTAATTGATCTAGCATCTGGTTCCTAAAATTCTGAGTCAATCAGAAAGCCAAACTTGAAT	53761
Qy	3869	TTTCTTTTCTTTTTTTTAAAAACAATCTTTGACAACTTTTGCAATAATAATACAAATCTTGCA	3928
Db	53762	GCTTTTGGAAAAGAGCYAGCCTCATACCACTTCAGTTGGGAAGGGGAGTACTGAGGTGTAC	53821
Qy	3929	TCTGCTTTTTCACCTTATCACCTTGTGTATGACTTTTTTCATATATGCTCAAAACCTTTATTGT	3988
Db	53822	CTTGGCAGGACAGTGGAAATGATTGCT-GGTTCCTTAGTTTGTCTATACCAAGAACTGC	53880
Qy	3989	TACTGTTTCTTCTTACTATTTTTAGTCACTGAATAATATGCGTTAATTTGCTTTATAC	4048
Db	53881	TATAACATGTTTCTAAACCAGGGCTATGCAAGCACTAGAGTTCCTGACCAGCAATGCCAA	53940
Qy	4049	ATCCTCTGCTCCACTTTAGAAGGCCAAAATTTACAAATCTGATGAAGCTATGAACCTTC	4108
Db	53941	ACCAGTGGCATACAAATTCAAAATACTGTATMCAGGCCCTGACTCCAGCCCAACCAAGG	54000
Qy	4109	TCCCCAGAGAAATACACACACACACACTCACACAGTTTTTTTTTAAATGTTTGCA	4168
Db	54001	CTGGAGGGCATCCAGGGGATGTGTTTCCCAAGGGGTAGCATCTTGGTTATGTGAGATC	54060
Qy	4169	ACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAAT-----	4213
Db	54061	ACCAAGACACCAARCTGTTTTTATGAGCTGAATCCTCAGCTTGTGTGATTTGTGGCT	54120

Qy	4214	-TAAAAATAACTAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTGGAAGTC	4272
Db	54121	GATAAAAAARTACAGCAGGGCCCAGTGGCTACRCCTGTAAATCCCAACACTTTGGGAGGC	54180
Qy	4273	CAAGGTGGGTGGATCACTTGAGGTGAGAAAGTTTCGAGACCAGCCTGGTCAATATGGTGAAA	4332
Db	54181	TGAGGCAGGCAGACCACCTGAGGCCRGAGTTTGAAAAC'TAGCCTGGCCAACATGGTGAAA	54240
Qy	4333	CCCTATCTCTAC-TAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCC	4391
Db	54241	TCCTGTATGTACTTAAAAATACAAAAATTACCCAGGCATATTTGGTGAGTGCCTGTCTATCC	54300
Qy	4392	CAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAG-AGSTTGCAG	4450
Db	54301	CAGCTACTCGGAAGGCTGAAGCAGGAGAATCGCTTGAATCTAGGAGGCTGCAGSTTGCAG	54360
Qy	4451	TGAGCCGAGATCCCACCACCTGCACCTCCAGCCTGGCGGACACAGCGAGACTCTATCTCAAA	4510
Db	54361	TGAGCTGAGAAAGGCCCACTGCACCTCCAGCCYGGGAGACGGAATCTCACTCTGTCTAGTCA	54420
Qy	4511	AAAAATAATAATAATAAAGGA	4534
Db	54421	CAACAACAACAAAAAATAGAGCA	54444
RESULT 35			
US-11-114-798-46/c			
; Sequence 46, Application US/11114798			
; Publication No. US20060035246A1			
; GENERAL INFORMATION:			
; APPLICANT: WU, RINA			
; APPLICANT: MARQUEZ, ABBEY			
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND			
; TITLE OF INVENTION: COMPOSITIONS			
; FILE REFERENCE: 0618.011.0004			
; CURRENT APPLICATION NUMBER: US/11/114,798			
; CURRENT FILING DATE: 2005-04-26			
; PRIOR APPLICATION NUMBER: 10/173,525			
; PRIOR FILING DATE: 2002-06-17			
; PRIOR APPLICATION NUMBER: 09/952,851			
; PRIOR FILING DATE: 2001-09-14			
; NUMBER OF SEQ ID NOS: 58			
; SOFTWARE: PatentIn Ver. 3.3			
; SEQ ID NO 46			
; LENGTH: 85980			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic			
; OTHER INFORMATION: nucleotide sequence			
US-11-114-798-46			
Query Match 7.1%; Score 353; DB 18; Length 85980;			
Best Local Similarity 59.1%; Pred. No. 2.2e+02;			
Matches 889; Conservative 1; Mismatches 521; Indels 94; Gaps 13;			
Qy	3104	TTTTTTTTTGTGTTTGTAGAGACAGGGTCTTGCTCTGTCA-CCCAGGCATGAGCACAG	3162
Db	38778	TTTTTCTTTTTTTTTTGAGATAGAGTCTTGCTGTCAACCCAGGCTGAAGTGCAG	38719
Qy	3163	TGGTCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTC	3222
Db	38718	TGGTGCATCTCGGCTCACTGCAACTTCTGCCTCCTGAGTTCAGTGATTTCTCTACCTC	38659
Qy	3223	AGCTCCCAAGTAGCTGGGACTACGAGCGTGCAACCAACCCAGCCTGGCTAATTAACCAAT	3282
Db	38658	AGCTCCCGAGTAGCTGGGATTACAGGCTCCCAACCAACCATGCCTTGCTAATTTTGTA--	38601
Qy	3283	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCA	3342
Db	38600	TTTTTAGTAGAGATGGGGTTTCACTATGTTGGTTAGGCTGCTCTGGAACCCCTGACCTAA	38541
Qy	3343	AGCAATCCTCCTACCTTGGCATCCCAAAAGTGTGGGATTACAGGGGTGAGCCACCATGTG	3402


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; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 168656
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-59

Query Match
Best Local Similarity 7.0%; Score 352.2; DB 17; Length 168656;
Matches 871; Conservative 1; Mismatches 524; Indels 75; Gaps 13;

QY 3098 TTTGGGTTTTTTTTTTGTTGTTTATAGACAGGGTCTTGCTCTGCACCCAGGCATGAG 3157
||| | ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 132627 TTTTGTGTTTTGTTTTTTTTTTGAGACGGAGTCTCACTCTGTGCCCCAGGCTGGAG 132568

QY 3158 CACAGTGTGCAACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGGATCTGCTG 3217
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132567 TGCAGTGGCAGCATCTCGGCTCACTGCAAGCTCCACCTCCGGGTTCAAGCCATTCTCCT 132508

QY 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACAGCCTGGCTAATTAAA 3277
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132507 GCCTCAGCCTCCTGAGTAGCTGGGACAACAGGCACCCACCAAGCTCCGGCTAATTTT 132448

QY 3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACCTCGG 3337
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132447 TGTA-TTTTGTAGTAGACAGGGTTTCACTGTGTTAGCCAGGATGGTCTCGATCTCCTGA 132389

QY 3338 CTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACC 3397
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132388 CCTCATG--ATCCACCACCTCGGCCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACC 132331

QY 3398 ATGTGGGGTACTTATTTCTTTTACATTCATCTTTTCCAATGAATGTAAGATCCACAGAA 3457
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132330 GCGCCCGGC-----CTTTGTGTGTTTTTTTTTTTAGATGGAGTCTCATTTCTGTCA 132280

QY 3458 CAGGGATTACTGCCTATTTTCTTCCTTCTTTTTTTTGAGACAGAGTCTCACTTCATCACT 3517
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132279 CAGGCTTGAGTGAATGGTGCAGC----- 132255

QY 3518 CAACCTCCGTTCAGCTCACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTA 3577
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Db 132254 -----TCGGCTCACTTCAACCTTCACTTCCACCTCCAGGTTCAAGCGATTCTCCTGCCTC 132205

QY 3578 AGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTTGTAT 3637
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132204 AGCCTCCCGAGTAGCTGGGACTACAGGCGCATGCCACCACACCTGGCTAA-TTTTTGCAT 132146

QY 3638 TTTTAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAA 3697
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132145 TTTTCTTAGACAGAGGTTTTCAC--TGTAGCCAGGCTGGTCTCGAACTCCTGACCTC-- 132090

QY 3698 GTGATCTGCCCTCAGTCTCCCAAAGTGTCTGGAATTATAGGCGTGAGTCACTGTGCCT 3757
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132089 GTGATCTGCCCTCAGCCTCCCAAAGGCTGGGATTACAGGCATGAGTCACCATGCCT 132030

QY 3758 GGCCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACA 3817
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 132029 GGCTGAGTCTGCGTTCTTAATGTCTCGGCTGGTGACTTTCCACCCATACCATATCCAATGT 131970

QY 3818 TATA-GTAGTGTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTT 3876
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Db 131969 CACAGGGTCTGCTCCGTCAACCCAGGCTGGAATGCAGTAGCACAATCATAGGTGGCTGTA 131910

QY 3877 TCTTTTTTAAACAAATCTTGACAACTTTGCAGAAATAAATAACAATC---TTGCATTCTG 3932
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Db 131909 ACTTGGAACCTCAAGGTTCAAGCAATCTGCCACAGCTTCCAAATAGCTGTGACTACAG 131850

QY 3933 CTTTTTCACTTATCACCTTGTTATGACTTTTTTTCATATTGCTCTCAACCTTTATTGTTACT 3992
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Db 131849 GCCCACACCACCATGCCCAGCTAAATTTTTTTTTTTTGTGTTTGTAGTAGACAAAGTCTCACT 131790

QY 3993 GTTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCC 4052
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131789 GTGTTACCCAGGCTGATCTGGAACGCCTAGGTTCCAGTGATCCTCCTGCTTAGCCTCCT 131730

QY 4053 TCCTGCTCCACTTTAGAAGGCCAAATTTTACAAATCTGATGAAAGCTATGAACCTCTCTCC 4112
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131729 AGAGTGTCTGGGATTACATGTGTAAGCCACTACACCCAGTCCCAATGTTCTCTTCTATAA 131670

QY 4113 CAGAGAAATACACACAC-----ACACACACACTCACACACAGTTTTTTTTTAAATGTTTGC 4167
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131669 CAAATATTTTGCAACACTAATATCCCAAAGTGAATGAACAGATAATATAACCTGCTGG 131610

QY 4168 AACTAAGACAAGAAACCTGCAATTAGAGGATGTTGTTTCATATTAATTTAAAAATAAATCAG 4227
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Db 131609 ACACATGATTTCAAAAAACAAATCAATATGATGTCCTTGATTATAA-AAAAAGACAAATAGG 131551

QY 4228 TTGGGCACAGTGACTCAAGCCTGTAACCCACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATC 4287
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Db 131550 CCGGGCACGGTGGCTCACACTTGCAATCCCAGCACTTTGGTAGGCCAAGCGGGTGGATT 131491

QY 4288 ACTTGAGGTGAGAAGTTTCGAGACCAGCCTGGTCAATATGTTGAAACCCATCTCTACTAA 4347
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131490 ACCTGAGGTTAGGAGTTCAAGACCAGCCTGGCCAAACATGGGAAATCTCATCTCTACTAA 131431

QY 4348 AAATACAAA-AATTAGCTGGGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGG 4406
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131430 AAATATAAAGAAATTAGCCAGGCATGATGGTGGGCACCTTTAATCGCAGCTACTCAGGAGG 131371

QY 4407 CTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCAC 4466
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131370 CTGAGGCAGGAGAAATTGCTTGAACCCGGGAAGCAGAGGTTGCAGTGAGTAAGAGATGC 131311

QY 4467 CACTGCACCTCCAGCCTGGGCGA-CACAGCGAGACTCTATCTCAAAAAATAAATAATAA 4525
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131310 CATTGCACTCCAGCCTGGGCAATGAGAGTGAACCTCCGTCTCAAAAAAAAAAAGACA 131251

QY 4526 AATAAAGGATCGGAGAGAAAAACAAACTAATA 4556
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Db 131250 AATAGAAGGATGCGGTTTCAATATGCAATA 131220
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RESULT 38

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US-11-112-908-58/c
; Sequence 58, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 170285
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-58
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Query Match 7.0%; Score 352.2; DB 17; Length 170285;
Best Local Similarity 59.2%; Pred. No. 1.3e+02;
Matches 871; Conservative 1; Mismatches 524; Indels 75; Gaps 13;
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[illegible]

RESULT 39
US-11-112-908-38/c
; Sequence 38, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 171162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-38

	Query Match	7.0%;	Score 352.2;	DB 17;	Length 171162;
	Best Local Similarity	53.4%;	Pred. No. 1.3e+02;		
	Matches 1217;	Conservative	2;	Mismatches 915;	Indels 147; Gaps 17;
QY	2278	AAAAATCGCTTTTCAGGCCAGGCGCGGTGGCTCATGCCTGTAAATCCCAGCACATTG---GG	2334		
Db	165308	AAATAAACTTTTTTAGGCCAGGCATGATGGCTGACGTTTGTAAATCTCAGCACCTTAGGGAGG	165249		
QY	2335	AGGCCGAGCGCGGCGGATCACTTGAGTCAAGGAGTTCGAGACCAGCCCTGGCCAAACATGGT	2394		
Db	165248	AGGCCAAGGCTGGAGACTGCTTGAGCCTAGGCATTCAAGACCAACCTTGGCCAACAAAGT	165189		
QY	2395	GA-AACCCCTGTCTCTACTAAAAAATACAAAAAATTAGCCGGACATGGTGGCGAGCGCCTGT	2453		
Db	165188	GAGACCCCTGTCTCTACAAAAAATTTAAAAAATTAGCCAGGCATGGTGGCATGCAACCTAT	165129		
QY	2454	AACCCCAGCTACTTTGGGAGACTGAGTTGG-----AGGTT	2487		

Db	165128	GGTCCCAAGTACTTGGGAGGCTGAGGCAGGAGGATTGCTTTGCACCCAGGAGGCAAGGTT	165069
Qy	2488	TCAGTGAGCCAAGGTCGTGTCACTGTGTCCAGCCTGGGTTAACAGAGCAA	2547
Db	165068	GCAGTGAGCCATGATCGCACCACTGCACTCCAGCCTGGCGAAAGAGTGAAACTCTCAAA	165009
Qy	2548	AAAAAAAAAATGCTTTCAATAAATATATATGATAAAAGGACTTATATTTTTCAAGCCATA	2607
Db	165008	AAAATAATAATAATAAAATAAAAAATAAAAAATAATAAAATAAATGTCTTACTCTTATTGA	164949
Qy	2608	GGATCATTTCTCCTGAAGCATCTTTGSGGAAGTCATCCCCACCTGTTCTCTGAGAGTGGSCA	2667
Db	164948	AAAGAAAAAAATACATTAGGTGACCTGAAAAAATTTCTGGATTCTTAGCTACTATTGACGG	164889
Qy	2668	GGTGAGGGCTGACCTATTGGCTCTGCACCTTACTCCTATCTCAGCTGTCCCTCCCACITTTCC	2727
Db	164888	GAGCTTCCTCTATGAGCCCATCTGAAATCAGTGATTTTTCTGGCAGGACAGGCTGAGGCA	164829
Qy	2728	AGGTGCTGCCAGACACATGACAACTGCTAYGACCAGGCCAAGAAGCTGGACAGCTGTAAA	2787
Db	164828	TTGAACCTGC--AAACCTGAGCAATGTCAGACCCCTTTTTTAAATCTGGACCCACAGAT	164772
Qy	2788	TTTCTGTGACAMMCCGTACACCCACACCTATTTCATACCTGTCTCTGGCTCGGCAATC	2847
Db	164771	ACCATCTAGCCACCTCTGTCTGAAACACTGCAGTAAAAAGT--TACTTCAGATGGTAACTC	164714
Qy	2848	ACCTGTAGCAGTAGGTTTATCCCTTCCTTGACCTATGAATTC	2907
Db	164713	GGCATCAGCATAATAGGAAGTTCAAAACACAGGCCCTGAGCTGTGTATAGTATTGGTTT	164654
Qy	2908	CCGGGGGGAATAATAGTAACAACAGCCATGATTTAGTGTTAAATTTCTTTGGTTC	2967
Db	164653	TAAGGTTCTTATCCAGATAATCCCAGATATTATTAACCTTTTTTTTCGTTGGCTGGGCGC	164594
Qy	2968	AGTGTCTCCTTTAATCCTCAGAAACACACTATGGGATAGGTACAATATCCTCACTTAAC	3027
Db	164593	AGTGGTTTCAT-----GCTTGTAAATCCCAGCACITTTGG	164562
Qy	3028	AGATAAGAAAACTGAGGCTCAGAAGGCTGAGCTATTTGCCAAGATCACACAGCTTGTA	3087
Db	164561	GAGGCTGAGGTGGCGGATCATGAGGTCATGAGTTTGAGACCAGCCTGGCCAACATGATG	164502
Qy	3088	GTGGTGACAGTTTGGGTTTTTTTTTGTGTGTTTAGAGACAGGGTCTTGCTCTGTCA	3147
Db	164501	AAACCTTGCTCTACTAAAAATTA	164442
Qy	3148	CAGGCATGACACAGTGGTGCAACCA-TAGGTCACTGCAGCCTCAACCTCCTGAGCTCAA	3206
Db	164441	CCCAGCTACTCAGGAGGCTGAGGCAAGTTGCTCACAGCAACCTCCACCACCCAGGTTCAA	164382
Qy	3207	GGGATCTGTGACCTCAGCCCTCCCAAGTGTGGACTACGAGCGTGCACCCACCGCCT	3266
Db	164381	CGGATTCTCTGCCTCAGCTTCCCAAGTAGCTGGGATTACCGGTGTGTGCCACCCACGCC	164322
Qy	3267	GGCTAATTA	3326
Db	164321	AGCTAATTTTGCATTTTTTAT--TAGAGATGGGGTTTCACCATGTTGACCAGGATGGTCT	164264
Qy	3327	TAAACTCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGTCTGGGATTACAGG	3386
Db	164263	TGATCTCCTGACCTC--GTGATCCGCCACCTTTGGCCTCCCAAGTGTCTGGGATTACAGG	164206
Qy	3387	GGTGAGCCACATGTGCGGCTACTTATTTCTTTTACATTCATCTTTTCCAATAGAAATGTAA	3446
Db	164205	CATGAGCCACACGCCCCGACCTATTTTATTCTTTTGAGACTAAGTCTCACTCTGTCA	164146
Qy	3447	GATCCACAGACAGGGATTACTGCCTATTTTCTTCTCTTTTGTGAGACAGAGTCTCA	3506
Db	164145	CC-----AAGG	164140
Qy	3507	CTTCATCACCTCAACCTCCGGTTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTTCAAGYGAT	3566

Db	164139	CTGGAGTACAGTGGCATGATCTTTGGCTCACTACAACCTCTGCCTCCCAAGTTCAA-CAAT	164081
Qy	3567	TCTCCTGCCTAAGCCTCCTGAGTAGCTGGAATTTACAAGCGTGCACCAACCATGCTTGGCTA	3626
Db	164080	TCTCATGCTTCAGCTTCCGAGTGGCTGGGATTACAGGCGTGCACCAACACCCAGCTA	164021
Qy	3627	ATTTTTTGTATTTTAGCAGAGATGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACT	3686
Db	164020	A-TTTTTGTATTTTAGTAGAGATGAGGTTTCACCATGTTGACCAGGCTGGTCTCGAACT	163962
Qy	3687	CCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAGTGTGGAATTTATAGGCGTGAG	3746
Db	163961	CCTGACCTCAAGTGATCCACCTTCCTTGGCCTCCCAAGTACTGGGATTACAGGCATGAG	163902
Qy	3747	TCACTGTGCCTGGCCGATTACTGTCTATTTTCTTATTGCTATATCCCCAGATCTAGAGC	3806
Db	163901	CCACCACGCCCAGCAAGCCATT--TAATATACATCCAAATATGAGTTAATTGTTACAAC	163845
Qy	3807	AGTGTCTGACATATAGTAGGTGCTCAATAATAATAAATTAATGATGAATGCACAGCCTAGATATA	3866
Db	163844	TTTATAAGACTTTTTTGCAGGGC-----GCAGTGGCTCATGCCTGTAATCCCAGCACTTG	163790
Qy	3867	ACTTTCCTTTTCTTTTAAACAATCTTGACAACCTTTGCAGAAATAAATAACAATCTTGC	3926
Db	163789	AGAAGCGGAGGCAGTAGATCAGTTGAGGTGAGGAGTCAAGACCAGCCCGACCGCTGG	163730
Qy	3927	ATTCTGCTTTTTTCACCTTATCACCTTGTATTGACTTTTTTCATATTGCCCTCAAACTTTATT	3986
Db	163729	TGAACCTTGTCTCTACTAAAAA	163670
Qy	3987	GTTACTGTTTTTTTCAITGTTACTATTTTTAGTCACTGAATAATATGGCTTAAATTTGCTTAT	4046
Db	163669	GGCACACACCTGTAAATCCCAGCTACTCAGGAGGCTGAGGCA-----GGAAATCACTTGG	163615
Qy	4047	ACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACA	4106
Db	163614	ACCCGGGAGGTGGAGATTGCAGTGAGCCGTGATTTGCACACCCAGGGCGACAGAGCAAGACA	163555
Qy	4107	TCTCCCCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTTAAATGTTTG	4166
Db	163554	CCATCTCA	163502
Qy	4167	CAACTAAGACAAAGAACTGCATTAGAGGATGTTTGTTCATATTAAATTA	4226
Db	163501	CAAAATTACAAAATTTACTTCAAAATAAAAAGTTTAAAGAAAAAAGAGATCAG	163442
Qy	4227	GTTGGGCACAGTGACTCAAGCCTGTAACCAACAGTACTTTGGAAGTCCAAAGGTGGGTGGAT	4286
Db	163441	GCCAGGCATGGTGGCTCATGCCTATA--ATAGGACTTTGGGAGGCCAAGGTAGGTGGAT	163385
Qy	4287	CACCTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTA	4346
Db	163384	CACCTGAGGTGAGAAAGTTCGAGACCAGCCTGACCCACATGTTGAAACTCTGTCTCTACTG	163325
Qy	4347	AAAAACA	4406
Db	163324	AAAAACA	163265
Qy	4407	CTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCAC	4466
Db	163264	CTGAGGCAGAAAGATCGATTGAACCTGGGAGGTGGAGGTTGCAGTGAGCCGAGATCACGC	163205
Qy	4467	CACCTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGCTCTCA	4526
Db	163204	CACCTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCGCTCTCA	163145
Qy	4527	A	4527
Db	163144	A	163144

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/ Sequence 13421, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13421
; LENGTH: 403278
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)....(403278)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13421

Query Match          7.0%; Score 352.2; DB 10; Length 403278;
Best Local Similarity 52.6%; Pred. No. 72;
Matches 770; Conservative 2; Mismatches 614; Indels 79; Gaps 13;

QY 3114 TTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGATGAGCACAGTGGTGCAACCA 3173
    ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158895 TTTTAATCTGAGACAGGGTCT--CACTGTGCCCCAGACTGGAGTGCGAGTGCGCATCA 158838

QY 3174 TAGTCACTGCAGCCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAG 3233
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158837 TGGCTCACTGCAGCCTCAAAACACTTGGGCTCAAGTGAT--CTTGCCTCAGCCTCCCAAG 158781

QY 3234 TAGCTGGGACTACGAGCGGTGCACACCACCGCTGGCTAATTAATAAATAATTTTGTGTA 3293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158780 TAGCTAGAACTATAGGTTTGTGCCATCGTGCCTGGCTAAATTTTAAATTTTATAGA 158721

QY 3294 GACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCAAGCAATCCTCC 3353
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 158720 GA--TGGGAGTCTTATGTTGCTCAGGCTGGTCTGGAACCTCTG-----GCT 158680

QY 3354 TACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTAT 3413
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158679 -----TGGCCTCCCAAAGTGCTGAGATTATAGGCATGAACCA-----CTGCCACCGT 158632

QY 3414 TTCTTTACATTCCATCTTTCCAAATAGAATGTAAGATCCACAGAACAGGGATTACTGCCTA 3473
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 158631 TCAGGAGCTTTCTTTTTTTTTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 158572

QY 3474 TTTTCTTCCTTTCTTTTTTTTGACACAGAGTCTCACTTCATCACTCAACCTCCGTTCAGCT 3533
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 158571 AGTTTCGCCCTTGTGTGCCAGGCTGGAGTGCAATGGCATGATCTCG-----GCT 158523

QY 3534 CACTGCAACCTCTGCCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCT 3593
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158522 CACTGCAACCTCTGCCTCCTCGGTTCAAGTGATTCTCCTGCCTCAACCTCCCCAGTAGCT 158463

QY 3594 GGAATTACAAGCGTGCACACCACCATGCTTGGCTAATTTTGTATTTTGTAGCAGAGATGGG 3653
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158462 TGGATTACAGGCATGTGCCACCACGCCAGCTAA--TTTGTATTTTGTAGTAGAGATGGG 158405

QY 3654 GTTTTACCATGTTGCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTGATCTGCCCTGCCCTC 3713
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 158404 GTTTCTCCATGTTGGTCCGGTGGTCTCAAAACACCTGACCTCAGGTGATCCACCTGCCCTC 158345

QY 3714 AGTCTCCCAAAGTGCGAATTATAGGCGTGAGTCACTGTCCTGGCCGATTACTGTCTA 3773
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 158344 AGCCTCCCTAAGTGCTAGGATTACAGGCGTGAGCCACCATGCCCCGCNNNNNNNNNN 158285

QY 3774 TTTTCTTTATTGCTATATCCCCAGATCTAGACGAGTGCTGACATATAGTAGGTCCTCAA 3833

Db 158284 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 158225
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QY 3834 TAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTAAACAAT 3893
Db 158224 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 158165

QY 3894 CTTGACAACTTTGCAGAAATAAACAATCTTGCATTTCTGCTTTTTCACITATCACCTTGT 3953
Db 158164 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 158105

QY 3954 TATGACTTTTTCATATATGCTCAACCTTTATTTGTTACTGTTTTCATGTTACTATTT 4013
Db 158104 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 158045

QY 4014 TAGTCACTGAATA-----ATATGGCTTAATTTGCTTATACATCCTCCTGCTCCA 4062
Db 158044 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 157985

QY 4063 ----CTTTAGAGGCCAAATTTACAAATCTGATGAAAAGCTATGAACCTCTCCCCAGAGA 4118
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 157984 GAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCGAAGGTTACAGTAAGCAAGATT 157925

QY 4119 AATACACACA---CACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGA 4175
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 157924 GCGTAAATCATTTTCAAAACAGAAACATTACCAATATCCTAATTTGCTTTTAGACGCTCAAC 157865

QY 4176 CAAGAAACCTGCAATTAGAGGATGTTTGTTCATATTAATAATAAATAAATACTCA-----G 4227
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 157864 TCAACACAAGGCATTAAAGTAAAGCTACAGTAAATAAATAATGATTATATAAGTGATAAAACAGG 157805

QY 4228 TTGGGCACAGTGACTCAAAGCCTGTAAACCACAGTACTTTTGAAGTCCAAGGTGGTGGATC 4287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 157804 CTGGGCGTGGTGGCTCATGCTGTAAATCCCAGCACTTTGGGAGGCTAAGGTGGCGGATC 157745

QY 4288 ACTTGAGGTGAGAGTTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCTACT-- 4345
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 157744 ACA--AAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTGA 157687

QY 4346 AAAAATACAAAATTAGCTGGTGTAGTGATGCATGCCCTGTAGTCCCAGCTACTCGGGAG 4405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 157686 AAAAATACAAAATTAGCCGGGCATGGTGGCATGCACCTGTAAATCCCAGCTACTTGGGAG 157627

QY 4406 GCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGCAGAGGTTGCAGTGAGCCGAGATCCCA 4465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 157626 GCTGAGGCAAGAGAAATTGCTTGAACCCAGGAGCAGAGGTTGCAGTGAATGAGATGTCG 157567

QY 4466 CCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAATAA 4525
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 157566 CCACTGCACCTCCAGCCTGGGCGACAAAGCAAGCAAGACTCCGTTCCACCGCCCCCAAAAAGA 157507

QY 4526 AATAAAGGATCGGAGAGAAAAA 4550
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 157506 GATGGAACAATTGAGAAAAARCCCAA 157482
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RESULT 41

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US-10-995-561-13319
; Sequence 13319, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13319
; LENGTH: 27509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13319
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Query Match		7.0%;	Score 351.6;	DB 10;	Length 27509;
Beat Local Similarity		53.5%;	Pred. No. 5.2e+02;		
Matches 1208;		Conservative 9;	Mismatches 878;	Indels 165;	Gaps 17;
Qy	2322	CCAGCACTTTGGGAGGCCGAGGCGGCGGATCACTTGAGGTCAGGAGTTCGAGACCAAGCC	2381		
Db	1	CCAGCACTTTGGGAGGCCGAGGCGGCGGAGTGAACAC--GAGGTGAGGAGATTGAGACCATCC	58		
Qy	2382	TGGCCAAACATGGTGAACCCCTGTCTCTACTAAAAAATAC-AAAAATTAGCCGACATGGT	2440		
Db	59	TGGCTAACACGGTGAACCCCGTCTCTACTAAAAAATACAAAAAATAGCCGGCGCGGT	118		
Qy	2441	GGCGAGCGCCTGTAAACCCAGCTACTTGGGAGACT-----	2475		
Db	119	GGTGGGTGCCTGTAGTCCAGCTACTCAGGAGGCTGAAGCAGGAGAAATGGCAGGAACCGG	178		
Qy	2476	-GAGTTGGAGTTTCAGTGAGCCAAAGGTCGTCTCACTGCTGCCAGCCCTGGGTAACAGAG	2534		
Db	179	GGAGGCAGAGGTTGTAGTGAGCTGAGATCGCGCCATTGCACTCCAGCCTGGCGACAGAG	238		
Qy	2535	C--AACTCTGTCTCAAAAAAATAAATGCTTTCAATAAATATATGATAAAAGGACTTATA	2592		
Db	239	CGAGAATCCGTCTCGAAAAAATAAATAAATACACACACACAAAAAACTGTGTTAAT	298		
Qy	2593	TTTTTTCAAGCCATAGGATCATTTCTCTGAAGCATCTTGGCGAAGTCATCCCCACCTGT	2652		
Db	299	GCTTAACATACACAAAAATGATAATCAGATAAAATATGCATTTATTTAGAGAACTGCATGTT	358		
Qy	2653	TCCTGAGAGTGGGCAGGTGAGGGCTGACCTATTGCTCTGCACCTTACTCTCATCTCAGCTG	2712		
Db	359	GGTCAGTCCAGTCCCTGCAGAGGGAAATCCCAGCATGACCTCATTCACATTGTGAAGACAG	418		
Qy	2713	TCCCTCCCACCTTCCAGGTGCTGCCAGACACATGACAACTGCTAYGACCAGGCCAAGAAG	2772		
Db	419	AGCAATCCCTGTGTTTTATTATTTTAAAGATGKATCTCACTCTGTGCCCCAGACTGGAGTG	478		
Qy	2773	CTGGACAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCACACCTATTTCATACCTCGTGC	2832		
Db	479	CAGTGGCATGATCTCAGCCCTCTGCCACCTCCACCTTCCGGGTTCAAGAGATTCTCATGC	538		
Qy	2833	TCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCCTTGACCTATGAATTTCTAG	2892		
Db	539	CTCAGCCTCCTGAGTAGCTGAGATTACAGGCTTGTGCCTCCRTGCCAGCTAATTTTTTT	598		
Qy	2893	TTGGTTCTCAGTAGGCCGGGGGAAATAATAGTAACAACAGCCATGATTTAGTGTTAATT	2952		
Db	599	ATTTTACTAGAGATGAGGTTTTCACCAGTTTGGGCAGGCCG-----GTCTCAAAC	648		
Qy	2953	TTCTTGGTTCTGGGCAGTGTCTCCTTTAATCCTCAGAACAACTATGGGATAGGTACAA	3012		
Db	649	TCCTGACCTCAAGTGATCCACCACCTCGGCCCTCCCGAAGTGTGGGATGACAGGTGC--	706		
Qy	3013	TTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGGCTGAGCTATTTGCCCAAGA	3072		
Db	707	-----CTGGTCAGCAACTGTTGTTTAGACATACACATTTTATCTGCTCGTCCAGCA	757		
Qy	3073	TCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTGTGTTGTTTAGAGACAGGG	3132		
Db	758	TGGTCAGCCCTCCACTT-----TTTAAATTTTATTTTATTTATTTTGTGAGACAGAG	810		
Qy	3133	TCTTGCTGTGCACCAGGCATGAGCACAGTGGTGCAACCATAGGTCACTGCAGCCTCAA	3192		
Db	811	TCTCACTCTGTGTCCAGGTTGGAGTCCAGTGGCGTGATTTTCGGCTCACTGCAACCTCTA	870		
Qy	3193	CCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGT	3252		
Db	871	CTTCCCAGGTTTCGASCAATTTCTCCTGCCTCAGCTTCCCAGTAGCTGGGATTACAGGCC	930		
Qy	3253	GCACCACCAAGCTGGCTAAATTAATAAATAATTTTTTGTAGAGACTGGGTCTTACTACGTT	3312		
Db	931	CGGTCCCCACACCTAGCTAAATTTTTTGTA--TTTTTAGTAGAGACAGGGTTTCACCATGTT	988		

Qy	3313	GGCCAGGCTTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGT	3372		
Db	989	GGCCAGGCTGGTCTCGAACTSCTGACCTCAGGTGATYCTCCTGCCTTGGCCTCCCAAAGT	1048		
Qy	3373	GCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTTACATTCCATCTTT	3432		
Db	1049	GCTGAGATTACAGGTGTGAGCCACTGCACACGCGCTTAAATTTTATTTATTTATTTA	1108		
Qy	3433	CCAATAGAAATGAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCTCTTTCTTTT	3492		
Db	1109	TTTATTTATTTAGAGA-----CCTAGTCTCACTCTG	1139		
Qy	3493	GAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTCAGCTCACTGCAACCTCTGCCTCC	3552		
Db	1140	TTGCCMSGCTGGAGTGCAGTGGCATGRTCTCGGCTCACTGCACTCCA-----CCTCC	1192		
Qy	3553	CGGGTTCAAGYGATTCTCCTGCCCTAAGCCCTCCTGAGTAGCTGGAAATTACAAGCGTGCACC	3612		
Db	1193	TGGGTTACGCCAFTTCTCCTGCCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCACC	1252		
Qy	3613	ACCATGCTTGGCTAATTTTTTGTATTTTGTATTTTAGCAGAGATGGGTTTTTACCATGTGCCCAG	3672		
Db	1253	ACCACCTCCCGGCTAA-TTTTGTATTTTGTAGTAGAGATGGGTTTCACTGTGTAGCCAG	1311		
Qy	3673	GCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCCTGCCTCAGTCTCCCAAAGTGTGGA	3732		
Db	1312	GATAGTCTCGATCTCCTGACCTY--GTGATCCGCGCTGCCTCGGCCCTCCCAAAGTGTGGG	1369		
Qy	3733	ATTATAGGCGTGAGTCACTGTGCCCTGGCCGATTACTGTCTATTTTCTTTATTG--CTATA	3790		
Db	1370	ATTACTTATTTTGTGTTTGTAGAGACAGGTTCTCACTGTGTTGCCAGGCTGGTCTGA	1429		
Qy	3791	TCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAAATAATTGATGAATG	3850		
Db	1430	ACTCCTGATCTCAAGTGATCTTCCCACCTCAGTCTCTCAAAGGGCTGGGATTACAGGGGT	1489		
Qy	3851	CACAGCCTAGATATAAACTTCTTTTCTTTTCTTTTAAACAACTCTTGACAACTTTGCAGA	3910		
Db	1490	GAGCCACTGCACCCACCTTCCCTCTACTTTTT-----GACG	1526		
Qy	3911	ATAAATAACAATCTTGCAATCTGCTTTTTCACCTTATCACCTTGTATTAGACTTTTTCATATT	3970		
Db	1527	GTTTCTCTGCTATGAATGTGCATGTCCAGTGTCTGCTGCTTCTTAGAACTGATATTACC	1586		
Qy	3971	GCCTCAAAACCTTATTTACTGTTTTTTTCAATGTTACTATTTTAGTCACTGAATAATAT	4030		
Db	1587	TTCTTCATCCATCA-----GCCATTGGAGGAGGACTGGGACCGCTC	1627		
Qy	4031	GGCTTAATTTGCTTATACATCCTCCTGCTCCACTTTAGAAAGGCCAAAATTTACAAATCTGA	4090		
Db	1628	AGATTATTGATCTGACCCATTCTTTCGGCAGGGTTTCTGTTGGTGTCTTCCCATCACCA	1687		
Qy	4091	TGAAAGCTATGAACCTCTCCCCAGAGAAATACACACACACACACACACACACAGT	4150		
Db	1688	AAACTGGAATCAGAAGAGTTTCCATAGCCCTTTTTTTTCCCCACATCTTTTGTCTGAAGCA	1747		
Qy	4151	TTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCAATTAGAGGATGTTTGTTCATATT	4210		
Db	1748	GAGTTTTTGAA-----AAACAAAACCAACAACTAAGCTATTCCCCAGAGAAATCTGTA	1800		
Qy	4211	AATTAATAATAACTCAGTTGGGCACAGTGACTCAAGCTGTAAACCACAGTACTTTTGAAG	4270		
Db	1801	ATCAAGATAAAGCTCTGCCGGGCACAGTGGCTCACGC-----CTTTTGGAG	1846		
Qy	4271	TCCAAGGTGGTGGATCACTTGAGGTGAGAAGTTCCGAGACCAGCCTGGTCAATATGGTGA	4330		
Db	1847	GCCAAGGGGGCGGATCACCTGAGGTGAGGATTTCTAGACCTGCCAGGCCAACATGGTAA	1906		
Qy	4331	AACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGTGATGCATGCCCTGTAGTC	4390		
Db	1907	AACCTCATCTCTACTAAAAATACAAAAATTAGCTAGATGTGGTGGGTACCTGTAGTC	1966		
Qy	4391	CCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAG	4450		


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Db 1967 TCAGCTACCTGGGAGGCTGAGGCGAAGAGAATCGCTTGAACCTGGGAAGTAGAGGTTGCAG 2026
Qy 4451 TGAGCCGAGATCCACCACCTGCACCTCCAGCCCTGGGCGACACAGCGAGACTCTATCTCAAA 4510
Db 2027 TGAGCCGAGATTGCACCACCTGCACCTCCAGCCCTGGGCGACGGAAGTGAGACGACCTCACAA 2086
Qy 4511 AAATAAAATAAAATAAAAGGATCGGAGAGAAACAAAA 4550
Db 2087 AATTACATAATAATAAATRAAAAGTAAAAATAAAATACAA 2126
```

RESULT 42

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US-10-775-169-352
; Sequence 352, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 352
; LENGTH: 96256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-352
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Query Match 7.0%; Score 351.6; DB 10; Length 96256;
Best Local Similarity 57.4%; Pred. No. 2.1e+02;
Matches 851; Conservative 1; Mismatches 550; Indels 80; Gaps 9;

Qy 3093 GACAGTTTGGGTTTTTTTTTTGTTGTTGTTTGTAGAGACAGGGTCTGTCTGTCAACCCAGGC 3152
Db 60419 GTCAGATTCTATTTTGTGTTTTTTTGTGATGGGTCGCTCTGTGCGCCAGGC 60478

Qy 3153 ATGAGCACAGTGGTGTCAACCAATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATC 3212
Db 60479 TGGAGTGCAGTAGCACGATCTCAGCTCACTGTAACTCCGTCTCCAGATTCAAGCAATT 60538

Qy 3213 TGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGGTGCACCACCACCGCCTGCTAA 3272
Db 60539 CTCCTGCCTCTGCCTCCTGTAATAGCTGGGATTACAGGCGGCCACCACTATGCCCGGTAA 60598

Qy 3273 TTAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACT 3332
Db 60599 TTTTTCGTA-TTTTGTAGAGACAGGATTTCACCATGTTGGCCAAAGCTGGTCACGAACT 60657

Qy 3333 CCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAG 3392
Db 60658 CCTGACCTCAAGTGATCTGCTCGCCTCGGCTCCCAAAGTGTGGATTACAAGTGTGAG 60717

Qy 3393 CCACCATGTGGGCTACTTATTTCTTTACATTCCATCTTCCAATAGAATGTAAGATCCA 3452
Db 60718 CCACCGCGCCGGCACTTTTTTATTT-----TATTTTAAAGATGGAGTCTCGCTCTG 60771

Qy 3453 CAGAACAGGGATTACTGCCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCAGTTTCA 3512
Db 60772 TTGACCGAGCTGGAGTGCCGTGGTGCGATC----- 60801

Qy 3513 CACCTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCCTCCCGGTTTCAAGYATTCT-CC 3571
Db 60802 -----TCAGCTCACTGCAACCTCCGCTTCCAGGTTTCAAGCAATTCTCCC 60846

Qy 3572 TGCCTAAGCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCATGTCTTGGCTAATTT 3631
Db 60847 TGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACCCGCGCACCGCCTGGCTAA-TTT 60905
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Qy 3632 TTGTATTTTTCAGCAGAGATGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGA 3691
Db 60906 TTGTATTTTTCAGCAGCGAGTTTTTACCATAATTGGTCAGGCTGGTCTCAAACTCCCAG 60965
Qy 3692 CCTCAAGTGATCTGCCTGCCTCAGTCTCCCCAAAGTGTGGAATTATAGGCGTGTGAGTCACT 3751
Db 60966 CCTCAAGTAATCTGCCACCTCAGCCTCCCCAAAGTGTGGGATTACAGGCGTGTGAGCAACC 61025
Qy 3752 GTGCCTGGCCGATTACTGTCTATTTTCTTTA-----TTGCTATATATCCCCAGA 3798
Db 61026 ACGCCGGGCAACAGTCAGTCTTTAAATGTACACTGCCAGTGTGCCTGCTGGCTCACT 61085
Qy 3799 TCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAAATAAATTGATGAATGCACAGCCT 3858
Db 61086 GTCCTGATGCTGTTCAGATTCTCCATGGGACAAATACTCTGGGCCGCCCCCAGGGAA 61145
Qy 3859 AGATATAAACTTTCTTTTCTTTTAAACAACACTTTGACAACTTTTGAGAATAAAATAC 3918
Db 61146 AGAGTTCCTACTGCTGTGCCACTTGAGCAAAATGCTAGAATGCTTTGTGCCTCTGTTCCT 61205
Qy 3919 AATCTTGCAATCTGCTTTTTCACCTTATCACCCTTGTATGACTTTTTCATATATGCTCAAA 3978
Db 61206 CATTTGTCCAGCTGCAGAAATAGCTCCTTCCCTTGGTGGCCAGCATGGGGATTGAGGGAG 61265
Qy 3979 CCTTTATTGTTACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAAT 4038
Db 61266 CCAGTGAAGAGGCTAGCCCCCTGGGTGAACAGTAAAGACCTTGTCTCCTCCACCTGCGG 61325
Qy 4039 TTGCTTATACATCCTCCTGCTCCACTTTTAGAGGCCAAATTTTACAAATCTGATGAAAGCT 4098
Db 61326 GTAAATACAGCTCCTCATCCCCGGCCACACAGCGCTCAGCCAGTCTCTCCTTCAGCCGGT 61385
Qy 4099 ATGAACCTCTCCCCAGAGAAAATACACACAGACACACACTCACACACAGTTTTTTTTT 4158
Db 61386 TTGCCTCGCTGCAGGTCCTCCACTCCCAGCCTTGTCTGTCTGCTGCTCCTTGGCAGCTGT 61445
Qy 4159 AATGTTTGCAACTAAGACAAGAAACCTGCAATTAGAGGATGTTTGTTCATATTAATTAATA 4218
Db 61446 GCACTGTGCATTTCCACTGCCCTTCCCTCTGCTTACAGCTCCTTTAAGACTTAACCTACA 61505
Qy 4219 ATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAGT 4278
Db 61506 ACCATGCAGTGGCTACA-----CCCATAACTCTAGCACTTGAGGAGGCCAAGGC 61555
Qy 4279 GGGTGGATCACTTAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTAT 4338
Db 61556 AGCGGATCACCTGAGTAAAGAGTTCAAGACCAGCCTGGCCAACATGGTGAAGCCCCCT 61615
Qy 4339 CTCTACT-AAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCGTGTAGTCCCAGCTA 4397
Db 61616 CTCTACTAAAAAATACAAAAATTAGCCGGCGGT--GGGTGGGTGCTGTAAATCCCAGCTA 61673
Qy 4398 CTCGGAGGCTGAGSCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCG 4457
Db 61674 GTCCGGAGGCTTAGGAGGAGAAATCGCTTGAACCCGGGAGGTGGAAGCTGCAGTGAGCTG 61733
Qy 4458 AGATCCCACCACTGCACCTCCAGCCTGGGCGACACAGCCGAGACTCTATCTCAAAAAATAA 4517
Db 61734 AGATCATGCCATGGCACTCCAGCCTGAGCAACAGAGAGAGACTCCGCTCTCAAAAAAAA 61793
Qy 4518 ATAAATAAAATAAAGGATCGGAGAGAAACAAACTAATAAGA 4559
Db 61794 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAGAGAGA 61835
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RESULT 43

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US-10-786-065-3
; Sequence 3, Application US/10786065
; Publication No. US20040146924A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
```

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098DIV II
; CURRENT APPLICATION NUMBER: US/10/786,065
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-786-065-3

Query Match 7.0%; Score 350.8; DB 10; Length 53332;
Best Local Similarity 58.4%; Pred. No. 3.2e+02;
Matches 840; Conservative 1; Mismatches 518; Indels 79; Gaps 10;

QY 3099 TTGGGTTTTTTTGGTTGTTTGTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAGC 3158
||| ||||| ||| ||| ||| ||||| ||||| ||||| |||
Db 6290 TTTTTTTTTTTTTTTTTTCTCAGATGGAGTCTCACTCTGTCGCCAGGCTGGGT 6349

QY 3159 ACAGTGGTGAACCATAGGTCACCTGACGCGCTCAACCTCCTGAGCTCAAGGGATCTGTGA 3218
||| ||||| ||| ||| ||||| ||||| ||||| ||||| |||
Db 6350 GCAGTGGCGCAATCTCAGCTCACTGCAACCTCCGGCTCCCGGTTCAAGCGA--TTCTCC 6407

QY 3219 CCTCAGCCTCCCAAGTAGCTGGGACTAGAGCGTGCACCACCGCCTGGCTAAATTAATAA 3278
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db 6408 TCTCAGCCTCCTGAGTAGCTGGGATCACAGGCGCGTGCACCACTCCCGCTAATT--TT 6465

QY 3279 AAATTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTGTCTTAAACTCCTGGC 3338
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db 6466 TTGTATTTTAGTAGAGACGGGTTCACCATGTTGCCAGGCTGGTCTCAAACTCCCGAG 6525

QY 3339 TTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGCTGGGATTACAGGGGTGAGCCACCA 3398
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db 6526 CTCAGGCAATCCACCACCTCAACCTCCCAAGTGCTAGGATTACAGGCATGAGCCACTG 6585

QY 3399 TGTGGCGCTACTTATTTCTTTACATTCATCTTTCCCAATAGATGTAAGATCCACAGAAC 3458
||| ||||| ||| ||| ||||| ||||| ||||| ||||| |||||
Db 6586 CGCCTGGCTGAGGGTATGCATTTTTTTTTTTTGTGAGACGGA----- 6627

QY 3459 AGGGATTACTGCGCTATTTTCTTCTCTTTCTTTTGTAGACAGAGTCTCACTTCATCACCTC 3518
||| ||| ||| ||| ||||| ||||| ||||| ||||| |||||
Db 6628 -----GTCTTGCTCTGTCGCCCCAGGCTGGAGTGAGTGCCACGATC-- 6668

QY 3519 AACCTCCGTTACAGTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTAA 3578
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db 6669 -----TTGGCTCACTGCAAGCTCGCCTCCAGGTTACGCGCATCTCCTGCCTCA 6719

QY 3579 GCCTCCTGAGTAGCTGGAATTACAAGCGTGCACCA--CCATGCTTGGCTAAATTTTGT 3635
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db 6720 GCCTCCCCAGTAGCTGGGACTACAAGGTGCCCCACCACCCAGCTAAATTTTGT 6779

QY 3636 ATTTTGTAGCAGAGATGGGTTTTTACCATGTTGCCCGAGGCTGGTCTCAAACCTCCTGACCTC 3695
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db 6780 ATTTTGTAGTAGACGGGGTTTCACTGTGTAGGCAGGATGGTCTCGATCTCCTGACCTC 6839

QY 3696 AAGTGATCTGCTGCCTCAGTCTCCCAAAGTGCTGGAATTAAGCGTGAGTCACTGTGC 3755
||| ||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||
Db 6840 --CTGATCCACGGCCTTCGCCTCCCAAAGTGCTGGGATTACAGCGGTGAGCCACTGTGC 6897

QY 3756 CTGGCCGATTACTGTCTATTTTCTTTATTTGCTATATCCCCAGATCTAGAGCAGTGTCTGA 3815
||| ||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||
Db 6898 CCGGCCTGATGAATGTTAAATCTTTTAAATATCGGATTGTACAAGAAATGAACATAAA 6957

QY 3816 CATATAGTAGTGCTCAATAAATAATTGATGAANTGCACAGCCTAGATATAAACTTTCTTT 3875
||| ||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||
Db 6958 GAGAAA-----AGTTACATGGAGGAAAAAGGTTACTAACAATATGATTTTAATCC 7008

QY 3876 TTCTTTTTTAAAAACAATCTTGCACAACCTTTCAGAAATAAAATACAATCTTGCATTCTGCTT 3935
||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7009 CACTGTATTAANAACAATGGATTTTATACCTGCATTAAATCTTCTATTCTCAGCACTT 7068

QY 3936 TTTCACCTTATCACCTTGTATTAGACTTTTTCATATTGCCTCAAAACCTTTATTGTACTGTT 3995
| | | | | | | | | | | | | | | | | | | | | |
Db 7069 AGCTGATATGAATAAAATGATGAATGAGGGGACACTAGGAGGAATGAAGAGAGAGAGAA 7128

QY 3996 TTTTCATTGTTACTATTTTAGTCACCTGAATAATATGGCTTAATTTGCTTATACAT-CCTC 4054
| | | | | | | | | | | | | | | | | | | | | |
Db 7129 TAATGGTGTGGCCTGGGAAGATCAGGTAGCACATTAGAAGCCCGCTGCAAGAATTTGGCTT 7188

QY 4055 CTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCCTCTCCCCA 4114
| | | | | | | | | | | | | | | | | | | | | |
Db 7189 TTATTCTAAGTAATGCGTGGAGATATGGTGGCTTTTGAACAGAAAAAGTGACITGTCTCTGA 7248

QY 4115 GAGAAATACACACACACACACACTCACACAGATTTTTTTTAAATGTTTGGAACTAAG 4174
| | | | | | | | | | | | | | | | | | | | | |
Db 7249 TTGTCAATTTGAAAAGTATGCCTCCAAC-----TACTACTGCTGAGAGTAAAT 7295

QY 4175 ACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATAAATAAATAAATAAATAAATAA 4234
| | | | | | | | | | | | | | | | | | | | | |
Db 7296 AGTAGGAGTGCAAGTGTGCTCAGCAGGGAAACTGTTAGAAGACCACACTACAAGGCTGGGCT 7355

QY 4235 CAGTGACTCAAGCCTGTAAACCAACAGTACTTTTGGAAAGTCCAAAGGTGGGTGATCACTTGAG 4294
| | | | | | | | | | | | | | | | | | | | | |
Db 7356 TGGTGGCTCGTCCCTGTAATCCAGCACCTTTGGGAGCCTGACGTGGGCAGATCACTCTGAG 7415

QY 4295 GTGAGAAAGTTCGAGACCAAGCCTGGTCAATATATGGTGAAGTCCAAAGTGGGTGATCACTA 4353
| | | | | | | | | | | | | | | | | | | | | |
Db 7416 GTCAGGAGTTCGAGACCAAGCCTGGCCAAATGTTGAACCCCATCTCTGCTAAAAATAC 7475

QY 4354 AAAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC 4413
| | | | | | | | | | | | | | | | | | | | | |
Db 7476 AAAAAATTAGCCAGGTGTGGTGGGGTCCCTGTAAATCCCAGCTTCTTTGGGAGGCTGAGGC 7535

QY 4414 AAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCAGTGCA 4473
| | | | | | | | | | | | | | | | | | | | | |
Db 7536 AGGAGAAATTGCTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCCAAAGATCGTGCCACTGTA 7595

QY 4474 CTCCAGCCTGGCGACACAGCGAGACTCTATCTCAAAAAATAAAATAAAATAAAATAAA 4531
| | | | | | | | | | | | | | | | | | | | | |
Db 7596 CTCCAGCCTGGGCAACAGAGCGAGATTCTGTCTCAAAAAATAAAATAAAATAAAATAAA 7653

RESULT 44
US-11-121-086-2
; Sequence 2, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 191684
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-2

Query Match 7.0%; Score 350.4; DB 17; Length 191684;
Best Local Similarity 58.1%; Pred. No. 1.3e+02;
Matches 851; Conservative 1; Mismatches 527; Indels 85; Gaps 10;

QY 3106 TTTTTTTTGTGTTTAGAGACAGGGTCTTGTCTGTCAACCCAGGCATGAGCAGTGG 3165
||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||
Db 177129 TTATTTTCTTTTCTTTTGAGATAGAGTCTCACTTGTCAACCCAGGCTGGAGTGCAGTGG 177188

QY 3166 TGCAACCATAGGTCAGTCAGCGCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGC 3225
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177189 CGTGATCTCGGCTCACTGCAACCTCCACCGCCTGGGATCACGCGACTCTTCTGCCACAGC 177248

Qy	3510	CATCACCTCAACCTCCGTT	CAGCTCACTGCAACCTCTG	CCCTCCCGGTTCAAGYGATTCT	3569
Db	34535	-----TTGGCTCACTGCAACCTCCGTC	CTCCAGGTTCAA--GATTCT	34574	
Qy	3570	CCTGCCTAAGCCTCCTGAGTAGCTGGAA	TACAAGCGTGCAACCATGCTTGGCTAAAT	3629	
Db	34575	CCTGCCTCAGCTTCCCAAGTAGCTGGGATTACAGGTGCCCGCCACCAAGCTAAAT	34634		
Qy	3630	TTTTGTATTTTAGCAGAGATGGGTTTT	-----ACCATGTGCCAGGCTGGTCT	3680	
Db	34635	TTTTGTATTTGTAGTAGAGATGGGGTTT	CACCGTGTTCACCATGTTCACCAAGCTAGTCT	34694	
Qy	3681	CAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAGTGTGGAATTATAGG	3740		
Db	34695	CAAACTCCTCACTTCAGGTCATCCACCGCCTTGGCCTCCCAAGTGTGGGATTACAGG	34754		
Qy	3741	CGTGAGTCACTGTGCCTGGCCGATTACTGTCTATTTTCTTTTATTTGCTATATCCCCAGATC	3800		
Db	34755	CGTGAGCTACTGTGCCCGGCCTGTTGTGTTTTAAATAAACACGCTTTACTGAGATCTCA	34814		
Qy	3801	TAGAGCAGTGTCTGACATATAGTAGTGCTCAATAAATAATTGATGAATGCACAGCCTAG	3860		
Db	34815	TTACAAAATAAATTACCCATTTTAAAGTTCACATTTGTAGCGTACAACCATCACCA-----	34868		
Qy	3861	ATATAAACTTTCTTTTCTTTTAAAAA	CAATCTTGACAACTTTGCAGAATAAAATACAA	3920	
Db	34869	AAACCAATTTTAGAAACATTTTTCATCACCCCATAAAAGAAATTTCTGTACTCAAGGCCAGGCA	34928		
Qy	3921	TCTTGCACTCTGCTTTTTCACCTTATCACTTGTATG--ACITTTTCATATTGCCTCAA	3977		
Db	34929	TTGTGGCTCAAGCCTATAATCCCAGCACTTTGGGAGGCCAAGAGGAAGATCACTTGAG	34988		
Qy	3978	ACCTTTATTGTACTGTTTTTTTTCATTTGTACTATTTTAGTCACTGAATAATATGGCTTAA	4037		
Db	34989	GCTGGGAGTTGAGACCAGCCTGAGCCACATAGTGAGACACCCCGTTTCTACAAAAAAT	35048		
Qy	4038	TTTGCTTATACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAGC	4097		
Db	35049	TTAAAAATTTGCAGGGAGTGGTGACACCTGTGGTTCTAGCCACTCAGAAAGCTGAGGTG	35108		
Qy	4098	TATGAACCCCTCTCCCCAGAGAAATACACACACACA-CACACACTCACACACAGTTTTTTTT	4156		
Db	35109	GGAGGATCATCTGCGTCCAGGAGTGTGGGCCCTACAGTGAACATATTACTGAACCACTGCA	35168		
Qy	4157	TTAATGTTTGCAACTAAGACAAAGAAACCTGCAATTAGAGGATGTTGTTCATATTAATTA	4216		
Db	35169	TCCAGCCTAGTGACAGAACAGACCTCATCTCTAAAGACAAATTTAAAAAAGTCACAAAGT	35228		
Qy	4217	AAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCAACAGTACTTTGGAAGTCCAG	4276		
Db	35229	TAAAAATTAGCGCGGTGCAGTGGCTTATGCTCTAATCCTATCACTTTGGCAAGACAAG	35288		
Qy	4277	GTGGGTGGATCACTTGAGGTGAGAAGTTGAGACCAAGCCTGGTCAATATGGTGAAACCC-	4335		
Db	35289	GCAGGGGATCACCTGAGCTCAGGAGTTCGAGACCAGCCTGGCCAAACAAGGCCAAACCCA	35348		
Qy	4336	-TATCTCTATAAAAAATACAAAAATTAGCTGGGTGTAGTGTGATGCATGCCCTGTAGTCCAG	4394		
Db	35349	TCTCTACTGAATAAATACTAAAAATTCGCTGGATGTGGTGGCGCACACCTGTAATCCAG	35408		
Qy	4395	CTACTCGGGAGCTGAGGCAAGAGAAATTGCTTGAAACCTGGGAGCAGAGGTTGCAGTGAG	4454		
Db	35409	CTACTCGGAGCTGAGGCACTGGAAATTGCTTGAACCTGGGAGGAGAGTTTGCAGTTAG	35468		
Qy	4455	CCGAGATCCCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAA	4514		
Db	35469	CTGAGATCGTGCCACTGGACTCCAGACTAGGCGACAGAGTGAGACCTTATCTCAAAAGAA	35528		
Qy	4515	TAAATAAATAAATAAAGGATCGGAGA	4541		
Db	35529	AGAAAAAAAATTAAGAAACCCCTGA	35555		

RESULT 46				
US-10-330-773-698/c				
; Sequence 698, Application US/10330773				
; Publication No. US20060040262A1				
; GENERAL INFORMATION:				
; APPLICANT: David W. Morris				
; APPLICANT: Marc Malandro				
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer				
; FILE REFERENCE: 529452001300				
; CURRENT APPLICATION NUMBER: US/10/330,773				
; CURRENT FILING DATE: 2002-12-27				
; NUMBER OF SEQ ID NOS: 981				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 698				
; LENGTH: 178024				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: misc_feature				
; LOCATION: (1)...(178024)				
; OTHER INFORMATION: n = A,T,C or G				
US-10-330-773-698				
Query Match 7.0%; Score 348.4; DB 11; Length 178024;				
Best Local Similarity 58.3%; Pred. No. 1.4e+02;				
Matches 862; Conservative 1; Mismatches 452; Indels 163; Gaps 8;				
Qy	3104	TTTTTTTTTGTGTTTAGAGACAGGGTCTTGTCTGTCA	CCCCAGGCATGAGCACAGT	3163
Db	129644	TTTTTTTTTTTTTTTTTTTGAGACAGTCTCAATCTGT	TACCCAGGCTGGAGTGCAGT	129585
Qy	3164	GGTGCAACCATAGGTCACTGCAGCCTCAACCTCTGAG	CTCAAGGGATCTGTGACCTCA	3223
Db	129584	GGCGTGATCTCAGCTCACCGCAACCTCCGCCCTCC	CAGGTTTAAGCGATTCTCCTGCCTCA	129525
Qy	3224	GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCA	CCAGCCTGGCTTAATAAAAAAAT	3283
Db	129524	GCCTCCGAGTAGCTGGGATTACAGGCATGTGCCAT	CATGCTAGCTAATTTTGTGA--T	129467
Qy	3284	TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAG	GCTTGTCTTAAACTCCTGGCTTCAA	3343
Db	129466	TTTTAGTAGAGATGGGTTTCGCCATGTTGGCCAG	GCTGGTCTCAAAATCTTGACCTCAG	129407
Qy	3344	GCAATCCTCCTACCTTGGCATCCCAAAGTCTGGAT	TACAGGGGTAGCCACCATGTGC	3403
Db	129406	GTGATCCGCCCTGCCTCGCTTCCCAAAGTCTGSC	ATTACAGGCTTGAGTCAACACAGCT	129347
Qy	3404	GGCTACTTATTTCTTACATTCCATCTTTC--CAAT	AGAATGTAAGATCCACAGAACAGG	3461
Db	129346	GGCCAGCTTTTTTCATCTTCTCAAAAGCCATCAT	TTTGAGCTTTTCATCCGAGCTTTTAG	129287
Qy	3462	GATTACTGCCATTTTCTTCTTCTTCTTCTTCTTCT	-----TTTTTGAGACAGAGTCTCACTTCAT	3512
Db	129286	AATTTAGAACTATTGTTTCTGATTTTTTTTGTGT	TTTTTGAGACAGAGTCTCGCTCTGT	129227
Qy	3513	CACCTCAACCTCCGTTCA-----GCTCACTGCAA	CCCTCTGCCCTCCCGGTT	3558
Db	129226	CACTCAGACTGGAGTGCAGTGGCATGATCTTGGCT	CACCTGCAATCCCTGCCTCCTGAGTT	129167
Qy	3559	CAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCT	TGGAAATTACAAGCGTGCACCAACATG	3618
Db	129166	CCAGCAATTCTCGTGCCTCAGCCTCCCGAGTAG	CTGGGACTACAGGGGCATACCCACACA	129107
Qy	3619	CTTGGCTAATTTTTTGTATTTTAGCAGAGATGGG	TTTTTACCATGTTGCCCAGGCTGGT	3678
Db	129106	CCCAGCTAA-TTTTTGTATTTTAGTAGAGATG	TGTTTTTCACCATGTTGGCCAGGCTGGT	129048
Qy	3679	CTCAAACTCCTGACCTCAAGTGATCTGCCCTGC	CTCAGTCTCCCAAAGTCTCGGAATTATA	3738
Db	129047	CTTGAACCTCCTGGCATCAAGTGATCCACCCGCT	CCCGCCTCCCAAAGTCTGGGATTACA	128988
Qy	3739	GGCGTGAGTCACTGTGCTGGCCGATTACTGTCTA	TATTTTCTTT--ATTGCTATATCCCCA	3796

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Db 128987 AATGTGAGCCACTGTGCCAGCCAGCAGCATAACTTTTATGTTGAATATTTGTGCTCTCA 128928
Qy 3797 GATCTAGACAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTTGATGAATGCACAGC 3856
Db 128927 AATTAACAGTAAAGCCCTATGCTGGTGTCTAGTTTATATATTTTGTGAGAAATAGGTCTC 128868
Qy 3857 CTAGATATAAACTTTTCTTTTCTTTTAAACAATCTTCACAACTTTGCAGATAAAT 3916
Db 128867 TAGGAATCAAAATGGAGAACACTGCCCTAAA-----GCAGTATTCTCAACCCAGAG 128818
Qy 3917 ACAATCTGCATTTCTGCTTTTTCACCTTATCACCTTGTATTAGCACTTTTTCATATTGCTCA 3976
Db 128817 AAGCTTTTGCCTCCAGAGGACATGTGACAAATGTGTGGAGACATTTTGTATTGTCACAA 128758
Qy 3977 AACCTTTATTGTTACTGTTTTTCAATTGTTACTATTTTATGTCACCTGAATAATATGGCTTA 4036
Db 128757 CTCGGGAGTGTACTTGGCCTCTGCTGGGTAGAGGCCAGGATGCTGTAAACA----- 128705
Qy 4037 ATTTGCTTATACATCCTCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAG 4096
Db 128704 ----- 128705
Qy 4097 CTATGAACCTCTCTCCCAGAGAAATACACACACACACACTCACACAGTTTTTTT 4156
Db 128704 -----TTC 128701
Qy 4157 TTAATGTTGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATAA 4216
Db 128700 GAAATGCCCCCAACAAGAAATGATCTGGCCTGAGATAATGTCAAAAAGTGTGAAGGAA 128641
Qy 4217 AAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACCACAGTACTTTGGAAGTCCAAG 4276
Db 128640 CCCTGTTTGGCCGGGTGCAGTGGTTCACACCTGTAATCCTTAACACTTTTGGAGGCTGAG 128581
Qy 4277 GTGGGTGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTCAATATGGTGAAACCT 4336
Db 128580 GCGGGCGGATTACCTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAATATGGTGAAACCCC 128521
Qy 4337 ATCTCTACTAAAAATACAAAAATTAGCTGGGTGATGATGCATGCCCTGTAGTCCCAGCT 4396
Db 128520 GTCTCTCTAAAAATACAGAAATTAGCTGGCGTGGTGGCGGCGCCTGTAGTCCCAGCT 128461
Qy 4397 ACTCGGAGGCTGAGGCAAGAGAAATTGCTTGAACTGGGAGGCAGAGGTTGCAGTGAGCC 4456
Db 128460 ACTCAGAGGCTGAGGCAGGAGAAATCGCTTGAAACCCGGAGGTGGAGGTTGCAGTGACCC 128401
Qy 4457 GAGATCCACCACTGCACCTCCAGCCTGGCGGACACAGCGAGACTCTATCTCAAAAAATA 4516
Db 128400 AAGATCAGGCCACTGCACCTGAGCCTGGGCAACAGAGCGAGATTCATCTCAAAAAAGAAA 128341
Qy 4517 AATAAATAAAATAAAGGATCGGAGAGAGAAACAAAATA 4554
Db 128340 AAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAGAAAGAAA 128303
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RESULT 47
US-11-121-086-57/c
; Sequence 57, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 155989
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-57

Query Match      7.0%; Score 347.8; DB 17; Length 155989;
Best Local Similarity 54.0%; Pred. No. 1.6e+02;
Matches 1241; Conservative 4; Mismatches 871; Indels 183; Gaps 19;

Qy 2276 TTAAAAATCGCTTTCAGGCCAGGCGCGGTGGCTCATCCCTGTAATCCCGACACTTTGGGA 2335
Db 59130 TTGCAAAATGCACATGAGGCCAGCGTGGTGGTCAAGCCTGTATCCCGACACTTTGGGA 59071
Qy 2336 GGCCGAGGCGGGGATCACCTTGAGGTGAGGTCAGGAGTCGAGACCAGCCTGGCCAAACATGGTG 2395
Db 59070 GGCTGAGGCAGGCAGATCACTTGAAGTCAGGAACCTCAAGACCAGCCTGGCCAAACATGGTG 59011
Qy 2396 AAACCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCCTGTAA 2455
Db 59010 AAACCCCGTCTCTAGT-AAAAATACAAAAATGAGCCGGACATGGTGGCACATGCCTATAA 58952
Qy 2456 CCCCAGCTACTTGGGAGACT-----GAGTTGGAGGTTTCAGT 2492
Db 58951 TCCCAGGTACTCAGGAGGCTGAGGCAGAAATGCTTGAACCTGGGAGGTGGAGTTGCAGT 58892
Qy 2493 GAGCCAAAGTCTGTCTCACTGTCTCCAGCCTGGGTA-ACAGAGCAACTCTGTCTCAAAA 2551
Db 58891 AAGCCAAAGATCGTGCCACTGCACCTCCAGCCTGGAGCAGAGTGAGACTCCATCTCAAAACA 58832
Qy 2552 AAAAAAATGCTTTCATAAAATATATGATAAAAGACTTA-----TATTTT 2598
Db 58831 AACAAACAAAAACAAATGCACATGCAAGTAGGTAAACAGAGAAGATTCAAAAACCTCTTTA 58772
Qy 2599 CAAGCCATAGGATCATTTCTCCTGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCCTGA 2658
Db 58771 ACAGACTTAGAACCAATACCAATTATTTAAATTGGCAGAGTAATGACATGGAATACCAT 58712
Qy 2659 GAGTGGGCGAGGTGAGGCTGACCTATTGCTCTGCACCTTACTCCTATCTCAGCTGTCCCTC 2718
Db 58711 TAAATTC----GTTAGTAAGGTTATTTTATGAAAAAGCTAATGTTTTGCCACGTTATA 58656
Qy 2719 CCACCTTCCAGGTGCTGCCAGACACATGACAACTGCTAYGACCAGGCCAAGAGCT-GGA 2777
Db 58655 ATTTTGACACAAATGCTAAAAAATATATTGAAATGTACTTATTAAACCATTTAGTTAAGT 58596
Qy 2778 CAGCTGTAAATTTCTGCTGGACAMMCCGTACACCCACACACCTATTATCATACTCGTGTCTGG 2837
Db 58595 TTTCATGTATTTCAACTTTTGATACATTTCCCATGGGTCTTCATCACAATTTCTCTCTAG 58536
Qy 2838 CTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTCTTGACCTATGAATTTCTAGTTGGT 2897
Db 58535 CAGTGCTATCCCATAGGAATATAATGCAAGCCATATTATAATTTTAAATTTTCTCTCTTT 58476
Qy 2898 TCTCAGTAGGCCGGGGGAAATAATAGTAACAACAGCCCATGATTTTAGTGTAAATTTCTT 2957
Db 58475 CTTTTTTTTTTTGTAGATGGAGTCTCCCTCTGTGCGCCCAAGCTGGCATGCACTGGCAC 58416
Qy 2958 GGTTCTGGG-CAGTGTCTCCTTTTAAATCCTCAGAAACAACTATGGGATAGGTACAATTAT 3016
Db 58415 GATCTTGGCTCACTGCAACCTCCGCCCTCCTGGGTCAAACTTTAAATTTTCTAGTAGCCA 58356
Qy 3017 CCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAAGCTGAGCTATTTGCCAAGATCAC 3076
Db 58355 TATTAAAAAGTTTTCTTTAAAAAGGTGAATTAATTTTGATATTTTATTAAACCCCAATAGAT 58296
Qy 3077 ACAGCTTGTAAAGTGGTGACAGTTTGGGTTT---TTTTTGTGTTTGTAGACACAGGTT 3133
Db 58295 ACATAATATGATTTCAACACGTAATCACTTAGAAAAAATAAATGTTTTTGAGATAAAAT 58236
Qy 3134 CTTGCTCTGTCAACCCAGGCATGAGCACAGTGGTGCACCAACCATAGGTCACCTGCAGCCTCAAC 3193
Db 58235 CTCACCTTGTCTCCAGGTTGGCGTACAGTGGTACAAATACAGCTCACTGCAGTCTCAAA 58176
Qy 3194 CTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTG 3253
```


[illegible]

QY	3760	CCGATTACTGTCATAATTTCTTTATTGCTATATATCCCCAGATCTAGAGCAGTGTCTGACATA	3819
Db	100999	CCCAAAAGACAACATAAT-----AATCCCATTTTCATCTTAGAACTTTTCTTAA	101045
QY	3820	TAGTAGGTGCTCAATAAATAAATTGATGAATGCACAGCCTAGATATAAACTTCTTTTTCT	3879
Db	101046	ATTTTCATGCATTAGGTTTCTCAAGAACTACTGTCTCTCGAAAACTCTTATTTGC-	101104
QY	3880	TTTTTTAAACAACATCTTGACAACTTTGCAGAATAAATACAATCTTGCAATCTGCTTTTC	3939
Db	101105	--CTATATATTATACATCTTC---AACTCATTTACTAATAAGTTGTTAGATTTA	101158
QY	3940	ACTTATCACCTTGTTATGACTTTTTTCATATTGCCTCAAACCTTTATTGTTACTGTTTTT	3999
Db	101159	ACCCAATGCTTCCCTTGTAATTTCCCTCTCCAGCACAACTAGTGTACTTATGTTTTCT	101218
QY	4000	CATTGTTACTATTTTAGTCACCTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCT	4059
Db	101219	TGATGTTA-----ATGAAGATTGGTAAAGGGTACCCGGTA	101253
QY	4060	CCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAA	4119
Db	101254	CAATTTTAAAAATTTAAGTGAACCCAGCTGATATATTTGCCTTAAATTTATTGCTGACAG	101313
QY	4120	ATACACACACACACACTCACACACAGTTTTTTTAAATGTTTGCAACTAAGACAAG	4179
Db	101314	ACTACATCTAAATATGTGAAGAAAAAAGTGATCTCATAACTTCAGAGGTTTGAATG	101373
QY	4180	AAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATACTAGTTGGGCACAGTG	4239
Db	101374	TATTGAAGAT-----TGTGTTCAATTTAAGTTTTAATTGTTCCAGTTTACTCACTGA	101424
QY	4240	ACTCAAGCCTGTAAACACACAGTACTTTTGGAAAGTCCAAGTGGGTGGATCACTTGAGGTAG	4299
Db	101425	AC----ACCTGTAATCCAGCAGCACTTTGGAGGCCGAGGTGGGTGGATCACTTAGGTCAG	101480
QY	4300	AAGTTCGAGACCCAGCCTGGT---CAATATGTTGAAACCCCTATCTCTACTAAAAATAC---	4353
Db	101481	GAGTTCAGAGACCCAGCTTGCCCAACAACATGTTGTAACCCCACTCTACTAAAAATACAAA	101540
QY	4354	-----AAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCAGCTACTCGGGAGGCT	4408
Db	101541	AAAAAAAATAATTAGCTGGGCGTGTTCGTGCACACCTGTAATCCAGCTACTCGGGAGGCT	101600
QY	4409	GAGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCCACCA	4468
Db	101601	GAGGCACAAGAAATCGCTTGAACCGGGAGGCCAAGGTTGCGGTGAGCCAGATCACGCCG	101660
QY	4469	CTGCACTCCAGCCTGGGCCGA	4488
Db	101661	CTGCACTCCAGCCTGGGTGA	101680

RESULT 49

US-11-121-086-57
; Sequence 57, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 155989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-57

Query Match		6.9%;	Score 344.8;	DB 17;	Length 155989;
Best Local Similarity		58.9%;	Pred. No. 1.7e+02;		
Matches 848;		Conservative 1;	Mismatches 493;	Indels 98;	Gaps 11;
Qy	3105	TTTTTTTGTGTTT	TAGAGACAGGGTCTT	GTCTGTCTGTCACCCAGGCATGAGCACAGTG	3164
Db	75471				
		TTTTCTTTTTTCT	TTTTTGAGATGGAGTCTCACTCTGTCACCCCAGCTGGAGTGCAGTG	75530	
Qy	3165	GTGCAACCATAGGTC	ACTGCGCCTCAACCTCCTGAGCTCAAGGGATCTGTGACCTCAG	3224	
Db	75531				
		GTGCGATCACAGCT	CATGGCAACCTCTGCCTCCCGGTTCAAGCAGTTCTC--	CCTCGG	75587
Qy	3225	CCTCCCAAGTAGCT	TGGGACTACGAGCGTGCACCACCACCGCCTGGCTTAATAAAAAATTT	3284	
Db	75588				
		CCTCCTGAGTAG	TAGGATTACAGGGCTGCACCACCATGCCTGGCTAATTTTATA--	TT	75645
Qy	3285	TTTTGTAGAGACT	GGGTCTTACTACGTTGGCCAGGCTTGCTCTTAAACTCCTGGCTTCAAG	3344	
Db	75646				
		TTTAGTAGAGAC	AGGGTTTCAACATGTTGGCCAGGCTGGTCTTTAACTCCTGACCTCATG	75705	
Qy	3345	CAATCCTCCTACCT	TGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCG	3404	
Db	75706				
		--ATCTGCCCACT	CAGCCTCCCAAAGTGTGGGACTACAGGCATGAGCCACTGGGCGAG	75763	
Qy	3405	GCTACTTATTTCT	TTACATTCCATCTTTCCAAATAGAAATGTAAGATCCACAGAACAGGGAT	3464	
Db	75764				
		ACGGAGTCTTGC	-----	-----	75775
Qy	3465	TACTGCCTATTTCT	TCCTTCTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCTC	3524	
Db	75776				
		-----	-----	-TCTGTCACTGGCTGGAGTGCAGTGGCACAAATC--	75808
Qy	3525	CGTTCAGCTCACT	GCAACCTCTGCCTCCCGGTTCAAGYGATTTCTCCTGCCTAAGCCTCC	3584	
Db	75809				
		---TCGGCTCAT	TGCAACCTCTGCCTCCCGAGTTCAAGCAACTCTCCTGCCTCAGCCTCC	75865	
Qy	3585	TGAGTAGCTGGAAT	TACAAGCGTGCACCACCATGCTTGGCTAAATTTTGTATTTTT--	3641	
Db	75866				
		CGAGTAGCTGGGAT	TACTGGTGCCCAACACGAGGCCTGGCTAGTTTGTGTTTGTTTTTT	75925	
Qy	3642	--AGCAGAGAT	TGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAACTCCTGACCTCAAGT	3699	
Db	75926				
		AGTAGAGATTGG	GGGTTTTTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGT	75985	
Qy	3700	GATCTGCCTGCCT	CAGTCTCCCAAAGTGTGGAATTATAGGCTGAGTCACTGTGCCTGG	3759	
Db	75986				
		GATCCACCCCACT	CAGCCTCCCAAAGTGTGGGATTATAGACATGAGCCACCAAGCCTGT	76045	
Qy	3760	CCGATTACTGTCT	ATTCTTTATTGCTATATATCCCGAGATCTAGAGCAGTGTCTGACATA	3819	
Db	76046				
		CCTAAAACTTTT	TTTTTGTGGT-CTTCCTCTGTTGCCAGGCTAGAGTGTGGAGGTG	76104	
Qy	3820	TAGTAGGTGCTCA	ATAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTCT	3879	
Db	76105				
		CCATCTCGGCTCA	CTGCAACCTCCCAACCTCCTGGTTCAAGCAATTCTCATGCCTCAGCC	76164	
Qy	3880	TTTTTTAAAACAAT	CTTGACAACTTTTGAGAAATAAATACAATCTTGCAATTCTGCTTTTTTC	3939	
Db	76165				
		TCCTGAGTAGTG	GGGATGACAAAGCGTGTGCCACCATGCCTGGCTAAATTTTGTATTTTA	76224	
Qy	3940	ACTTATCACCTTG	TATGACTTTTTCATATTGCTCCTCAAAACCTTTATTGTTACTGTTTTTT	3999	
Db	76225				
		GTAGAGAAAGTGT	TTCACCATATTGCCCA---GGCTGGTCTTGAACCTCCTGAGCTCAGG	76280	
Qy	4000	CATTGTTACTAT	TTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCCTGCT	4059	
Db	76281				
		CAGTCCACCGCCT	TCGCCTCCCAAAGTGTAGGATTACAGGCGTGAGCCACCAACCTG	76340	
Qy	4060	CCACTTTTAGAAG	GCCAAATTTACAAATCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAA	4119	
Db	76341				
		GCCGGTACCTTAA	ACTTTTAAATTATTTCTAACTCCTATATTTTAAATTCAGCGAACACTAAGAA	76400	

Qy	4120	ATACACACACACAC	ACACTCACACACAGT	TTTTTTTTTAATGTTTGCAACTAAGACAAG	4179
Db	76401				
		CTGCAGTGGAAAA	AGCCTTGGCTTTGGATCCCTGGCTCTGCTTCTTACTAGATACCTAAC	76460	
Qy	4180	AAACCTGCATTAG	AGGATGTTTGTTCATATTAAATTAATAAACTCAGTTGGGCACAGTG	4239	
Db	76461				
		CATCTTTTATTTT	TATTTT-TTTACTTTAAATTAGAGATGGGGGCTGGGCACAGTG	76519	
Qy	4240	ACTCAAGCCTGTA	ACCACAGTACTTTTGGAACTCCAAGGTGGGTGGATCACTTGAGGTGAG	4299	
Db	76520				
		GCTCATGCCTGCG	ATCCAGCACTTTGGGAGGCCAGGTGGAGGATCACCTGAGATGG	76579	
Qy	4300	AAGTTCGAGACC	AGCCTGTCAAATATGGTGAAACCCCTATCTCTACTAAAAATACAAAAAT	4359	
Db	76580				
		GAGTTCGAGACCA	CGCTGACCAACATGGAGAAACCCCGTCTCTACTAAAAATAC-AAAAAT	76638	
Qy	4360	TAGCTGGGTGTAG	TGATGCATGCCTGTAGTCCCAGTACTCGGAGGCTGAGGCAAGAGA	4419	
Db	76639				
		TAGCCAGGCGTGG	TGGCACATGCCTGTAATCCCAGTACTAGGGAGGCTGAGGCAGGAGA	76698	
Qy	4420	ATTGCTTGAACCT	TGGAGCAGAGGTTGCAGTGAGCGAGATCCCACCACCTGCATCCAG	4479	
Db	76699				
		ATCTCTGAACCTG	TAGGCAGAGGTTACAGTGAGCTGAGATCATGCCATTGCACCTCAG	76758	
Qy	4480	CCTGGGCGAC-AC	AGCGAGACTCTATCTCAAAAAATAATAATAATAAAAGGATCGG	4538	
Db	76759				
		CCTGGGCAACAAG	AGTGAACCTCCATCTCAAAAAAGAAAAATAATTAGAGGTGGG	76818	

RESULT 50

US-11-121-086-29
; Sequence 29, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 160226
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-29

Query Match 6.9%; Score 344.8; DB 17; Length 160226;
Best Local Similarity 57.0%; Pred. No. 1.6e+02;
Matches 836; Conservative 1; Mismatches 543; Indels 86; Gaps 8;

Qy	3104	TTTTTTTTTGTGTT	TGTAGAGACAGGGTCTT	GTCTGTGTCACCCAGGCATGAGCACAGT	3163
Db	147280				
		TCTTTTTTTTTT	TTTTTGAGATGGAGTCCCACTCTGTCACCCAGACTGTAGTGCACT	147339	
Qy	3164	GGTGCAACCATAG	GTCAGTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACTCA	3223	
Db	147340				
		GGCGGATCTCAG	CTCACTGCAACCTCTGCCTCCCTGGTTCAAGTGATTCTCCTGCCTCA	147399	
Qy	3224	GCCTCCCAAGTAG	CTGGACTACGAGCGTGCACCACCAACCGCTGGCTAATTAATAAAAT	3283	
Db	147400				
		GCCTCCTGAGTA	GCTGGGATTACAGGTGCGCGTCACCATGTCCGGCTAATTTTTTGA--	T	147457
Qy	3284	TTTTTGTAGAGAC	TGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCCTGGCTTCAA	3343	
Db	147458				
		TTTTAGTAGAGAC	CGGGGTTTCCCGGTGTTGGCCAGCAAGTTTCACACT-CTGACCTCAG	147516	
Qy	3344	GCAATCCTCCTAC	CCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGC	3403	
Db	147517				
		GTGATCCACCTGC	TGCCTTGGCCTCCCAAAGTCTGGGATTACAGGCGTGAGCCACCTCGCCT	147576	

Qy	3404	GGCTACTTATTTCTTTACATTCCATCTTTTCCAAATAGAAATGTAAGATCCACAGAACAGGGA	3463
Db	147577	GGCCCATAAATATTTTTTTTTTTTTTTTGTGACACAGAGTCTCGCTCTGTC-----	147626
Qy	3464	TTACTGCGCTATTTTCTTCCTTTCTTTTGTGACACAGAGTCTACATTACACCTCAACCT	3523
Db	147627	-----ACCCAGGCTGGAGTGCAGCGCGC	147650
Qy	3524	CCGTTACGTCACCTGCAACCTCTGCCCTCCGGGTTCAAGYGAATCTCCTGCCTAAGCCTC	3583
Db	147651	GATCTCGGCTCACTGCAAGCTCCACCTCCTGGGTTCAATGCCATTCTCCTGCCTCAGCCTC	147710
Qy	3584	CTGAGTAGTGGAAATTACAAGCGTGCACCAACCATGCTTGGCTAAATTTTGTATTTTAG	3643
Db	147711	CCAAGTAGTGGGACTACAGGCGCATACTGCCACGCTGGCTAAATTTTGTATTTTAG	147770
Qy	3644	CAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC	3703
Db	147771	TAGAGATGGGTTTCACCTTGTTAGCCAGGATGGTCTCAATCTCTGACCTC--GTGATC	147828
Qy	3704	TGCCTGCCTCAGTCTCCCAAAGTCTGGAATTATAGGCGTAGTCACCTGTGCCTGGCCGA	3763
Db	147829	TGCCCGCCTCGGCCTCCCAAAGTCTGGAATTACAGGTGTAGGCCACCATGCTGGCCTT	147888
Qy	3764	TTACTGTCTATTTTCTTTATTGCTATATATCCCCAGATCTAGAGAGTGTCTGACATATAGT	3823
Db	147889	TTTTTTTTTTTTTAGACCAAGTCTCACTCTATCACTCTGGCTAGAGTGCAGTAGAGCGA	147948
Qy	3824	AGGTGCTCAATAAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTT	3883
Db	147949	TCTCGGCTCACTACAACCTCTGCCTCCAGGTTTCAAGTGAATTTCTCTGCCTCAGCCTCCA	148008
Qy	3884	TTAAACAACATCTTGACAACTTTGCAGAATAAATAACAATCTTGCATTCTGCTTTTTCACTT	3943
Db	148009	GAGTAGCTGGGATTACAGGCGTGTGCCAATGCCTGGCTAAT-----TTTGTATTT	148059
Qy	3944	ATCACCTTGTATGACTTTTTCATATATGTCCTCAAAACCTTTATGTACTGTTTTCATT	4003
Db	148060	TTTTTAGTAGAGATGGGTTTTTCACCATATTTGGCCAGGCTGGTCTGAACTCCTGACCTCA	148119
Qy	4004	GTTACTATTTTAGTCACTGAATAATATATGGCTTAATTTTGCITTATACATCCTCCTGCTCCAC	4063
Db	148120	TGATCCACCCACCTCAGCCTCCCAAAGTCTGGGATTACAGGCTGAGCCACTGCACCTG	148179
Qy	4064	TTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAAATAC	4123
Db	148180	GCCACCTGGCCCATAAATTTTATATGCACTGGG-----AATCCAAAAG	148222
Qy	4124	ACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAAC	4183
Db	148223	ATTCATGTGCATTGCTTTTTTGCAGTATTGCTTTATTGCGGTGGTCTGGAACCAAACCT	148282
Qy	4184	CTGCATTAGAGGATGTTGTTCATATTAATTAAAAATAACTCAAGTTGGGCACAGTGACTC	4243
Db	148283	CGCATATCTCTGAGGTATGTGTGTAATTAGAAAAGGAGGTTGGGCTGGATGCG-----	148336
Qy	4244	AAGCCTGTAACCAACAGTACTTTTGGAACTCCAAGTGGGTGGATCACTTGAGGTGAGAACT	4303
Db	148337	--GTGGCTCACATCTGTAATCCGTACAGCCGAGGCAGGTGGATCACCTGA-GTCAGGGGT	148393
Qy	4304	TCGAGACACGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGC	4363
Db	148394	TTGAGACCAGCTTAGTCAACATGGTGAAACCCCGTCTCTACTAAAAATACAGAAATTAGC	148453
Qy	4364	TGGGTGATGATGCATGCCTGTAGTCCCAGCTACTCGGAGGCTGAGGCCAAGAGAAATG	4423
Db	148454	CAGGCATGATGGTGCACGCCTGTAATCCCAGCTGCTCGGAGGCTGAGGCAGGAAAATGG	148513
Qy	4424	CTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACTGCCACTGCACCTCCAGCCTG	4483
Db	148514	CTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCTGAGATCGTGCCTGCACTGCACCTCCAGCCTG	148573

Qy	4484	GGCGACACAGCGAGACTCTATCTCAAAAAATAAATAAAAAATAAAGGATCGGAGAGA	4543
Db	148574	GGTGACAGAGGAAGACTCCATCCGAAGGAAAAAAGACAAGGAGTTGGGGGTAGT	148633
Qy	4544	AACAAAACTAATAAGATTCTCTGAAGG	4569
Db	148634	CAGACTGCAGTGAGGGTTGAAGAAGG	148659
RESULT 51			
US-09-925-065A-667241/c			
; Sequence 667241, Application US/09925065A			
; Publication No. US20040181048A1			
; GENERAL INFORMATION:			
; APPLICANT: Wang, David G.			
; TITLE OF INVENTION: Identification and Mapping of Single			
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome			
; FILE REFERENCE: 108827.135			
; CURRENT APPLICATION NUMBER: US/09/925,065A			
; CURRENT FILING DATE: 2001-08-08			
; PRIOR APPLICATION NUMBER: US 60/243,096			
; PRIOR FILING DATE: 2000-10-24			
; PRIOR APPLICATION NUMBER: US 60/252,147			
; PRIOR FILING DATE: 2000-11-20			
; PRIOR APPLICATION NUMBER: US 60/250,092			
; PRIOR FILING DATE: 2000-11-30			
; PRIOR APPLICATION NUMBER: US 60/261,766			
; PRIOR FILING DATE: 2001-01-16			
; PRIOR APPLICATION NUMBER: US 60/289,846			
; PRIOR FILING DATE: 2001-05-09			
; NUMBER OF SEQ ID NOS: 957086			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 667241			
; LENGTH: 1561			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-925-065A-667241			
Query Match 6.9%; Score 344.6; DB 7; Length 1561;			
Best Local Similarity 58.6%; Pred. No. 4.9e+03;			
Matches 864; Conservative 2; Mismatches 496; Indels 113; Gaps 11;			
Qy	3105	TTTTTTTGTGTTGTAGAGACAGGGTCTTGCTG-TGTACCCAGGCGATGAGCACAGT	3163
Db	1445	TTTTGTTTTTGTGTTGTAGACGGAGTTTCGCTCTGTTGCCAGGCTGGAGTACAAT	1386
Qy	3164	GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA	3223
Db	1385	GGCGTGATCTCAGCTCAAAACAACCTCTACCTCCAGATTCAAGCGATTCTCCTGCCTCA	1326
Qy	3224	GCCTCCCAAGTAGCTGGACTACGAGCGTGCACCACCGCTGGCTAAATTAATAAATT	3283
Db	1325	GCCTCCAAAGTAGCTGGGATTTCAGTCAATGCAACACCATGCCCGGCTAATTTTGTA--C	1269
Qy	3284	TTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTGTCTTAAACTCCTGGCTTCAA	3343
Db	1268	TTTTTAGTAGGGATGGGTTTCTCCATGTTGGTCAGGCTGGTCTCGAACTCCTGACCTCAA	1209
Qy	3344	GCAATCCTCCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGC	3403
Db	1208	GGGATCTGCCCCCTCGGCCTCCCAAAGTCTGGGATTACAGGCGTGAGCCACCACACCC	1149
Qy	3404	GGCTACTTATTTCTTTACATTCCATCTTTTCCAAATAGAATGTAAGATCCACAGAACAGGGA	3463
Db	1148	AGCCTATATTTTTTTCTTTTTTTAGACACAGTCTGACTCCGTTGCCAG-----	1097
Qy	3464	TTACTGCCTATTTTCTCTTCTTTTGTGAGACAGAGTCTCACTTCATCACTCAACCT	3523
Db	1096	-----GCTGGAGTGCAGTAGCGC	1079
Qy	3524	CCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCTTAAGCCTC	3583
Db	1078	GATCTTGGTTCACTGTAACTTCTGCCTCCACAGGTTCAAGCGATTCTCCTGCCTCAGCCTC	1019

QY	3021	ACTTAACAGATAAAGAAAAC	TGAGGCTCAGAAAGGCTGAGCTATTTGCCAAGATCACACAG	3080
Db	14657	CTTTGAGAAACAGAACCCAT	TGGCCTTCCCAGTCCCTCCCTAGACTTTATGTCGTGGTC	14716
QY	3081	CTTGTAAGTGGTGACAGTT	TGGGTTTTTTTTTTTGTGTGTTGTTA--GAGACAGGGTCTTGCC	3138
Db	14717	CTCTGCGCTTCCATTTCT	CTCTTTTTTTTGGTGGGGAGGACGGGGGACAGAGTCTCGT	14776
QY	3139	TCTGTCACCCAGGCATGAGC	CAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCCT	3198
Db	14777	TCTGTGCCCCAGGCTGGAG	TGCAGTGGCGTGATCTCAGCTCACTGCAGCATCTGCCTCCC	14836
QY	3199	GAGCTCAAGGGATCTGCTG	ACCTCAGCCTCCCAAGTAGTGGGACTACGAGCGTGACCA	3258
Db	14837	AGTTTCAAGTGATGCTCCT	CCCTCAGCCTCCCAATTAGCGAGACTACAGGCGGTGCCA	14896
QY	3259	CCACGCTGGCTAATTAAAA	AAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAG	3318
Db	14897	CCACGCCAGCTTATTTTGT	GA--TTTTTTCTAGAGACAGGTTTTCATCATGTTGGCCAG	14954
QY	3319	GCTTGCTTAAACTCCTGG	CTTCAAGCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGG	3378
Db	14955	GCTGGTCTCGAACTCCCA	ACTTCAAGTGATCTGCCCTGACTCGGCCCTCTCAAAGTGCTGGG	15014
QY	3379	ATTACAGGGGTGAGCCACC	ATGTCGGGCTACTT----ATTCTTTTACATTCCATCTTTTC	3433
Db	15015	ATTACAGCGTGAGCCACC	TTCGCGGCCCTTGCCCGGCCCTTCCATTTCTTTTAT	15074
QY	3434	CAATAGAATGTAAGATCC	ACAGAACAGGGATTACTGCCTATTTTCTTCTCTTTTCTTTTG	3493
Db	15075	CCTCAAAAAACCTCCTTG	CCAAAGCCGGCTGAGCAGGCACCATCTTCTTTTTTTTTTTTG	15134
QY	3494	AGACAGAGTCTCACTTCA	TCACTCAACCT-----CCGTTCAGTCACTG	3538
Db	15135	AGACAAAGTCTTGCTCTT	GTCAACCCAGGCTGGAGTGAGTGGCGCGATCTCAGCTCACTG	15194
QY	3539	CAACCTCTGCCCTCCCGG	GTTCAAAGYGATTCTCCTGCCTAAGCCTCCTGAGTAGCTGGAAT	3598
Db	15195	TAACCTCCACCTCCCAGG	TTCAGGTGATTCTCCTGCCCTCAGCCTCCTGAGTAGCTGGAT	15254
QY	3599	TACAAGCGTGCAACCACCA	TGCTTGGCTAAATTTTTTGTATTTTTTAGCAGAGATGGGGTTTT	3658
Db	15255	TACAGGCACATGCCACCA	CCGCTGGCTAA--TTTTTGTATTTTTTAGTAGACACAGGGTTTC	15313
QY	3659	ACCATGTTGCCCAGGCTG	GCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCT	3718
Db	15314	ACCATGTTTGCAGGCTGG	TCTCAAACTCCTGACCTCAGATGATCCGCCCTGCCTCAGCTT	15373
QY	3719	CCCAAAGTGCTGGAATTA	TAGCGGTGAGTCACTGTGCCCTGGCCGATTACTGTCTATT	3775
Db	15374	CCCAAAGTGTAGGATTAC	AGGCGTGCAGCCACCACCCCCCAGGCCCATCATCCCCCTTTT	15430

QY	942	AAAGGCGCCTGCCACCA	CAGCCCCGGCTAATTTTTTTTGTATTTTTTAATAAAGACGGGGTTTC	1001
Dd	48306	ACAGGCACCTGCCACC	ACGCCCGGCTAATTTTTTTTGTATTTTTTAGTAGAGATGGGGTTTC	48247
QY	1002	ATCGTGTTAGCCAGGAT	GCTCGATCTCATGACCTTGATCCGCTGCCTCGGCCTCC	1061
Dd	48246	ACCATGTTAGCCAGGAT	GCTCGATCTCCTGACCTTGATCTGCCTGCCTGGCCTCC	48187
QY	1062	CAAAGTGCTGGGATTAC	AGGCATGAGCCACCGTGCCCGGCCTTATCACATTTATTA	1117
Dd	48186	CAGAGTGCTGGGATTAT	AGGCATGAGCCACCGCATGGCTGTTTTTTTA	48131

RESULT 54
US-10-330-773-278
; Sequence 278, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro

RESULT 54
US-10-330-773-278
; Sequence 278, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro

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; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 278
; LENGTH: 127722
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(127722)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-278

Query Match          6.9%; Score 344.4; DB 11; Length 127722;
Best Local Similarity 57.4%; Pred. No. 1.9e+02;
Matches 833; Conservative 1; Mismatches 547; Indels 71; Gaps 9;

QY 3107 TTTTTTGTGTTGTATTAGAGACAGGGTCTTGCTCTGTCACCCCAGGCATGAGCACAGTGGT 3166
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5161 TTTTTTTTTTTTTTTTGAAATGGAGTTTCACCTCTTGTGTGCCCAGGCTGCCGTGCAGTGGC 5220
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3167 GCAACCATAGGTCACCTGCAGCCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCC 3226
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5221 ATGATCTCGGCTCACTAAATGTTTCGGCTCCTGGGTTCAAGCGATTTTCCTGCCTCAGCC 5280
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3227 TCCCAAGTAGTGGGACTACGAGCGTGCAACCACCGCTGGCTGCTTAATAAAAAATTTT 3286
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5281 TCCTGAGTAGTAGGATTACAGGGGCTTCCACCACACCTGGCTAAATTTTGTGA--TTT 5338
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3287 TTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCCTGGCTTCAAGCA 3346
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5339 TAGTAGAGACGGGGTTTCAACCAGGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAGGTG 5398
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3347 ATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGC 3406
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5399 ATCCACCTGACTCAGCCTCCCAAAGTGTGGAATTAAGGTGTGAGCCATCACACCCGGA 5458
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3407 TACTTATTTCTTTACATTTCCATCTTTTCCAAATAGAATGTAAGATCCACAGAACAGGGATT 3466
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5459 CCTTTTAATCTTTTTTTTGA----- 5479
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3467 CTGCCTATTTTCTTCTTTCTTTTGTGACAGAGTCTCATTTCATCACCTCAACCTCCG 3526
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5480 ---GACAGAGTCTCGCTCTGTGCGCCCAAGCTGGAGTGCAGTGGCATGATC----- 5526
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3527 TTCAGCTCACTGCAACCTCTGCTCCTCCGGGTTCAAGYGATTTCTCTGCCTAAGCCTCCTG 3586
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5527 -TCGGCTCACTGCAACCTCTGCTCCTCCAGGTTCAGGCGATTTCTCTGCCTCAGCCTCCCA 5585
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3587 AGTAGCTGGAATTACAAGCGTGCACCACCATGCTTGGCTAAATTTTGTATTTTAGCAG 3646
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5586 AGTAGCTGGGACTACAGGCGCCCGCCACACGAGTGGTCTCGATCTCCTGACCTC--GTGATCCAT 5645
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3647 AGATGGGGTTTACCATGTTTGCCCAAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGC 3706
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5646 AGACGGGGTTTACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTC--GTGATCCAT 5703
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3707 CTGCCTCAGTCTCCCAAAGTGTCTGGAATTATAGGCGTGAGTCACTGTGCCCTGGCCGATT 3766
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5704 CTGCCTTGGCCTCCCAAAGTGTTAGGATTACAGGAGTGAGCCACTGGCCCGCCTAATC 5763
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3767 CTGCTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATAT-AGTAG 3825
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5764 ATTTTAAAGTGTATAGTTCAGTGTCTATAAGTACAACCACCACCGCCATCCATCTCCAGAA 5823
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3826 GTGCTCAATAAATAATTGATGAATGCACAGCCCTAGATATAAACTTTCTTTTCTTTT 3885
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5824 CTTTTTCATCTTCCCAAACTGAAACTCTATCCCCGTTAAATACCAAGTCCCCCATTTCCCC 5883
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3886 AAAACAAATCTTGACAACTTTTGAGAAATAAATACAATCTTGTGATTTCTGCTTTTTCACATT 3945
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 5884 TCCCCGAGCCCCCTGGCACCCACCATTCCACTTCTGTCTCTATGAGTCTGACTACTCCAG 5943
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3946 CACCTTGTATGACT-TTTTTCATATTGCCTCAAACCTTTATTGTTACTGTGTTTTTCATTG 4004
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5944 GACCCCTCATATGAGTGAATCCTACAGTATTTATGCAATTTGTGTCTGCTCATTTCAATT 6003
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4005 TTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCTCTCTGCTCCACT 4064
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6004 AGCATAGTAT---CCTCAAGGTTTCATGCATGTTGTTAAACAGGTGTCAAGGACTCCCTCCT 6059
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4065 TTAGAAGGCCAAATTTACAAAATCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAAATACA 4124
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6060 TTTTAAGGCTGGATCATCTTCTATTGTGTGGATAGACTGCATTTTGTCTTATTCATTCATC 6119
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4125 CACACACACACACACTCACACACAGTTTTTTTAAATGTTTGCAACTAAGACAAGAAACC 4184
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6120 AGCTGATAACATCAGGTGCTCCACTTTTGGCTATTGTGAATAATGCTGCTATAAACAT 6179
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4185 TGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATAAATCAGTTGGGCACAGTACTCA 4244
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6180 TGGTGTACAGATATCTACTCCAATCT-----CTGCTTTTGGCCGGGCATGGTGGCTCA 6232
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4245 AGCCTGTAACACACAGTACTTTTGAAGTCCAAGTGGTGGATCACCTTGAGGTGAGAAGTT 4304
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6233 CGCCTGTAATCCCAGCACTTTGGAGGCTGAGGCAGGTGGATCACCTGAGGTCAAGGAGTT 6292
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4305 CGAGACCAGCCTGGTCAATATGGTGAAACCCCTATCTCTACTAAAAATACAAAAATTAGCT 4364
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6293 CAAGACCAGCCTGGCCACCATGGTGAAACCCCGTCTCTACTAAAAATTAATAAATTAGCC 6352
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4365 GGGTGTAGTATGCATGCTGCTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAATTGC 4424
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6353 AGCATGGTGGTGGGCACCTGTAATCCCAGCTATTTTGGAGGCTGACACAGGAGATCAC 6412
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4425 TTGAACCTGGGAGGCACAGGTTGCAGTGAGCCCGAGATCCCACCACCTGCACCTCCAGCCTGG 4484
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6413 TTGAACCCAGGAGGCACAGGTTGCAGTGAGCCCGAGATCACGCCACTGCACCTCTAGCCTGG 6472
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4485 GCGACA-CAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGA 4543
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6473 ACAATAAGAGGGAACTCCATCTCAAAAGCAAAACAAAAGAAAACAACAACAACAAAAAC 6532
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4544 AACAAAACTAAT 4555
      ||||| ||||| |||||
Db 6533 AAACAAAAAAAT 6544
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 55
US-10-995-561-13341
; Sequence 13341, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13341
; LENGTH: 28693
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13341

Query Match          6.9%; Score 344; DB 10; Length 28693;
Best Local Similarity 50.1%; Pred. No. 5.9e+02;
Matches 1599; Conservative 15; Mismatches 1355; Indels 221; Gaps 23;

QY 752 TTCTTCCCCTTTTCTAATGCAGTATCCAGTTTCTTACTATATCATTATTATTATTTCTT 811
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Db 23800 TTTTACTTCTTTGAAC TAGAATTTAACTTCTTCAAGTCTCAGTTTTTKTTTTTTTTTTT 23859

Qy 812 ATTATTATTGAGACAGAGTCTTGCTTTTGTGCGCCAAAGCTGGAGTACAGTGGTGGCATCTC 871

Db 23860 TTTTTTTTGAGACGRAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGGCGGATCTC 23919

Qy 872 GGCTCACTGCAAGCTCCACCTGCTGGGTTTCAAGCCATTTCTCCGCTCAGCCCTCCCCAGT 931

Db 23920 GGCTCACTGCAAGCTCCGCTCCCGGTTTCAAGCCATTTCTCGCTCAGCCCTCCCAAGT 23979

Qy 932 AGCTGGGACTAAAGGCGCTGCCACCAAGCCCGCTAAATTTTTTTTGTATTTTAAATAAAG 991

Db 23980 AGCTGGGACTACAGGCGCGGCCACTACGCGCGGCTAA-TTTTTTGTATTTTAGTAGAG 24038

Qy 992 ACGGGTTTCATCGTTAGCCAGGATGGTCTCGATCTCATGACCTTGTGATCCGCTGC 1051

Db 24039 ACGGGTTTCACCATTTTAGCCGGGATGGTCTCGATCTCGTACCTCGTGATCCGCCAC 24098

Qy 1052 CTCGGCTCCCAAAGTCTGGGATTACAGGCATGAGCACCGTGCCCGCTTATCACAT 1111

Db 24099 CTCGGCTCCCAAAGTCTGGGATTACAGGCGTGAGCCAGCCGCGCGCC----- 24149

Qy 1112 TTATTATTATTGTTTTCTCTCCCACTAGGTTGTAAGCTCCATGAGGTTAGAGATTATT 1171

Db 24150 -TAAGTCTCAGTTTTTTTTTGTTCCTCCAAATGGTATTAAATAAATATACCAAGGTTCTAAG 24208

Qy 1172 ATT 1231

Db 24209 AAAAAAATAACCCA-ATTATAAAGGCATGAAGAGTATTAAATAAAAGTATATATGTAAA 24267

Qy 1232 TCTAGTCTCTAGGACAGAGCTGGCACATAGTAAGTGCTCAATAAATAATTCACTGGATAA 1291

Db 24268 ATAATATGCCAAGCGCAAGCTGGGCACGGTGGCTCATGCTGTAATCCCAGCACTTTGGG 24327

Qy 1292 ACAGTGCAGATAGTTTAAAACTATCTGACCTAGGGAGGCTGAGGCAGGAGAAATGGCGTGA 1351

Db 24328 AGCCGAGGCGGGGATCACAAAGGTCAGGAGATCGAGACCATCTCTGACTAACACAGTGA 24387

Qy 1352 ACCCGGAAGCAGAGTTTGCAGTGAGCTGAAATCGTGTCACTGCACCTCCAACCTGGGCAA 1411

Db 24388 AACCTGTCTC---TACTAAACAATAAACAATAATAGCCGGGCATGGTTGCGGGCGCCT 24444

Qy 1412 CAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAAAAAACTATCAGGCCTAGCTGGTGGCACA 1471

Db 24445 GTAGTCCCAGCTCCTCGGAGGCTGAGGCAGGAGATGGCATGAATCCGGGAGGCAGAGC 24504

Qy 1472 TGCCTGTAATCCTAGCTAGCGGGTAGGGTCCCAGAGAAGAAGAAGAAGAAAAAGAAGA 1531

Db 24505 TTGCAGTGAGCCGAGATCAGCCCACTGCACCTCCAGCCTGGCGACAGAGTGAGA----- 24558

Qy 1532 AGATATATATATATACACACACACAAAAGATATAAACTTTATATATAATAAGTTTTCAT 1591

Db 24559 -----CTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAATGCCAAAYGCAATGACTGGCTC 24612

Qy 1592 TAAAAAAAAAAAAAAAAACCTCTACCCACTTTTCACTTTTACCAGGTTCTCTGGGTCCAACGGTC 1651

Db 24613 ACACCTGTAATCCCAACACTTTGGGAGGCAGAGGCAGGAGGATTGCTTGAGCTCAGGGGT 24672

Qy 1652 TTCAGAGGAGGCAGCTGGCAGGGGTTCAGGGAGGCAGCGTGGGACCCGAGGGGAGCAGGAAG 1711

Db 24673 TTGAGACCAGCCTAGACAACATAGTGAGACCCCTGTCTACAAAAAATAAGAAAAAAT 24732

Qy 1712 GCAGTGTGTCCCGGGGTGCTGGCAGACCGGATTTGAATCTCTGGCTATGTTCTTGTGCAGT 1771

Db 24733 TAGCTG-----GGCATGGTGGTGGGCTGTAGTTTCCAGTTACTCAAGA 24777

Qy 1772 GCGCGCGCGCMCAGCGGCATCAGCCCTCGGGCGGTGTGGCAGTTCCGCAAAATGATCAA 1831

Db 24778 GCGTGAGGTAAGAGGATTGCTTGAGCCCAAGGTTGAGGCTGCAYTGAGCCATGATCGT 24837

Qy 1832 GTGCGTGATCCCGGGAGTGACCCCTTYYTTGGAATACAACTACGGCTGCTACTGTGG 1891

Db 24838 GCCACCACACTGCAGCCTGGCAACAGACCAAGAAAAAAGATAGTGATGTATA 24897

Qy 1892 CTTGGGGGGCTCAGGCACCCCGTGGATGAACACTGGACAAAGTAAGTATCCGCTGCAGGA 1951

Db 24898 GTCAGTAAATACAGCAGTGGCTTCTGATCTCCAGACCTCTCATTTGCATTGATTTCTTTAA 24957

Qy 1952 AAATTGGAGTGCTGCTCCGGGGCGGGTGGGGCACACGCCAAGGATCTCAGAGGCATAC 2011

Db 24958 AATCATCTCTACCTTAATGTTCTGTAG-----ACATTTCAAAATCAACATGTTCAAAAT 25011

Qy 2012 AAAGGGGACTTGCATATCTGCTAAGGATAACATATTTTACCTCTTGTCTAAATAAAACAAA 2071

Db 25012 CAAATTTATTATCTATCTCCCCAAATCTGCTCTCTACTTCTGATGTTTACTGTTCAATT 25071

Qy 2072 TATGTTCCAGAGGACCCCTGTAGCGAACGCAACCCCGTTAGAGATGGAACAATGACCGAC 2131

Db 25072 AATG-----GATAACAGAAATAACCATCAAATCATGTAAGTGGAGAGAACTCAGTGTAA 25125

Qy 2132 GTGCAAAAACAGTGGGCGGATGCTGCCCTCCAGTGGCAGAAATGTAGCAACAGTAAACATCA- 2190

Db 25126 CCTTTATTACTCCCTCTTATTATTATCCCATCTACCAACTACAGTATCTATAAAACACAT 25185

Qy 2191 ---CAGCAACTATCCACGTGTCAATTTTCTAGCAGTGGTTGTCACTGCACTTCTGAAATA 2246

Db 25186 TCACTCCTTTCTACCCCATTTGCTTTTGTCAAGATAYCATAATTCCCTCTCTTTCTTTGTG 25245

Qy 2247 CAGGATTTTACTGTATTCTTTGCAA-----CCATGTTAAAAATCGCTTTCAGGCCAGG 2298

Db 25246 GTAAACATGAAGGTGTACCATCCAGTTCTACCTCCAAAGAAAGACTTCTCTGTGGCYGGG 25305

Qy 2299 CGCGTGGCTCATGCCTGTAATCCCAGCACTTTTGGAGGCCGAGCGGGCGGATCACTTG 2358

Db 25306 CATGATGGTTCACGCTTGTAATCGCAGCACTTTTGGAGGCCGAGGTGGGGGATCACCTG 25365

Qy 2359 AGTCAGGAGTTCGAGACCAGCCTGGCCAAACATGGTGAAACCCCTGTCTCTACTAAAAAAT 2418

Db 25366 AGTCAGGAGTTGGAGACCAGCCTGGCCAACTGGCGAAACCCCTGTCTCTACT-AAAAAT 25424

Qy 2419 AAAAAAATTAGCCGACATGGTGGCGAGCGGCTGTAAACCCACGTA----- 2464

Db 25425 AAAAAAATTAGCGGGCGGGTGATGCACGCTTGTAAATCCCAGCTACTAGCAGGGGCTGA 25484

Qy 2465 -----CTTGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCAAAGTGGTGTCACT 2511

Db 25485 GGCAGGAGAAATCTCTTGAACCCCAAGAGGCAGAGGTGCAATGAGCTGAGATCTCGCCACT 25544

Qy 2512 GCTGTCCAGCCTGGGTAAC-AGAGCAACTCTGTCTCAAAAAAAAAAATGCTTTCAATAA 2570

Db 25545 GCACTCCAGCCTGGGCAACAAGAGCAAAATTCATCTCAAAATAAATAAATAAYATAA 25604

Qy 2571 ATATATGATAAAG-----GACTTATATTTTTTCAAGCCATAGGATCATTTCTCC 2620

Db 25605 ATAAGAAAAAAGACTTTGCCGTTACGCTATAGGGGGAATAGCCAGCAGATAGCTTCCGC 25664

Qy 2621 TGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCTCTGAGAGTGGGCGAGGTAGGGCTGAC 2680

Db 25665 TTGCTTCAGTTCTTTCAATGTCTGCCCTCAGCTGTAGAGGACAGTCTTGCAAGATCATG 25724

Qy 2681 CTATTGCTCTGCACCTTACTCTATCTCAGTGTCTCTCCACTTTCCAGGTGCTGCCAGA 2740

Db 25725 CCCATCCCAGGCTGCCCTCACTCGTGCTTAAGCAAGCAGGGGTATFAAAAGTTCGGTY 25784

Qy 2741 CACATGACAACTGCTAYGACCAGGCCAAGAGCTGGACAGCTGTAAATTTCTGCTGGACA 2800

Db 25785 ATTTTGGCCAACTGCAGGACAACTCTGAGAATARGTTGGATTGACAAGGCTAGCCAGGG 25844

Qy 2801 MMCCGTACACCCACACCTATTTCATACT-----CGTGCTCTGGCTCGGCAATCACC 2850

Db 25845 CTGGAAATATTCACTCCAGAGCTCCCTGCCAGGGAGGCTGGGTCTTTGTCTGAGATCTGCAT 25904

Qy 2851 TGAGCAGTAGGTTTATCCCTTCCCTTGACCTATGAATTTCTAGTTGGTTCTCAGTAGGCCG 2910

Db 25905 TGCCGTTTGACTTCTCTCTTAKCTCAKCCCTACTTCTTCCCCCTGGTAAGCATCTTTGCAC 25964

QY	2911	GGGGAATAATAGTAACAACAGCCATGATTAGTGTAAATTTCTTGTTCTGGSCAGT	2970
Db	25965	CTCAAACTCTGTCTCAGCCTCTGTCTCCAGATAAACCCAACTGTGTGTGTGTCTCTCT	26024
QY	2971	GTCTCCTTTAATCCTCAGAACAACACTATGGGATAGGTAC-----	3010
Db	26025	CTCTTTCAAAAATTGAGAAATTTTCTCAATCYTGTCTGGACCATGGCAGCCTCCTCCT	26084
QY	3011	-----AATTATCCTCACCTTAACAGATAAGAAAACTGAGGCTCAGAAGGCT	3055
Db	26085	AAGAAATTGCCTCTAAATTTCTCCATATTTAATTCACTCTTACATGGCAGTAAGAAACA	26144
QY	3056	GAGCTATTGCCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTGT	3115
Db	26145	CAGATCTAATTGTGTCAATTATTCGGTTTTTTTGTGTGTTTTTTTGTGTGTGT	26204
QY	3116	G-----TTGTTTAGACACAGGGTCTTGCTCTGTCAACCAGGCATGAGCACAGTGGTGC	3168
Db	26205	GTTTTGTTTTTGTGTTGAGACAGAGTCTCTCTGTCAACCAGGCTGGAGTGCAGTAGTGT	26264
QY	3169	AACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGCCTC	3228
Db	26265	GAACTTAGCTCACTGCAACCTCTGCTCACAGGTTCAAGCAATCTCCTGCCCTCAACCTC	26324
QY	3229	CCAAGTAGCTGGGACTACGAGCGTGACACCACCGCTGGCTAAATTAATAAAATTTTTTT	3288
Db	26325	CCGAGTAGCTGGGATTACAGGCATGTGCCACCAACCGCCGGCTAAATTTTTTGTA-TTTT	26383
QY	3289	GTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCAAGCAAT	3348
Db	26384	GTAGAGTCGGGTTTACCATGTTGGTCAGGCTGGTCTTGAGCTCCTGACCTCAAGTGAT	26443
QY	3349	CCTCCTACCTTGGCATCCC AAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCGG---	3405
Db	26444	CTACCCGCTTGGCCTCACAAAGTGTGGGATTACAGGGGTGAGCCACCACCGCTGGACT	26503
QY	3406	-----CTACTATTCTTTACATTCCATCTTTCCAAATAGAAATGTAAGATCCACAG	3455
Db	26504	GTTTTTTAAATTTCTCATTGAGTTAAATTCAGAAATCCTCAAAATGACATTC AAGGCTTG	26563
QY	3456	AACAGGG-----ATTACTGCCATATTTCCTTCTTCTCTCT	3483
Db	26564	CACAAATGGGCCCCAACCTAATTTCTAAATTTAAATTTTWWTTTATTTTATTWATTTTA	26623
QY	3484	TTCCTTTTTGAGACAGAGTCTCACTTCATCACTCAACCTCCGT-----TC	3529
Db	26624	TTTTATTTTGAGATGGAGTCTCACTCTGTCAACCCAGGCTGSAGTAAAGTGGTGCATCTC	26683
QY	3530	AGCTCACTGCAACCTCTGCTCCCGGTTCAAGYGATTCTCCTGCCTAAGCCTCCTGAGT	3589
Db	26684	TGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCTATTCTCTACCTCAGCCTCCCRAGT	26743
QY	3590	AGCTGGAATTACAAGCGTGCACCAACCATTGCTTGGCTAATTTTTTGTATTTTTTAGCAGAG	3649
Db	26744	AGCTGGGATTGAGGCATGTGCCACCAACGCCCCGGCTAA-TTTTGTATTTTTTAGTAGTA	26802
QY	3650	TGGGGTTTACCATTGTTGCCAGGCTGGTCTCAAACCTCCTGACCTCAAGTGATCTGCCTG	3709
Db	26803	CGGGGTTTCACCATGTTGGTCAGGCTGGTCTTGAACCTCCTGACCTCA--TGATCTGCTCT	26860
QY	3710	CCTCAGTCTCCCAAAGTCTGGAAATTATAGGCGTGAGTCACTGTGCCTGGCCGATTA	3769
Db	26861	CCTTGGCCTCCCAAAGTCTGGGATTGCCGGCGTGAGCCACTGTGCCCCGCCCTCAAAAT	26920
QY	3770	TCTATTTTCT	3779
Db	26921	TTTATTTTCT	26930

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; Publication No. US20040181048A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Wang, David G.
;
; TITLE OF INVENTION: Identification and Mapping of Single
;
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;
; FILE REFERENCE: 108827.135
;
; CURRENT APPLICATION NUMBER: US/09/925,065A
;
; CURRENT FILING DATE: 2001-08-08
;
; PRIOR APPLICATION NUMBER: US 60/243,096
;
; PRIOR FILING DATE: 2000-10-24
;
; PRIOR APPLICATION NUMBER: US 60/252,147
;
; PRIOR FILING DATE: 2000-11-20
;
; PRIOR APPLICATION NUMBER: US 60/250,092
;
; PRIOR FILING DATE: 2000-11-30
;
; PRIOR APPLICATION NUMBER: US 60/261,766
;
; PRIOR FILING DATE: 2001-01-16
;
; PRIOR APPLICATION NUMBER: US 60/289,846
;
; PRIOR FILING DATE: 2001-05-09
;
; NUMBER OF SEQ ID NOS: 957086
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 667240
;
; LENGTH: 1561
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; US-09-925-065A-667240

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Query Match 6.9%; Score 343; DB 7; Length 1561;
Best Local Similarity 58.5%; Pred. No. 5e+03;
Matches 863; Conservative 2; Mismatches 497; Indels 113; Gaps 11;

Qy	3105	TTTTTTTGTGTTGTTTATAGACACAGGGTCTTTGCTC-TGTACCCACAGGCATGAGCACAGT	3161
Db	1445	TTTTGTTTGTGTTGTTGAGACGGAGTTTCGCTCTTGTGTGCCAGGCTGGAGTACAAT	1386
Qy	3164	GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA	3223
Db	1385	GGCGTGATCTCAGCTCAAAACAACCTCTACCTCCAGATTCAAGCGATTCTCTGCTCA	1326
Qy	3224	GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACACGCTTGGCTAAATTAATAAAAT	3283
Db	1325	GCCTCCAAAGTAGCTGGGATTTCACTCATGCAACACCATGCCCCGGCTAAATTTGTA---C	1269
Qy	3284	TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCTGGCTTCAA	3343
Db	1268	TTTTTAGTAGGGATGGGGTTTCTCCATGTTGGTCAGGCTGGTCTCGAACTCCTGACCTCAA	1209
Qy	3344	GCAATCCTCCTACCTTGGCATCCCAAAGTGCTGGGATTACAGGGGTGAGSCACCATGTGC	3403
Db	1208	GGGATCTGCCCGCCTCGGCCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCAACCC	1149
Qy	3404	GGCTACTTATTTTCTTTTACATTCCATCTTTTCCAATAGAATGTAAGATCCACAGAACAGGA	3463
Db	1148	AGCCTATATTTTTTTCTTTTTTTTATAGACACAGTCTGACTCCGTTGCCAG-----	1097
Qy	3464	TTACTGCCTATTTTCTTCTCTTTCTTTTGTGAGACAGAGTCTCACTTCATCATCCTCAACCT	3523
Db	1096	-----GCTGGAGTGCAGTAGCGC	1079
Qy	3524	CCGTTACGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCCTGCCCTAAGCCTC	3583
Db	1078	GATCTGGTTCACTGTAACTTCTGCCTCCAGGTTTCAAGCGATTCTCCTGCCTCAGCCTC	1019
Qy	3584	CTAGTAGCTGGAATTACAAGCGTGACCAACCATGCTTGGCTAATTTTTTGTATTTTTTAG	3643
Db	1018	CCAAGTAGCTGGGATTACAGGCATGCACCAACCAACATCCGACTAA-TTTTTGTATTTTTTAG	960
Qy	3644	CAGAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC	3703
Db	959	TAGAGATGGGGTTTCAACCATGTTGGCCAGGCTGGTCTCAAACTCCTCAACCTCAAGTAATC	900
Qy	3704	TGCCTGCCTCAGTCTCCCAAAGTGTGGAATTA-TAGGCGTGAGTCACTGTGCCTGGCC-	3761
Db	899	CGYCGCCTCGGCCTCCCAAAGTGTGGGATTACAAGGCGTGACCCACCGGGCCTGGCCC	840

QY	3762	-----GATTACTGTCTATTTTCTTTTATTGCTATATCCCCAGATCTAGAGCAGTGTCT	3811
Db	839	TGTTGTTGTTTTATGTATGTTTCTATATGTTTATAATTTCAAAATAAACTAAATATAA	780
QY	3814	GACATATAGTAGGTGCTCAAATAAAAATAATTGATGAATGCACAGCCCTAGATATAAACCTTCT	3873
Db	779	AACAAGAATAAAGTATGCTATGCACAAAGGTATTTAAAAATTCACCCTCACAAATAAAT	720
QY	3874	TTTTCTTTTTTAACAACATCTTGACAACCTTTGCAGAATAAAATACAATCTTGCAATCTGC	3933
Db	719	TTTTTTTTTTGAGACAGGATCTCACTCTGTTACCCAGCGTGGAGTGCAGTGGCACCACT	660
QY	3934	TTTTTCACTTATCAC----CTTGTATGACTTTTTTTCATATTCCTCAAACCTTTATTTGTT	3989
Db	659	TGGTTCACTGCAGCCCTGACCTCCCAGGCCCAAGCGATCCTTCTACCTCAGCCCTCCTGAG	600
QY	3990	ACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTTGCATTATACA	4049
Db	599	TAGCTGGGACTACAGGCACACTCCACACACCCACCTAAATTTTGTATTTTGGTAAAGA	540
QY	4050	TCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCT	4109
Db	539	TGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAA--CTTCTGGGATCAAGGAATCCTCC	482
QY	4110	CCCCAGAGAAATACACA-----CACCACAC	4133
Db	481	AACCTTGGCTTTCCAAGTCTGGTATTACAGGCGTGAGCCACTGTACCCGGCCCAAGAT	422
QY	4134	ACACACTCACACACAGTTTTTTTTTAATGTTTGCACCTAAGACAAGAACCTGCATTAGA	4193
Db	421	AGTTTCTTCTCCTTACCCTAGGTAGAGACCTCTGCAGAAATGCTGGGAGATCTTTGGAGAG	362
QY	4194	GGATGTTTGTTCATATTAATTAATAAATAAATACTCAGTTGGGCACAGTCACTCAAGCCCTGTAA	4253
Db	361	GGGAGATTTTTTAATAAATAAATAATTTAATACTTGGAGGGGCGTGGTGGCTTACCCCTGTAA	302
QY	4254	CCACAGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAAG	4313
Db	301	TCCAGCACCTTTGGGAGGCCAAGCGGCAGACAGATCA--GGAAGTCAGGAGATTGAGACCAC	244
QY	4314	CCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAATAC---AAAAATTAGCTGGGTG	4369
Db	243	CCTGGCTAACACCGTGAACACCCCATCTCTACTAAAAAAAATACAAAAAATTAGCTGGSCA	184
QY	4370	TAGTGATGCATGCCCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTCCTTGAA	4429
Db	183	TCGTGGCGGGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGTCAGGAGACTGGCGTGAA	124
QY	4430	CCTGGGAGGCAGAGGTTGCAGTGAGCCGAGATCCCACCACCTGCACCTCCAGCCTGGGCGAC	4489
Db	123	CCTGGGAGGGGAGCTTGCAGTGAGCCGACATCGGGGCCACTGCACCTCCAGCCTGGGCGAC	64
QY	4490	ACAGCGAGACTCTATCTCAAAAAATAAAATAAATA	4524
Db	63	ACAGCAAGACTTCGTCTCAAAAAAAAAAAAAAAAAAAAA	29

RESULT 57

US-09-925-065A-667242/c
; Sequence 667242, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20

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; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 667242
; LENGTH: 1561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-667242

Query Match          6.9%;   Score 343;   DB 7;   Length 1561;
Best Local Similarity 58.5%;   Pred. No. 5e+03;
Matches 863;   Conservative 2;   Mismatches 497;   Indels 113;   Gaps 11;

QY 3105 TTTT TTTT TTTG TTTG TTTAGAGACAGGGTCTTGCTC-TGTCACCCAGGCATGAGCACAGT 3163
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1445 TTTT GTTT TTTG TTTG TTTGAGACGGAGTTTCGCTCTTGTGCCCCAGGCTGGAGTACAAT 1386

QY 3164 GGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGACCTCA 3223
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1385 GCGTGATCTCAGCTCAAAACAACCTCTACCTCCAGATTCAAGCGATTCTCTGCTCTCA 1326

QY 3224 GCCTCCAAAGTAGCTGGGACTACGAGCGTGCACCAACCCAGCCTGGCTTAATAAAAAAATT 3283
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1325 GCCTCAAAGTAGSTGGATTTCAGTCATGCAACACCATGCCCGGCTAATTGTGTA--C 1269

QY 3284 TTTT TGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAACTCCTGGCTTCAA 3343
      |||| |||| || |||| || |||| || |||| || |||| || |||| || |||| || ||||
Db 1268 TTTTAGTAGGATGGGTTTCTCCATGTTGGTCAGGCTGGTCTCGAACTCTGACCTCAA 1209

QY 3344 GCAATCCTCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGTGAGCCACCATGTGC 3403
      |||| |||| || |||| || |||| || |||| || |||| || |||| || |||| || ||||
Db 1208 GGGATCGCCCGCCTCGGCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCACCAACCC 1149

QY 3404 GGCTACTTATTTCTTTACATTCATCTTTTCCAAATAGAAATGTAAGATCCACAGAACAGGA 3463
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1148 AGCCTATATTTTCTTTCTTTTATTTTAGACACAGTCTGACTCCGTTGCCAG----- 1097

QY 3464 TTACTGCGCTATTTCTTCCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCT 3523
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1096 -----GCTGGAGTGCAGTAGCGC 1079

QY 3524 CCGTTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGYGATTCTCTCGCTCAAGCCTC 3583
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1078 GATCTTGGTTCACTGTAACTTCTGCCTCCAGGTTTCAAGCGATTCTCTGCCTCAGCCTC 1019

QY 3584 CTGAGTAGCTGGAAATTACAAGCGTGCAACCAACCATGCTTGGCTAATTTTGTATTTTGTAG 3643
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1018 CCAAGTAGCTGGGATTACAGGCATGCACCACCAACATCCGACTAA-TTTTGTATTTTGTAG 960

QY 3644 CAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC 3703
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 959 TAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTCACCTCAAGTAATC 900

QY 3704 TGCTGCGCTCAGTCTCCCAAAGTGTGGAATTA-TAGGCGTGAGTCACTGTGCCTGGCC- 3761
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 899 CGCCCGCTCGGCCTCCCAAAGTGTGGGATTACAAGGCGTGACCCACCGGCGCTGGCCC 840

QY 3762 -----GATTACTGTCTATTTTCTTATTGCTATATCCCCAGATCTAGAGCAGTGTCT 3813
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 839 TGTGTGTTGTTTATGTATGTTTCTATATGTGTTATATTTCACAAATAAACTAAATATAA 780

QY 3814 GACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCT 3873
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Db 779 AACAAAGAATAAAGTATGCTATGCAAAAGGTATTTAAATTTTCAACCTCACAAATAATT 720

QY 3874 TTTTCTTTTAAAAACAATCTTGACAACTTTGCAGAATAAAATACAACTTGCAATTCTGC 3933
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 719 TTTT TTTT TTTT TGAGACAGGATCTCACTCTGTTACCCAGGCTGGAGTGCAGTGGCACCACT 660

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QY 4176 CAAGAAACCTGCATTAGAGGATGTTGTTTCATATT----- 4210
Db 25892 GCAGAAACCTACTTTAAATTTTTCAAATAATTGTCATTATACCCTAATTCATCACC 25951
QY 4211 -----AATTAAAAATAACTCAGTTGGGCACAGTCAAGCCTGTAACACAGT 4260
Db 25952 AATCATTTAAAAAACTATCTTTCTTGGCCAGGCGGTGGCTCAGCCTATAATCCAGC 26011
QY 4261 ACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAAGTTCGAGACCAGCCTGGTC 4320
Db 26012 ACTTTGGGAGGCAGAGGCGGTGGATCAC--GAGGTCAGGAGTTCGAAGACCAGCCTGGCC 26069
QY 4321 AATATGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCAT 4380
Db 26070 AAGATGGTGAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCACAGTGGCAGAT 26129
QY 4381 GCCTGTAGTCCAGCTACTCGGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGG-- 4438
Db 26130 GCCTGTAAATCCAGCTACTTTGGGAGGCTGAGGCAGGAGAAATTGCTTGAACCTGCGSGGG 26189
QY 4439 --CAGAGGTTGCAGTGAGCCGAGATCCCACCACCTGCACCTCCAGCCTGGGCGACACAGCGA 4496
Db 26190 TACGGAGGTTGCAGTGAGCCCAAGATCATGCCACTGCACCTCCAGCTTGGGCAACAGAGTGA 26249
QY 4497 GACTCTATCTCAAAAAATAATAAA 4522
Db 26250 GACTGCCTCAAAAAATAAAAAA 26275

RESULT 59
US-11-121-086-27
; Sequence 27, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 153142
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-27
Query Match 6.8%; Score 341.2; DB 17; Length 153142;
Best Local Similarity 58.1%; Pred. No. 1.8e+02;
Matches 850; Conservative 1; Mismatches 529; Indels 82; Gaps 11;
QY 3098 TTTGGGTTTTTTTTTGTGTTGTTTAGAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAG 3157
Db 101687 TTTTGTGTTTTTTTTTTTTTTTTTTTGTGACGGAGTCTCGCTTGTGCGCCAGGCTGGAG 101746
QY 3158 CACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGGATCTGCTG 3217
Db 101747 TGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCCCTCCCGGGTTCACGCCATTCTCCT 101806
QY 3218 ACCTAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACCCAGCCTGGCTAATAAA 3277
Db 101807 GCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGCCCGCCACTATGACCGGCTAATTTT 101866
QY 3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTGTCTTAAACTCCTGG 3337
Db 101867 TTGTATTTTAGTAGAGACGGGTTTCACCGTTTTAGCCGGGATGGTCTCGATCTCCTGA 101926
QY 3338 CTTCAAGCAATCCTCCTACCTTGSCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACC 3397

Db 101927 CCTC--GTGATCCGCCCGCCTCGGCCTCCCAAAGTGTGGATTACAGGGGTGAGCCACC 101984
QY 3398 ATGTGCGGCTACTTATTTCTTTACATTCCATCTTTTCCAATAGAATGTAAAGATCCACAGAA 3457
Db 101985 GCGCCCGGCTGTTTTTTTTT----- 102006
QY 3458 CAGGGATTACTGCTATTTTCTTCTCTTTTGTGAGACAGAGTCTCAGTTCATCACCT 3517
Db 102007 -----TTTTTTTGAGACTGAGTCTCGCACTGTGCCCCAGGCTGGAGTGCAG 102052
QY 3518 CAACCTCCGTTCAAGTCACTGCAACCTCTGCCTCCCGGTTTCAAGYGATTCTCCTGCCTA 3577
Db 102053 TGGCGGATCTCGGCTCACTGCAACCTCCACCTCCAGGTTCAAGCAATTCTCCTGCCTC 102112
QY 3578 AGCTCCTGAGTAGCTGGAATTACAAGCGTGCACCACCACCATGCTTGGCTAA----- 3627
Db 102113 AGCTCCTGAGTAGTGAGATTACAGGTGCCCAACACCATGCCAGTAACTTTTTTTT 102172
QY 3628 -TTTTTTGTATTTTAGCAGAGA-TGGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAAC 3685
Db 102173 TTTTGTGATTTTAGTAGAGACGGGGGTTTCACCATGTTGGTCAGGCTGGTCTCGAAC 102232
QY 3686 TCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGTGGAATTATAGGCGTGA 3745
Db 102233 TCCTGACCTC--GTGATCCGCCCGCCTTGGCCTCCCAAAGTGATGGATTACAGGCGTGA 102290
QY 3746 GTCAGTGTGCCTGGCCGATTACTGTCTATTTTCTTTATTGCTATATCCCCAGATCTAGAG 3805
Db 102291 GCCACCGTGCCCCAGC---TTTTTTTTTTTTTTTTTAAAGAGACGGGGTCTTACTATGTTG 102346
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Db 102347 CCCAGGCTGGACTCTCAAACTCCTGGGCTCAAGGAATCCTTCTACCACAGCTTCTGAGT 102406
QY 3866 AACTTTCTTTTTTTTTTAAACAATCTTGACAACATTTGCAGAATAAATAACAATCTTG 3925
Db 102407 AGCTGGGGCTACAAGCCCTGCCACAGTACCTGGCTGTTT-TTGTTTTTTTTATAATTGTG 102465
QY 3926 CATTCGTCTTTTCACTTATCACCTTGTGTTATGACTTTTTTCATATTGCCCTCAAACCTTTAT 3985
Db 102466 GTAAAAATATAAACACATGGCCGGGTGTGTGGTCAAGGCTGTAATCTCAACACTCT-- 102523
QY 3986 TGTACTGTTTTTTCATTTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTA 4045
Db 102524 --GGGAGGTTGAGGTGGGAGGATTACTTGAACCCAGGAGTTCAAGACCAGTCTGGGCAAC 102581
QY 4046 TACATCCTCCTGCTCCACTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACC 4105
Db 102582 TTGGCAAACTGTGTTTCTACAAAAATAAAAAATATTAGCTGGGCGCCAGGCGCAGTGG 102641
QY 4106 CTCTCCCCAGAGAAATACACACACACACACTCAACACAGTTTTTTTTTAAATGTTT 4165
Db 102642 CTCATGCCTGCAATCCCAGCACCTTTGGGAGGCTGAGGTGGATCACCTGAGAGGTCA 102701
QY 4166 GCAACT--AAGACAAGAAAACTGCAATTAGAGGATGTTTGTTCATATTAAATTAATAATAA 4222
Db 102702 GGAGTTTGAGACCACCTGGCCAAACATGGTGAAAAACCTGTCTCTTTAAAAAATACAAAAAA 102761
QY 4223 CTCAGTTGGGCACAGTCACTCAAGCCTGTAACCAAGTACTTTTGGAAAGTCCAAGGTGGGT 4282
Db 102762 ATGAGCCAGCCATGTTGGCTCAGCCTGTAATCCAGCACTTTTGAGAGGCCAAGGCAGGT 102821
QY 4283 GGATCACTTGAGGTGAGAAAGTTCGAGACCAGCCTGGTCAATATGGTGAACCCCTATCTCT 4342
Db 102822 GGATCACCTGAGGTGAGGATTCAGACCACCACTGGCCAACATTTGTGAACCCCGTCTCT 102881
QY 4343 ACTAAAAATAC-AAAAATTAGCTGGGTGTAGTGATGCATGCCTGTAGTCCCAGCTACTCG 4401
Db 102882 ACTAAAAATACAAAAAATTAGCTGGGCATGGTGGCAGGCGCTTATAATTCCAGCTACTAA 102941
QY 4402 GGAGGCTGAGGCAAGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCAGTGAGCCGAGAT 4461
Db 102942 GGAGGCTGAGGCCGAGAAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGTCAAGAT 103001

